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(54) Title: MANIPULATION OF ORGANIC ACID BIOSYNTHESIS AND SECRETION

(57) Abstract: The present invention relates to nucleic acid fragments encoding amino acid sequences for organic acid biosynthetic enzymes in plants, and the use thereof for the modification of, for example, organic acid biosynthesis and secretion in plants. In particularly preferred embodiments, the invention relates to the combinatorial expression of citrate synthase (CS) and/or malate dehydrogenase (MDH) and/or phosphoenolpyruvate carboxylase (PEPC) in plants to modify, for example, organic acid synthesis and secretion.

MANIPULATION OF ORGANIC ACID BIOSYNTHESIS AND SECRETION

The present invention relates to nucleic acid fragments encoding amino acid sequences for organic acid biosynthetic enzyme polypeptides in plants, and the use thereof for the modification of organic acid biosynthesis and secretion in plants. In particularly preferred embodiments, the invention relates to the combinatorial expression of malate dehydrogenase (MDH) and/or phosphoenolpyruvate carboxylase (PEPC) and/or citrate synthase (CS) in plants to modify organic acid biosynthesis and secretion.

Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

Organic acids, such as citrate and malate, are key metabolites in plants. They are involved in numerous processes, including C4 and Crassulacean acid metabolism (CAM) photosynthesis, stomatal and pulvinual movement, nutrient uptake, respiration, nitrogen assimilation, fatty acid oxidation, and providing energy to bacteroids in root nodules. For example, malate plays a key role in root nodule metabolism and nitrogen fixation, serving as the primary carbon source for bacteroid maintenance and nitrogenase activity, and is also tightly linked to nodule nitrogen assimilation. Furthermore, the complexing role of organic acids produced and excreted from plant roots has also been associated with tolerance to the aluminium cation Al^{3+} which is toxic to many plants at micromolar concentrations. Aluminium toxicity has been recognized as a major limiting factor of plant productivity on acidic soils, which account for approximately 40% of the earth's arable land.

The tricarboxylic acid cycle (TCA), also known as Krebs cycle (after its discoverer Hans Krebs) or citric acid cycle, moves electrons from organic acids to the oxidized redox cofactors NAD^+ and FAD, forming NADH, $FADH_2$, and carbon dioxide (CO_2). The reaction sequence of the TCA cycle involves: in a reaction catalysed by citrate synthase (CS), acetyl-CoA formed by the pyruvate dehydrogenase complex combines with oxaloacetate to produce the C_6 tricarboxylic acid, citrate. In the overall cycle, the citrate is oxidized to produce two molecules of CO_2 in a series of reactions that leads to the formation of one oxaloacetate, three NADH, one $FADH_2$, and one ATP. The resulting oxaloacetate

reacts with another molecule of acetyl-CoA to continue the cycle. The oxidative decarboxylation of pyruvate yields an additional CO_2 and NADH. Thus the TCA cycle brings about the complete oxidation of pyruvate to three CO_2 plus 10 electrons, which are stored temporarily as 4 NADH and 1 $FADH_2$.

Cytosolic reactions generate products that are transported into the mitochondria to feed the TCA cycle. The nature of the end product of the glycolytic reactions in the cytosol of plants is determined by the relative activities of the three enzymes that can utilize phosphoenol-pyruvate (PEP) as substrate. Both pyruvate kinase and PEP-phosphatase form pyruvate; while PEP-carboxylase (PEPC) generates oxaloacetate. Pyruvate is transported directly into the mitochondrion. Oxaloacetate is either transported directly into the mitochondrion or first reduced to malate by cytosolic malate dehydrogenase (MDH).

Before entering the TCA cycle proper, pyruvate is oxidised and decarboxylated by the pyruvate dehydrogenase enzyme complex to form CO_2, acetyl-CoA, and NADH. The pyruvate dehydrogenase enzyme complex, which requires the bound cofactors thiamine pyrophosphate, lipoic acid, and FAD as well as free coenzyme A (CoASH) and NAD^+, links the TCA cycle to glycolysis.

It is known that the TCA cycle includes the following enzymes: pyruvate dehydrogenase, citrate synthase, citrate hydrolase, isocitrate dehydrogenase, oxoglutarate dehydrogenase, succinyl-CoA synthetase, succinate dehydrogenase, fumarase, malate dehydrogenase, NAD-malic enzyme and phosphoenolpyruvate carboxylase.

In particular, citrate synthase (CS) catalyses the condensation of acetyl-CoA and oxaloacetate to form the C6 molecule citrate and free CoASH, as the TCA cycle proper begins.

Malate dehydrogenase (MDH) catalyses the final step of the TCA cycle, oxidizing malate to oxaloacetate and producing NADH. This reaction catalysed by MDH is reversible, thus allowing also for the reversible reduction of oxaloacetate to malate. The enzyme MDH is important in several metabolic pathways, and higher plants contain multiple forms that differ in co-enzyme specificity and subcellular localization. Chloroplasts contain an $NADP^+$-dependent MDH that plays a critical role in balancing reducing equivalents between the cytosol and

stroma. Plants also contain NAD-dependent MDHs which are found in a) mitochondria as part of the TCA cycle; b) cytosol and peroxisomes involved in malate-aspartate shuttles; and c) glyoxisomes functioning in β-oxidation. In root nodules of nitrogen-fixing legumes, such as white clover (*Trifolium repens*) and alfalfa (*Medicago sativa*), malate serves as the primary carbon source to support the respiratory needs of the bacterial microsymbiont and the fixation of N_2 by nitrogenase, and a nodule-enhanced MDH is thus critical for nodule function.

Phosphoenolpyruvate carboxylase (PEPC) catalyses the reaction of phosphoenol-pyruvate with HCO_3^- releasing the phosphate and producing the C4 product, oxaloacetate. Oxaloacetate is commonly reduced to malate by NADH through the action of malate dehydrogenase (MDH). PEPC is a homotetrameric enzyme widely distributed in most plant tissues. In plants, PEPC fulfils various physiological roles such as the photosynthetic CO_2 fixation in C_4 and Crassulacean Acid Metabolism (CAM) plants, and the anaplerotic pathway.

While nucleic acid sequences encoding some organic acid biosynthetic enzymes have been isolated for certain species of plants, there remains a need for materials useful in modifying organic acid biosynthesis; in modifying organic acid secretion; in modifying phosphorus acquisition efficiency in plants; in modifying aluminium and acid soil tolerance in plants; in modifying nitrogen fixation and nodule function, particularly in forage legumes and grasses, including alfalfa, medics, clovers, ryegrasses and fescues, and for methods for their use.

This invention is directed towards overcoming, or at least alleviating, one or more of the difficulties or deficiencies associated with the prior art.

In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the organic acid biosynthetic polypeptides CS, MDH and PEPC, from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or functionally active fragments or variants of these polypeptides.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of polypeptides which are related to CS, MDH and PEPC (from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species) of CS, MDH

and PEPC, or functionally active fragments or variants of CS, MDH and PEPC. Such polypeptides are referred to herein as CS-like, MDH-like and PEPC-like respectively and include polypeptides having similar functional activity.

The present invention also relates to individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants to enhance or otherwise alter organic acid biosynthesis; to enhance or reduce or otherwise alter organic acid secretion; to enhance or reduce or otherwise alter phosphorous acquisition efficiency in plants; to enhance or reduce or otherwise alter aluminium and acid soil tolerance in plants; and/or to enhance or reduce or otherwise alter nitrogen fixation and nodule function in legumes.

The individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants has significant consequences for a range of applications in, for example, plant production, plant performance, plant nutrition and plant tolerance. For example, it has applications in increasing plant tolerance to aluminium-toxic acid soils; in improving plant nutrient acquisition efficiency for example in increasing acquisition of phosphorus from soils; in increasing nodule function in nitrogen-fixing legumes for example leading to enhanced nitrogen fixation; in modifying the accumulation of organic acids such as citrate in fruits; in modifying the secretion of organic acids for example citrate and/or malate from plant roots.

Manipulation of CS, MDH and/or PEPC or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species) may be used to facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to aluminium toxic soils; enhanced nutrient acquisition efficiency; forage legumes with enhanced nitrogen fixation; fruits with enhanced organic acid content leading to enhanced flavour and health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium*

multiflorum), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). White clover (*Trifolium repens* L.) and perennial ryegrass (*Lolium perenne* L.) are key pasture legumes and grasses, respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof. The RNA is readily obtainable, for example, by transcription of a DNA sequence according to the present invention, to produce a RNA corresponding to the DNA sequence. The RNA may be synthesised *in vivo* or *in vitro* or by chemical synthesis to produce a sequence corresponding to a DNA sequence by methods well known in the art. In this specification, where the degree of sequence similarity between an RNA and DNA is such that the strand of the DNA could encode the RNA, then the RNA is said to "correspond" to that DNA.

The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living plant is not isolated, but the same nucleic acid or polypeptide separated from some or all of the coexisting materials in the natural system, is isolated. Such an isolated nucleic acid could be part of a vector and/or such a nucleic acid could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment. An isolated polypeptide could be part of a composition and still be isolated in that such a composition is not part of its natural environment.

By "functionally active" in respect of a nucleic acid it is meant that the fragment or variant is capable of modifying organic acid biosynthesis in a plant. A variant in this context can be an analogue, derivative or mutant and includes naturally occurring allelic variants and non-naturally occurring variants. Additions, deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity

of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the functional part of the above mentioned sequence, more preferably at least approximately 90% identity, most preferably at least approximately 95% identity. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 30 nucleotides, more preferably at least 45 nucleotides, most preferably at least 60 nucleotides.

By "functionally active" in respect of a polypeptide it is meant that the fragment or variant has one or more of the biological properties of the proteins CS, CS-like, MDH, MDH-like, PEPC and PEPC-like. A variant in this context includes additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 60% identity to the functional part of the above mentioned sequence, more preferably at least approximately 80% identity, most preferably at least approximately 90% identity. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

The term "construct" as used herein refers to an artificially assembled or isolated nucleic acid molecule which includes the gene of interest. In general a construct may include the gene or genes of interest, a marker gene which in some cases can also be the gene of interest and appropriate regulatory sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes vectors but should not be seen as being limited thereto.

The term "vector" as used herein encompasses both cloning and expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

By "operatively linked" in respect of a regulatory element, nucleic acid or nucleic acid fragment and terminator, it meant that the regulatory element is capable of causing expression of said nucleic acid or nucleic acid fragment in a plant cell and said terminator is capable of terminating expression of said nucleic acid or nucleic acid fragment in a plant cell. Preferably, said regulatory element is upstream of said nucleic acid or nucleic acid fragment and said terminator is downstream of said nucleic acid or nucleic acid fragment.

By "an effective amount" of a nucleic acid or nucleic acid fragment it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Such nucleic acids or nucleic acid fragments could be assembled to form a consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid fragments can be compared and aligned in order to identify common or overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encodes a CS or CS-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102, 104,

114, 118 and 122 hereto (SEQ ID NOS 1, 3 to 10, 11, 13 to 16, 17, 19, 327, 329 to 335, 336, 338 to 344, 349, 351, 353 respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encodes a MDH or MDH-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequence shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto (SEQ ID NOS. 21, 23 to 29; 30, 32 to 33, 34, 36, 38, 40, 42 to 43, 44, 46, 48 to 110, 111, 113, 115, 117 to 182, 183, 185, 205, 207 to 217, 218, 220 to 251, 252, 254 to 270, 271, 273 to 275, 276, 278 to 287, 288, 290 to 292, 293, 295 to 296, 297, 299 to 301, 304 to 305, 306, 308); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encodes a PEPC or PEPC-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95, 97 and 110 hereto (SEQ ID NOS 187, 189, 191 to 197, 199, 201, 203, 310, 312 to 314, 315, 317 to 318, 319, 321 to 322, 323, 325 and 347 respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

Nucleic acids or nucleic acid fragments encoding at least a portion of several CS, MDH and PEPC polypeptides have been isolated and identified. Genes encoding other CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins, either as cDNAs or genomic DNAs, may be isolated directly by using all

or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling, nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or RNA. For example, polymerase chain reaction may be performed on a library of cloned nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol (Frohman *et al.* (1988) *Proc. Natl. Acad Sci. USA* 85:8998, the entire disclosure of which is incorporated herein by reference) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated (Ohara *et al.* (1989) *Proc. Natl. Acad Sci USA* 86:5673; Loh *et al.* (1989) *Science* 243:217, the entire disclosures of which are incorporated herein by reference). Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a further aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*),

ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like polypeptides; and functionally active fragments and variants of these polypeptides.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*).

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CS or CS-like polypeptide includes an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 10, 100, 103, 115, 119, 123 hereto (SEQ ID NOS 2, 12, 18, 20, 328, 337, 350, 352 and 354 respectively); and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated MDH or MDH-like polypeptide includes an amino acid sequence selected from the group consisting of sequences shown in Figures 12, 15, 18, 20, 22, 24, 27, 29, 32, 34, 36, 39, 41, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83 and 85 hereto (SEQ ID NOS 22, 31, 35, 37, 39, 41, 45, 47, 112, 114, 116, 184, 186, 206, 219, 253, 272, 277, 289, 294, 297, 303, 307 and 309, respectively) and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated PEPC or PEPC-like polypeptide includes an amino acid sequence selected from the group consisting of sequences shown in Figures 43, 45, 48, 50, 52, 54, 87, 90, 93, 96, 98 and 111 hereto (SEQ ID NOS 188, 190, 198, 200, 202, 204, 311, 316, 320, 324, 326, and 348 ,respectively); and functionally active fragments and variants thereof.

In a further embodiment of this aspect of the invention, there is provided a polypeptide produced (e.g. recombinantly) from a nucleic acid or nucleic acid

fragment according to the present invention. Techniques for recombinantly producing polypeptides are known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is allelic between organisms because it then may serve to unambiguously identify an individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 9, 13, 16, 30, 37, 57, 60, 63, 79, 89, 92 and 104 hereto.

Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment

according to the present invention, for example a SNP from a nucleic acid sequence shown in Figures 3, 6, 9, 13, 16, 30, 37, 57, 60, 63, 66, 67, 72, 78, 88, 94, 101 and 104 hereto; or complements or sequences antisense thereto, and functionally active fragments and variants thereof. The invention further provides a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) isolated by the method of this invention.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library. The method includes the step of identifying the SNP.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragment may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs, and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping, DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to abiotic stresses such aluminium toxic acid soils; in relation to nutrient acquisition efficiency including phosphorus; in

relation to nitrogen fixation; in relation to nodulation. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a construct or vector including a nucleic acid or nucleic acid fragment according to the present invention.

In a particularly preferred embodiment the construct or vector may include nucleic acids or nucleic acid fragments encoding both CS or CS-like and MDH or MDH-like polypeptides.

In yet another preferred embodiment the construct or vector may include nucleic acids or nucleic acid fragments encoding both MDH or MDH-like and PEPC or PEPC-like polypeptides.

In yet another preferred embodiment the construct or vector may include both CS or CS-like and PEPC or PEPC-like polypeptides.

In another preferred embodiment the construct or vector may include nucleic acids or nucleic acid fragments encoding all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like polypeptides.

In a preferred embodiment of this aspect of the invention, the vector may include one or more regulatory element such as a promoter, one or more nucleic acids or nucleic acid fragments according to the present invention and one or more terminators; said one or more regulatory elements, one or more nucleic acids or nucleic acid fragments and one or more terminators being operatively linked.

In a preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both CS or CS-like and MDH or MDH-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both CS or CS-like and MDH or MDH-like polypeptides are expressed.

In another preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both CS or CS-like and PEPC or PEPC-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both CS or CS-like and PEPC or PEPC-like polypeptides are expressed.

In yet another particularly preferred embodiment of the present invention the vector or construct may contain nucleic acids or nucleic acid fragments encoding both MDH or MDH-like and PEPC or PEPC-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both MDH or MDH-like and PEPC or PEPC-like polypeptides are expressed.

In another particularly preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like, operatively linked to a regulatory element or regulatory elements, such that all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like polypeptides are expressed.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg.

monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter, the maize Ubiquitin promoter, and the rice Actin promoter. Particularly suitable tissue-specific promoters include root-prevalent promoters.

A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (*nos*) and the octopine synthase (*ocs*) genes.

The vector, in addition to the regulatory element, the nucleic acid or nucleic acid fragment of the present invention and the terminator, may include further elements necessary for expression of the nucleic acid or nucleic acid fragment, in different combinations, for example vector backbone, origin of replication (ori), multiple cloning sites, spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene, the phospho-mannose isomerase (*pmi*) gene], and reporter genes (such as beta-glucuronidase (GUS) gene (*gusA*)]. The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid or nucleic acid fragment. Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example including one or more restriction enzyme sites.

The vectors of the present invention may be incorporated into a variety of plants, including monocotyledons (such as grasses from the genera *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as Arabidopsis, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species), more preferably perennial ryegrass, including forage- and turf-type cultivars. In an alternate preferred embodiment, the vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

Techniques for incorporating the vectors of the present invention into plant cells (for example by transduction, transfection or transformation) are known to those skilled in the art. Such techniques include *Agrobacterium* mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, a vector, nucleic acid or nucleic acid fragment of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a monocotyledon, preferably a grass species, more preferably a ryegrass (*Lolium* species) or fescue (*Festuca* species), more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment the plant cell, plant, plant seed or other plant part may be from a dicotyledon, preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*).

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

In a further aspect of the present invention there is provided a method of modifying organic acid biosynthesis; of modifying organic acid secretion; of modifying phosphorous and other nutrients acquisition efficiency in plants; of modifying aluminium and acid soil tolerance in plants; of modifying nitrogen fixation and nodule function, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to the present invention. Preferably the nucleic acid or nucleic acid fragment is part of a vector.

Using the methods and products of the present invention, organic acid biosynthesis; organic acid secretion; phosphorous and other plant nutrient acquisition efficiency; aluminium and acid soil tolerance; nitrogen fixation and nodule function, may be increased or otherwise altered, for example by incorporating additional copies of a sense nucleic acid or nucleic acid fragment of the present invention. They may be decreased or otherwise altered, for example by incorporating an antisense nucleic acid or nucleic acid fragment of the present invention.

In a particularly preferred embodiment the method may include introducing into said plant nucleic acids or nucleic acid fragments encoding both CS or CS-like and MDH or MDH-like polypeptides.

In another preferred embodiment the method may include introducing into said plant nucleic acids or nucleic acid fragments encoding both CS or CS-like and PEPC or PEPC polypeptides.

In yet another preferred embodiment the method may include introducing into said plant nucleic acids or nucleic acid fragments encoding both MDH or MDH-like and PEPC or PEPC-like polypeptides.

In an even more preferred embodiment the method may include introducing into said plant nucleic acids or nucleic acid fragments encoding all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like polypeptides.

The present invention will now be more fully described with reference to the accompanying Examples and drawings. It should be understood, however, that the description following is illustrative only and should not be taken in any way as a restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of LpCSa.

Figure 2 shows the deduced amino acid sequence of LpCSa.

Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSa.

Figure 4 shows the consensus contig nucleotide sequence of LpCSb.

Figure 5 shows the deduced amino acid sequence of LpCSb.

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSb.

Figure 7 shows the nucleotide sequence of LpCSc.

Figure 8 shows the deduced amino acid sequence of LpCSc.

Figure 9 shows the nucleotide sequence of LpCSd.

Figure 10 shows the deduced amino acid sequence of LpCSd.

Figure 11 shows the consensus contig nucleotide sequence of LpMDHa.

Figure 12 shows the deduced amino acid sequence of LpMDHa.

Figure 13 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHa.

Figure 14 shows the consensus contig nucleotide sequence of LpMDHb.

Figure 15 shows the deduced amino acid sequence of LpMDHb.

Figure 16 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHb.

Figure 17 shows the nucleotide sequence of LpMDHc.

Figure 18 shows the deduced amino acid sequence of LpMDHc.

Figure 19 shows the nucleotide sequence of LpMDHd.

Figure 20 shows the deduced amino acid sequence of LpMDHd.

Figure 21 shows the nucleotide sequence of LpMDHe.

Figure 22 shows the deduced amino acid sequence of LpMDHe.

Figure 23 shows the consensus contig nucleotide sequence of LpMDHf.

Figure 24 shows the deduced amino acid sequence of LpMDHf.

Figure 25 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHf.

Figure 26 shows the nucleotide sequence of LpMDHg.

Figure 27 shows the deduced amino acid sequence of LpMDHg.

Figure 28 shows the consensus contig nucleotide sequence of LpMDHh.

Figure 29 shows the deduced amino acid sequence of LpMDHh.

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHh.

Figure 31 shows the nucleotide sequence of LpMDHi.

Figure 32 shows the deduced amino acid sequence of LpMDHi.

Figure 33 shows the nucleotide sequence of LpMDHj.

Figure 34 shows the deduced amino acid sequence of LpMDHj.

Figure 35 shows the consensus contig nucleotide sequence of LpMDHk.

Figure 36 shows the deduced amino acid sequence of LpMDHk.

Figure 37 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHk.

Figure 38 shows the nucleotide sequence of LpMDHl.

Figure 39 shows the deduced amino acid sequence of LpMDHl.

Figure 40 shows the nucleotide sequence of LpMDHm.

Figure 41 shows the deduced amino acid sequence of LpMDHm.

Figure 42 shows the nucleotide sequence of LpPEPCa.

Figure 43 shows the deduced amino acid sequence of LpPEPCa.

Figure 44 shows the consensus contig nucleotide sequence of LpPEPCb.

Figure 45 shows the deduced amino acid sequence of LpPEPCb.

Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpPEPCb.

Figure 47 shows the nucleotide sequence of LpPEPCc.

Figure 48 shows the deduced amino acid sequence of LpPEPCc.

Figure 49 shows the nucleotide sequence of LpPEPCd.

Figure 50 shows the deduced amino acid sequence of LpPEPCd.

Figure 51 shows the nucleotide sequence of LpPEPCe.

Figure 52 shows the deduced amino acid sequence of LpPEPCe.

Figure 53 shows the nucleotide sequence of LpPEPCf.

Figure 54 shows the deduced amino acid sequence of LpPEPCf.

Figure 55 shows the consensus contig nucleotide sequence of TrMDHa.

Figure 56 shows the deduced amino acid sequence of TrMDHa.

Figure 57 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHa.

Figure 58 shows the consensus contig nucleotide sequence of TrMDHb.

Figure 59 shows the deduced amino acid sequence of TrMDHb.

Figure 60 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHb.

Figure 61 shows the consensus contig nucleotide sequence of TrMDHc.

Figure 62 shows the deduced amino acid sequence of TrMDHc.

Figure 63 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHc.

Figure 64 shows the consensus contig nucleotide sequence of TrMDHd.

Figure 65 shows the deduced amino acid sequence of TrMDHd.

Figure 66 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHd.

Figure 67 shows the consensus contig nucleotide sequence of TrMDHe.

Figure 68 shows the deduced amino acid sequence of TrMDHe.

Figure 69 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHe.

Figure 70 shows the consensus contig nucleotide sequence of TrMDHf.

Figure 71 shows the deduced amino acid sequence of TrMDHf.

Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHf.

Figure 73 shows the consensus contig nucleotide sequence of TrMDHg.

Figure 74 shows the deduced amino acid sequence of TrMDHg.

Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHg.

Figure 76 shows the consensus contig nucleotide sequence of TrMDHh.

Figure 77 shows the deduced amino acid sequence of TrMDHh.

Figure 78 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHh.

Figure 79 shows the consensus contig nucleotide sequence of TrMDHi.

Figure 80 shows the deduced amino acid sequence of TrMDHi.

Figure 81 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHi.

Figure 82 shows the nucleotide sequence of TrMDHj.

Figure 83 shows the deduced amino acid sequence of TrMDHj.

Figure 84 shows the nucleotide sequence of TrMDHk.

Figure 85 shows the deduced amino acid sequence of TrMDHk.

Figure 86 shows the consensus contig nucleotide sequence of TrPEPCa.

Figure 87 shows the deduced amino acid sequence of TrPEPCa.

Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCa.

Figure 89 shows the consensus contig nucleotide sequence of TrPEPCb.

Figure 90 shows the deduced amino acid sequence of TrPEPCb.

Figure 91 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCb.

Figure 92 shows the consensus contig nucleotide sequence of TrPEPCc.

Figure 93 shows the deduced amino acid sequence of TrPEPCc.

Figure 94 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCc.

Figure 95 shows the nucleotide sequence of TrPEPCd.

Figure 96 shows the deduced amino acid sequence of TrPEPCd.

Figure 97 shows the nucleotide sequence of TrPEPCe.

Figure 98 shows the deduced amino acid sequence of TrPEPCe.

Figure 99 shows the consensus contig nucleotide sequence of TrCSa.

Figure 100 shows the deduced amino acid sequence of TrCSa.

Figure 101 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSa.

Figure 102 shows the consensus contig nucleotide sequence of TrCSb.

Figure 103 shows the deduced amino acid sequence of TrCSb.

Figure 104 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSb.

Figure 105 shows the plasmid map in pGEM-T Easy of TrMDH.

Figure 106 shows the nucleotide sequence of TrMDH.

Figure 107 shows the deduced amino acid sequence of TrMDH.

Figure 108 shows the plasmid map of sense construct of TrMDH in the binary vector pPZP221:35S^2.

Figure 109 shows the plasmid map in pGEM-T Easy of TrPEPC.

Figure 110 shows the nucleotide sequence of TrPEPC.

Figure 111 shows the deduced amino acid sequence of TrPEPC.

Figure 112 shows the plasmid map of sense construct of TrPEPC in the binary vector pPZP221:35S^2.

Figure 113 shows the plasmid map in pGEM-T Easy of TrCSa.

Figure 114 shows the nucleotide sequence of TrCSa.

Figure 115 shows the deduced amino acid sequence of TrCSa.

Figure 116 shows the plasmid map of sense construct of TrCSa in the binary vector pPZP221:35S^2.

Figure 117 shows the plasmid map in pGEM-T Easy of TrCSb.

Figure 118 shows the nucleotide sequence of TrCSb.

Figure 119 shows the deduced amino acid sequence of TrCSb.

Figure 120 shows the plasmid map of sense construct of TrCSb in the binary vector pPZP221:35S^2.

Figure 121 shows the plasmid map in pGEM-T Easy of TrCSd.

Figure 122 shows the nucleotide sequence of TrCSd.

Figure 123 shows the deduced amino acid sequence of TrCSd.

Figure 124 shows the plasmid map of sense construct of TrCSd in the binary vector pPZP221:35S^2.

Figure 125 shows the plasmid maps of the modular vector system comprising a binary base vector and 7 auxiliary vectors.

Figure 126 shows an example of the modular binary transformation vector system comprising plasmid maps of the binary transformation vector backbone and 4 expression cassettes for combinatorial expression of chimeric CS and MDH and PEPC genes in auxiliary vectors (A) and the plasmid map of the T-DNA region of the final binary transformation vector (B).

Figure 127 shows the results of RT-PCR experiments performed as described in Example 6. Samples were isolated from: L, leaf; S, stolon; St, stolon tip; R, root; Rt, root tip. –C: negative (no reverse transcriptase) control; +C, positive (plasmid) control. The numbers indicate cycle numbers. A: phosphate transporter homolog; B: root iron transporter homolog.

Figure 128 shows the screening of a white clover BAC library using the phosphate transporter cDNA as a probe (A); Southern hybridisation blot of six BAC clones identified in A using the same probe (B); physical map of the phosphate transporter genomic region including the coding region and the promoter region (C).

Figure 129 shows white clover cotyledons, various stages of selection of plantlets transformed with a binary transformation vector constructed as described in Examples 4 and 5, transgenic white clover on root-inducing medium, and white clover plants transformed with genes involved in organic acid biosynthesis.

Figure 130 shows the molecular analysis of transgenic white clover plants for the presence of the chimeric MDH gene with real time PCR amplification plot and agarose gel of PCR product.

Figure 131 shows the molecular analysis of transgenic white clover plants for the presence of the chimeric PEPC gene with real time PCR amplification plot and agarose gel of PCR product.

Figure 132 shows the molecular analysis of transgenic white clover plants for the presence of the chimeric CS gene with real time PCR amplification plot and agarose gel of PCR product.

EXAMPLE 1

Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CS, CS-like, MDH, MDH-like, PEPC and PEPC-like polypeptides from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)

cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

TABLE 1

cDNA libraries from white clover (*Trifolium repens*)

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 &28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated white clover
04wc	Nodulated white clover cut leaf and stem collected after 0, 1, 4, 6 &14 h after cutting
05wc	Non-nodulated Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at –80°C, imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf

Library	Organ/Tissue
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials
15wc	Senescing stolon
16wc	Senescing leaf

TABLE 2

cDNA libraries from perennial ryegrass (*Lolium perenne*)

Library	Organ/Tissue
01rg	Roots from 3-4 day old light-grown seedlings
02rg	Leaves from 3-4 day old light-grown seedlings
03rg	Etiolated 3-4 day old dark-grown seedlings
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)
05rg	Senescing leaves from mature plants
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)
07rg	Roots from mature plants grown in hydroponic culture
08rg	Senescent leaf tissue
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
10rg	Embryogenic suspension-cultured cells
11rg	Non-embryogenic suspension-cultured cells
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
13rg	Shoot apices including vegetative apical meristems
14rg	Immature inflorescences including different stages of inflorescence

Library	Organ/Tissue
	meristem and inflorescence development
15rg	Defatted pollen
16rg	Leaf blades and leaf sheaths (*rbcL*, *rbcS*, *cab*, *wir2A* subtracted)
17rg	Senescing leaves and tillers
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
22rg	Spikelets with open and maturing florets
23rg	Mature roots (specific subtraction with leaf tissue)

The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into *Escherichia coli* Epicurian coli XL10-Gold

ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.

Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analysed using an Applied Biosystems ABI 3700 sequence analyser.

EXAMPLE 2

DNA sequence analyses

The cDNA clones encoding CS, CS-like, MDH, MDH-like, PEPC and PEPC-like polypeptides were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the *e*Bioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.

The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to a multiple alignment using the CLUSTALw algorithm, and to generate a consensus contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT protein sequence database using the BLASTx algorithm to confirm the initial identification.

EXAMPLE 3

Identification and full-length sequencing of cDNAs encoding CS, MDH and PEPC polypeptides

To fully characterise for the purposes of the generation of probes for hybridisation experiments and the generation of transformation vectors, a set of cDNAs encoding white clover CS, MDH and PEPC polypeptides was identified and fully sequenced.

Full-length cDNAs were identified from our EST sequence database using relevant published sequences (NCBI databank) as queries for BLAST searches. Full-length cDNAs were identified by alignment of the query and hit sequences using Sequencher (Gene Codes Corp., Ann Arbor, MI 48108, USA). The original plasmid was then used to transform chemically competent XL-1 cells (prepared in-house, $CaCl_2$ protocol). After colony PCR (using HotStarTaq, Qiagen) a minimum of three PCR-positive colonies per transformation were picked for initial sequencing with M13F and M13R primers. The resulting sequences were aligned with the original EST sequence using Sequencher to confirm identity and one of the three clones was picked for full-length sequencing, usually the one with the best initial sequencing result.

Sequencing of all cDNAs was completed by primer walking, i.e. oligonucleotide primers were designed to the initial sequence obtained using M13F and M13R oligonucleotide primers and used for further sequencing. The sequences of the oligonucleotide primers are shown in Table 2.

Contigs were then assembled in Sequencher. The contigs include the sequences of the SMART primers used to generate the initial cDNA library as well

as pGEM-T Easy vector sequence up to the EcoRI cut site both at the 5' and 3' end.

Plasmid maps and the full cDNA sequences of TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC polypeptides were obtained (Figures 1, 2, 5, 6, 9, 10, 13, 14, 17, 18, 21, 22, 25, 26, 29 and 30).

TABLE 3

List of primers used for sequencing of the full-length cDNAs encoding CS, MDH and PEPC

gene name	clone ID	sequencing primer	primer sequence (5'>3')
TrCSa	05wc1HsB08	05wc1HsB08.f1	TTGCCCGAGGCTATACTGTGGC
		05wc1HsB08.f2	CAGCTCACCTAGTTGCTAG
		05wc1HsB08.f3	CCATGGCCTAATGTTGATGC
		05wc1HsB08.r1	TTGGCCTTTCAAGTGGCATTCC
		05wc1HsB08.r2	CAGAATGGGAGGCACGACTTC
		05wc1HsB08.r3	ATGTGAGCATAGTTTGCACC
TrCSb	05wc2HsD09	05wc2HsD09.f1	GACTGCCAGAAAACACTTCCAGG
		05wc2HsD09.f2	ATGACTGCTTTAGTGTGG
		05wc2HsD09.r1	CTCAAGTTTCTCCAGTGTGACAC
		05wc2HsD09.r2	TGACTTATGTATCCCACC
		05wc2HsD09.r3	GCTCTGAATGGTTTAGCTGG
TrCSd	10wc1BsF10	10wc1BsF10.f1	GCACTGCCTGTTTCTGCTCATCC
		10wc1BsF10.f2	AGCCAACTTATGAGGATAGC
		10wc1BsF10.r1	CTCCAATACTCCTCGCGACGCC
		10wc1BsF10.r2	AGGCACAACCTGGCCACTG
		10wc1BsF10.r3	ACGTTGCCACCTTCATGATC
TrMDH	13wc1NsD01	13wc1NsD01.f1	GTTGTTATACCTGCTGGTGTT
		13wc1NsD01.r1	CTCACTCAACCCTTGGAGAT
TrPEPC	15wc1DsH12	15wc1DsH12.f1	TCCTAAGAAACTTGAAGAGCTCGG
		15wc1DsH12.f2	AGATGTTTGCTTACTAGC
		15wc1DsH12.r1	GCCAGCAGCAATACCCTTCATGG
		15wc1DsH12.r2	TTGCTTCTCAACTGTTCC

EXAMPLE 4

Development of binary transformation vectors containing chimeric genes with cDNA sequences encoding CS, MDH and PEPC

To alter the expression of the polypeptides involved in organic acid biosynthesis to improve phosphorus acquisition efficiency as well as aluminium and acid soil tolerance in forage plants, a set of sense binary transformation vectors was produced.

The pPZP221 binary transformation vector (Hajdukiewicz *et al.*, 1994) was modified to contain the $35S^2$ cassette from pKYLX71:$35S^2$ (Schardl *et al.*, 1987) as follows: pKYLX71:$35S^2$ was cut with ClaI. The 5' overhang was filled in using Klenow and the blunt end was A-tailed with Taq polymerase. After cutting with EcoRI, the 2kb fragment with an EcoRI-compatible and a 3'-A tail was gel-purified. pPZP221 was cut with HindIII and the resulting 5' overhang filled in and T-tailed with Taq polymerase. The remainder of the original pPZP221 multi-cloning site was removed by digestion with EcoRI, and the expression cassette cloned into the EcoRI site and the 3' T overhang restoring the HindIII site. This binary vector contains between the left and right border the plant selectable marker gene aacC1 under the control of the 35S promoter and 35S terminator and the pKYLX71:$35S^2$-derived expression cassette with a CaMV 35S promoter with a duplicated enhancer region and an rbcS terminator.

A GATEWAY® cloning cassette (Invitrogen) was introduced into the multicloning site of the pPZP221:$35S^2$ vector obtained as described following the manufacturer's protocol.

cDNA fragments were generated by high fidelity PCR with a proofreading DNA polymerase using the original pGEM-T Easy plasmid cDNA as a template. The primers used (Table 3) contained *att*B sequences for use with recombinases utilising the GATEWAY® system (Invitrogen). The resulting PCR fragments were used in a recombination reaction with pDONR® vector (Invitrogen) to generate entry vectors. In a further recombination reaction, the cDNAs encoding the open reading frame sequences were transferred from the entry vector to the GATEWAY®-enabled pPZP221:$35S^2$ vector.

The orientation of the constructs (sense or antisense) was checked by restriction enzyme digest and sequencing which also confirmed the correctness of the sequence. Transformation vectors containing chimeric genes using full-length open reading frame cDNAs encoding white clover TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC proteins in sense orientation under the control of the CaMV 35S[2] promoter were generated (Figures 4, 8, 12, 16, 20, 24, 28 and 32).

TABLE 4

List of primers used to PCR-amplify the open reading frames of cDNAs encoding CS, MDH and PEPC

gene name	clone ID	primer	primer sequence (5'>3')
TrCSa	05wc1HsB08	05wc1HsB08f	GGGGACAAGTTTGTACAAAAAAGCAGGCTTGATCTTAATGGCGTTCTTTCG
		05wc1HsB08r	GGGGACCACTTTGTACAAGAAAGCTGGGTTTTCAATTTTAGGACGATGCG
TrCSb	05wc2HsD09	05wc2HsD09f	GGGGACAAGTTTGTACAAAAAAGCAGGCTTTGTTGATTGATCTTAATGGC
		05wc2HsD09r	GGGGACCACTTTGTACAAGAAAGCTGGGTTAGTAATCCACAGATAACCG
TrCSd	10wc1BsF10	10wc1BsF10f	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTAGATTGTTGATTGATCTAAATGGC
		10wc1BsF10r	GGGGACCACTTTGTACAAGAAAGCTGGGTCTAGATTCAATTTTAGGATGATGCACC
TrMDH	13wc1NsD01	13wc1NsD01f	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTAGAAATTCCCATTACCATTCATTCC
		13wc1NsD01r	GGGGACCACTTTGTACAAGAAAGCTGGGTCTAGATTGACATTCTCTCGCATGGACGC
TrPEPC	15wc1DsH12	15wc1DsH12f	GGGGACAAGTTTGTACAAAAAAGCAGGCTTGAGAAGGAGTGAATTGCTCC
		15wc1DsH12r	GGGGACCACTTTGTACAAGAAAGCTGGGTATGATATCTTAGCACACACTTAAC

EXAMPLE 5

Development of binary transformation vectors containing chimeric genes with a combination of 2 or more cDNA sequences encoding CS, MDH and PEPC

To alter the expression of the polypeptides involved in organic acid biosynthesis to improve phosphorus acquisition efficiency as well as aluminium

and acid soil tolerance in forage plants, a modular binary transformation vector system was used (Figure 125). The modular binary vector system enables simultaneous integration of up to seven transgenes the expression of which is controlled by individual promoter and terminator sequences into the plant genome (Goderis *et al.*, 2002).

The modular binary vector system consists of a pPZP200-derived vector (Hajdukiewicz *et al.*, 1994) backbone containing within the T-DNA a number of unique restriction sites recognised by homing endonucleases. The same restriction sites are present in pUC18-based auxiliary vectors flanking standard multicloning sites. Expression cassettes comprising a selectable marker gene sequence or a cDNA sequence to be introduced into the plant under the control of regulatory sequences like promoter and terminator can be constructed in the auxiliary vectors and then transferred to the binary vector backbone utilising the homing endonuclease restriction sites. Up to seven expression cassettes can thus be integrated into a single binary transformation vector. The system is highly flexible and allows for any combination of cDNA sequence to be introduced into the plant with any regulatory sequence.

For example, a selectable marker cassette comprising the nos promoter and nos terminator regulatory sequences controlling the expression of the nptII gene was PCR-amplified using a proofreading DNA polymerase from the binary vector pKYLX71:35S^2 and directionally cloned into the AgeI and NotI sites of the auxiliary vector pAUX3166. Equally, other selectable marker cassettes can be introduced into any of the auxiliary vectors.

In another example, the expression cassette from the binary vector pWM5 consisting of the ASSU promoter and the tob terminator was PCR-amplified with a proofreading DNA polymerase and directionally cloned into the AgeI and NotI sites of the auxiliary vector pAUX3169. Equally, other expression cassettes can be introduced into any of the auxiliary vectors.

In yet another example, the expression cassette from the direct gene transfer vector pDH51 was cut using EcoRI and cloned directly into the EcoRI site of the auxiliary vector pAUX3132.

TABLE 5

List of primers used to PCR-amplify plant selectable marker cassettes and the regulatory elements used to control the expression of CS, MDH and PEPC genes

expression cassette	primer	primer sequence (5'>3')
nos::nptII-nos	forward	ATAATAACCGGTTGATCATGAGCGGAGAATTAAGGG
	reverse	ATAATAGCGGCCGCTAGTAACATAGATGACACCGCG
35S::aacC1-35S	forward	AATAGCGGCCGCGATTTAGTACTGGATTTTGG
	reverse	AATAACCGGTACCCACGAAGGAGCATCGTGG
$35S^2$::rbcS	forward	ATAATAACCGGTGCCCGGGGATCTCCTTTGCC
	reverse	ATAATAGCGGCCGCATGCATGTTGTCAATCAATTGG
assu::tob	forward	TAATACCGGTAAATTTATTATGRGTTTTTTTCCG
	reverse	TAATGCGGCCGCTAAGGGCAGCCCATACAAATGAAGC

The expression cassettes were further modified by introducing a GATEWAY® cloning cassette (Invitrogen) into the multicloning site of the respective pAUX vector following the manufacturer's protocol. In a recombination reaction, the cDNAs encoding the open reading frame sequences were transferred from the entry vector obtained as described in Example 4 to the GATEWAY®-enabled pAUX vector. Any combination of the regulatory elements with cDNA sequences of TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC can be obtained. One typical example is given in Figure 126 with expression cassettes comprising the nptII plant selectable marker, TrPEPC, TrCSa and TrMDH.

Complete expression cassettes comprising any combination of regulatory elements and cDNA sequences to be introduced into the plant were then cut from the auxiliary vectors using the respective homing endonuclease and cloned into the respective restriction site on the binary vector backbone. After verification of the construct by nucleotide sequencing, the binary transformation vector

comprising a number of expression cassettes was used to generate transgenic white clover plants.

EXAMPLE 6

Isolation of regulatory elements to direct expression of chimeric genes encoding CS, MDH and PEPC involved in organic acid biosynthesis

To direct the expression of chimeric white clover genes TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC involved in organic acid biosynthesis to specific tissues, regulatory elements showing specificity for expression in root or root tip tissue were identified and isolated.

Using the BLASTn algorithm, white clover EST sequence collections prepared as detailed in Examples 1 and 2 were searched with nucleotide sequences representing genes with known root-specific expression identified in GenBank as queries. Suitable candidate ESTs were identified and oligonucleotide primers for reverse transcription-PCR (RT-PCR) were designed (see Table 4).

TABLE 6

Oligonucleotide primers used in reverse transcription-PCR to confirm tissue specificity of candidate white clover ESTs

gene	forward primer (5'->3')	reverse primer (5'->3')
histone (internal control)	CCGATTCCGTTTCAATGGCTCGTA	GCCATCCTTAACCCTAAGCACGT
white clover phosphate transporter homolog	TTGCATTTGCTTGGAACAACTAG	GCAAGAGCAAACATGAAACCA
white clover root iron transporter homolog	ATGGGTCTTGGTGGTTGCA	GCAGCAAGAAGATCAACCAAAGCCA

Total RNA for RT-PCR experiments was isolated from a leaf, stolon, stolon tip, root and root tip of white clover plants grown in the glasshouse using the TRIZOL method. Reverse transcription was performed using SuperScriptII (Invitrogen) following the supplier's instructions. Preliminary PCR reactions using Dynazyme as the DNA polymerase were set up to determine the correct amount of template using the PCR primers for the internal control (histone). The results of this preliminary PCR were used to set up another round of PCR to determine the optimum number of cycles for linear amplification. The final PCR amplifications

were performed using the following cycling conditions: 94 °C, 4 min., 1 time; 94 °C, 15 sec., 60 °C, 30 sec., 72 °C, 2 min., x times; 72 °C, 10 min., 1 time. The number of cycles in the amplification (x) was found to be dependent on the relative abundance of transcript and had to be optimised for each template.

RT-PCR results using a white clover histone gene as an internal constitutively expressed control confirmed the tissue-specificity of two candidate ESTs to be root-prevalent (Figure 127 A and B). These were a phosphate transporter homolog (clone name 02wc1DsG07) and a root iron transporter homolog (clone name 05wc1IsB11).

A spotted white clover BAC library consisting of 50,304 clones with an estimated 99% genome coverage (6.3 genome equivalents) was screened using the phosphate transporter homolog EST nucleotide sequence as a probe. A number of positive BAC clones could be identified (Figure 128 A). After Southern hybridisation blotting (Figure 128 B) a 7.5 kb EcoRV genomic DNA fragment was selected and fully sequenced. The fragment contained the phosphate transporter homolog open reading frame and 4 kb of upstream sequence including the promoter region. A physical map of the genomic DNA fragment including the promoter region is shown in Figure 128 C.

EXAMPLE 7

Production by *Agrobacterium*-mediated transformation and analysis of transgenic white clover plants carrying chimeric genes encoding CS, MDH and PEPC involved in organic acid biosynthesis

A set of binary transformation vectors carrying chimeric white clover genes to alter the expression of the polypeptides involved in organic acid biosynthesis to improve phosphorus acquisition efficiency as well as aluminium and acid soil tolerance in forage plants were produced as detailed in Examples 4 and 5.

Agrobacterium-mediated gene transfer experiments were performed using these transformation vectors.

The production of transgenic white clover plants carrying the white clover TrCSa, TrCSb, TrCSd, TrMDH and TrPEPC cDNAs, either singly or in combination, is described here in detail (Table 7).

Preparation of *Agrobacterium*

Agrobacterium tumefaciens strain AGL-1 transformed with one of the binary vector constructs detailed in Example 6 were streaked on LB medium containing 50 µg/ml rifampicin and 50 µg/ml kanamycin and grown at 27 °C for 48 hours. A single colony was used to inoculate 5 ml of LB medium containing 50 µg/ml rifampicin and 50 µg/ml kanamycin and grown over night at 27 °C and 250 rpm on an orbital shaker. The overnight culture was used as an inoculum for 500 ml of LB medium containing 50 µg/ml kanamycin only. Incubation was over night at 27 °C and 250 rpm on an orbital shaker in a 2 l Erlenmeyer flask.

Preparation of white clover seeds

1 spoon of seeds (ca. 500) was placed into a 280 µm mesh size sieve and washed for 5 min under running tap water, taking care not to wash seeds out of sieve. In a laminar flow hood, seeds were transferred with the spoon into an autoclaved 100 ml plastic culture vessel. A magnetic stirrer (wiped with 70% EtOH) and ca. 30 ml 70% EtOH were added, and the seeds were stirred for 5 min. The EtOH was discarded and replaced by 50 ml 1.5% sodium hypochlorite. The seeds were stirred for an additional 45 - 60 min on a magnetic stirrer. The sodium hypochlorite was then discarded and the seeds rinsed 3 to 4 times with autoclaved ddH_2O. Finally 30 ml of ddH_2O were added, and seeds incubated over night at 10 - 15°C in an incubator.

***Agrobacterium*-mediated transformation of white clover**

The seed coat and endosperm layer of the white clover seeds prepared as above were removed with a pair of 18 G or 21 G needles. The cotyledons were cut from the hypocotyl leaving a ca. 1.5 mm piece of the cotyledon stalk. The cotyledons were transferred to a petridish containing ddH_2O. After finishing the isolation of clover cotyledons, ddH_2O in the petridish was replaced with *Agrobacterium* suspension (diluted to an OD_{600} = 0.2 - 0.4). The petridish was sealed with its lid and incubated for 40 min at room temperature.

After the incubation period, each cotyledon was transferred to paper towel using the small dissection needle, dried and plated onto regeneration medium RM73. The plates were incubated at 25°C with a 16h light/8h dark photoperiod. On day 4, the explants were transferred to fresh regeneration medium. Cotyledons

transformed with *Agrobacterium* were transferred to RM73 containing cefotaxime (antibacterial agent) and gentamycin. The dishes were sealed with Parafilm and incubated at 25°C under a 16/8 h photoperiod. Explants were subcultured every three weeks for a total of nine weeks onto fresh RM 73 containing cefotaxime and gentamycin. Shoots with a green base were then transferred to root-inducing medium RIM. Roots developed after 1 – 3 weeks, and plantlets were transferred to soil when the roots were well established.

Preparation of genomic DNA for real-time PCR and analysis for the presence of transgenes

3 – 4 leaves of white clover plants regenerated on selective medium were harvested and freeze-dried. The tissue was homogenised on a Retsch MM300 mixer mill, then centrifuged for 10 min at 1700xg to collect cell debris. Genomic DNA was isolated from the supernatant using Wizard Magnetic 96 DNA Plant System kits (Promega) on a Biomek FX (Beckman Coulter). 5 μl of the sample (50 μl) were then analysed on an agarose gel to check the yield and the quality of the genomic DNA.

Genomic DNA was analysed for the presence of the transgene by real-time PCR using SYBR Green chemistry. PCR primer pairs were designed using MacVector (Accelrys) or PrimerExpress (ABI). The forward primer was located within the $35S^2$ promoter region and the reverse primer within the transgene to amplify products of approximately 150 - 250 bp as recommended. The positioning of the forward primer within the $35S^2$ promoter region guaranteed that endogenous genes in white clover were not detected.

5 μl of each genomic DNA sample was run in a 50 μl PCR reaction including SYBR Green on an ABI 7700 (Applied Biosystems) together with samples containing DNA isolated from wild type white clover plants (negative control), samples containing buffer instead of DNA (buffer control) and samples containing the plasmid used for transformation (positive plasmid control). Cycling conditions used were 2 min. at 50 °C, 10 min. at 95 °C and then 40 cycles of 15 sec. at 95 °C, 1 min. at 60 °C.

Preparation of genomic DNA and analysis of DNA for presence and copy number of transgene by Southern hybridisation blotting

Genomic DNA for Southern hybridisation blotting was obtained from leaf material of white clover plants following the CTAB method. Southern hybridisation blotting experiments were performed following standard protocols as described in Sambrook *et al.* (1989). In brief, genomic DNA samples were digested with appropriate restriction enzymes and the resulting fragments separated on an agarose gel. After transfer to a membrane, a cDNA fragment representing a transgene or selectable marker gene was used to probe the size-fractionated DNA fragments. Hybridisation was performed with either radioactively labelled probes or using the non-radioactive DIG labelling and hybridisation protocol (Boehringer) following the manufacturer's instructions.

Plants were obtained after transformation with all chimeric constructs and selection on medium containing gentamycin. Details of plant analysis are given in Table 5 and Figures 130, 131 and 132.

TABLE 7

Transformation of white clover with binary transformation vectors comprising cDNAs encoding CS, MDH and PEPC involved in organic acid biosyntheses, selection and molecular analysis of regenerated plants.

construct	cotyledons transformed	selection into RIM	soil	QPCR-positive	Southern	copy number range
pPZP221-35S2::TrMDH	2739	72	45	43	n/d	
pPZP221-35S2::TrCS	2550	39	7	nd	n/d	
pPZP221-35S2::TrPEPC	2730	44	10	nd	n/d	

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Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as outlined herein.

CLAIMS

1. A substantially purified or isolated nucleic acid or nucleic acid fragment encoding an organic acid biosynthesis enzyme polypeptide selected from the group consisting of a citrate synthase (CS) polypeptide; a CS-like polypeptide; a malate dehydrogenase (MDH) polypeptide; a MDH-like polypeptide; a phosphoenolpyruvate carboxylase (PEPC) polypeptide; and a PEPC-like polypeptide; or a functionally active fragment or variant of such a polypeptide, from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species.

2. A nucleic acid or nucleic acid fragment wherein said nucleic acid or nucleic acid fragment is from white clover (*Trifolium repens*) or perennial ryegrass (*Lolium perenne*).

3. A nucleic acid or nucleic acid fragment encoding a CS or CS-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102, 104, 114, 118 and 122 hereto (SEQ ID NOS 1, 3 to 10, 11, 13 to 16, 17, 19, 327, 329 to 335, 336, 338 to 344, 349, 351, 353 respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

4. A nucleic acid or nucleic acid fragment encoding a MDH or MDH-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequence shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto (SEQ ID NOS 21, 23 to 29; 30, 32 to 33, 34, 36, 38, 40, 42 to 43, 44, 46, 48 to 110, 111, 113, 115, 117 to 182, 183, 185, 205, 207 to 217, 218, 220 to 251, 252, 254 to 270, 271, 273 to 275, 276, 278 to 287, 288, 290 to 292, 293, 295 to 296, 297, 299 to 301, 304 to 305, 306, 308); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

5. A nucleic acid or nucleic acid fragment encoding a PEPC or PEPC-like polypeptide and including a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95, 97 and 110 hereto (SEQ ID NOS 187, 189, 191 to 197, 199, 201, 203, 310, 312 to 314, 315, 317 to 318, 319, 321 to 322, 323, 325 and 347 respectively); (b) complements of the sequences recited in (a); (c) sequences antisense to the sequences recited in (a) and (b); (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c); and (e) RNA sequences corresponding to the sequences recited in (a), (b), (c) and (d).

6. A construct including one or more nucleic acids or nucleic acid fragments according to any one of claims 1 to 5.

7. A construct according to claim 6 including nucleic acids or nucleic acid fragments encoding both (a) a CS polypeptide or a CS-like polypeptide and (b) a MDH polypeptide or a MDH-like polypeptide.

8. A construct according to claim 6 including nucleic acids or nucleic acid fragments encoding both (a) a CS polypeptide or a CS-like polypeptide and (b) a PEPC polypeptide or a PEPC-like polypeptide.

9. A construct according to claim 6 including nucleic acids or nucleic acid fragments encoding both (a) a MDH polypeptide or a MDH-like polypeptide and (b) a PEPC polypeptide or a PEPC-like polypeptide.

10. A construct according to claim 6 including nucleic acids or nucleic acid fragments encoding all three of (a) a CS polypeptide or a CS-like polypeptide; (b) a MDH polypeptide or a MDH-like polypeptide; and (c) a PEPC polypeptide or a PEPC-like polypeptide.

11. A construct according to any one of claims 6 to 10 wherein the one or more nucleic acids or nucleic acid fragments are operably linked to one or more regulatory elements, such that the one or more nucleic acids or nucleic acid fragments are each expressed.

12 A construct according to Claim 11, wherein the one or more regulatory elements include a promoter and a terminator, said promoter, nucleic acid or nucleic acid fragment and terminator being operably linked.

13. A plant cell, plant, plant seed or other plant part, including a construct according to any one of claims 6 to 12.

14. A plant, plant seed or other plant part derived from a plant cell or plant according to Claim 13.

15. A method of modifying one or more of organic acid synthesis; organic acid secretion; nutrient acquisition; aluminium and acid soil tolerance; or nitrogen fixation and nodule function; in a plant, said method including introducing into said plant an effective amount of a nucleic acid or nucleic acid fragment according to any one of claims 1 to 5, or a construct according to any one of claims 6 to 12.

16 A method according to claim 15 wherein said method includes introducing into said plant effective amounts of nucleic acids or nucleic acid fragments encoding both (a) a CS polypeptide or CS-like polypeptide and (b) a MDH polypeptide or MDH-like polypeptide.

17. A method according to claim 15 wherein said method includes introducing into said plant effective amounts of nucleic acids or nucleic acid fragments encoding both (a) a CS polypeptide or a CS-like polypeptide and (b) a PEPC polypeptide or a PEPC-like polypeptide

18. A method according to claim 15 wherein said method includes introducing into said plant effective amounts of nucleic acids or nucleic acid fragments encoding both (a) a MDH polypeptide or a MDH-like polypeptide and (b) a PEPC polypeptide or a PEPC-like polypeptide.

19. A method according to claim 15 wherein said method includes introducing into said plant effective amounts of nucleic acids or nucleic acid fragments encoding all three of (a) a CS polypeptide or a CS-like polypeptide; (b) a MDH polypeptide or a MDH-like polypeptide; and (c) a PEPC polypeptide or a PEPC-like polypeptide.

20. A method according to any one of claims 15 to 19 wherein the method is modifying nutrient acquisition and the nutrient is phosphorous.

21. Use of a nucleic acid or nucleic acid fragment according to any one of claims 1 to 5, and/or nucleotide sequence information thereof, and/or single nucleotide polymorphisms thereof as a molecular genetic marker.

22. A substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid fragment according to any one of claims 1 to 5.

23. A nucleic acid or nucleic acid fragment including an SNP according to Claim 22, wherein said nucleic acid or nucleic acid fragment is from white clover (*Trifolium repens*) or perennial ryegrass (*Lolium perenne*).

24. A substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CS and CS-like, MDH and MDH-like and PEPC and PEPC-like; and functionally active fragments and variants thereof.

25. A polypeptide according to Claim 24, wherein said polypeptide is from white clover (*Trifolium repens*) or perennial ryegrass (*Lolium perenne*).

26. A polypeptide encoded by a nucleic acid or nucleic acid fragment according to any one of claims 1 to 5.

27. A polypeptide according to Claim 24 or 25, wherein said polypeptide is CS or CS-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 2, 5, 8, 10, 100, 103, 115, 119, 123 hereto (SEQ ID NOS 2, 12, 18, 20, 328, 337, 350, 352 and 354 respectively); and functionally active fragments and variants thereof.

28. A polypeptide according to Claim 24 or 25, wherein said polypeptide is MDH or MDH-like and includes an amino acid sequence selected from the group consisting of sequences shown in Figures 12, 15, 18, 20, 22, 24, 27, 29, 32, 34, 36, 39, 41, 56, 59, 62, 65, 68, 71, 74, 77, 80, 83 and 85 hereto (SEQ ID NOS 22, 31, 35, 37, 39, 41, 45, 47, 112, 114, 116, 184, 186, 206, 219, 253, 272, 277, 289, 294, 297, 303, 307 and 309, respectively) and functionally active fragments and variants thereof.

29. A polypeptide according to Claim 24 or 25, wherein said polypeptide is PEPC or PEPC-like and includes an amino acid sequence selected from the

group consisting of sequences shown in Figures 43, 45, 48, 50, 52, 54, 87, 90, 93, 96, 98 and 111 hereto (SEQ ID NOS 188, 190, 198, 200, 202, 204, 311, 316, 320, 324, 326, and 348, respectively); and functionally active fragments and variants thereof.

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                 *        20         *        40         *        60
LpCSa : GNNTTATATTGACGGGGATGAGGGAATTCTTCGCTACAGAGGCTATCCAATTGAGGAGGT :  60
                 *        80         *       100         *       120
LpCSa : GGCTGAAAGCAGCTCGTTTGTTGAGGTCGCCTACCTCTTAATGTATGGGAATTTGCCCAC : 120
                 *       140         *       160         *       180
LpCSa : CCAGAGTCAACTGGCAGGCTGGGAGTTTGCAATTTCGCAGCACTCTGCTGTTCCTCAAGG : 180
                 *       200         *       220         *       240
LpCSa : ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG : 240
                 *       260         *       280         *       300
LpCSa : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 300
                 *       320         *       340         *       360
LpCSa : TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC : 360
                 *       380         *       400         *       420
LpCSa : AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTTGTCCTTCCTTCAAA : 420
                 *       440         *       460         *       480
LpCSa : TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA : 480
                 *       500         *       520         *       540
LpCSa : TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA : 540
                 *       560         *       580         *       600
LpCSa : CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT : 600
                 *       620         *       640         *       660
LpCSa : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA : 660
                 *       680         *       700         *       720
LpCSa : GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA : 720
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FIGURE 1

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                       *        740         *        760         *        780
LpCSa : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGTTTTGGGCACCGTGTGTATAAGAATTA :  780

                       *        800         *        820         *        840
LpCSa : TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG :  840

                       *        860         *        880         *        900
LpCSa : GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT :  900

                       *        920         *        940         *        960
LpCSa : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT :  960

                       *        980         *       1000         *       1020
LpCSa : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 1020

                       *       1040         *       1060         *       1080
LpCSa : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 1080

                       *       1100         *       1120         *       1140
LpCSa : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 1140

                       *       1160         *       1180         *       1200
LpCSa : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 1200

                       *       1220         *       1240         *       1260
LpCSa : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 1260

                       *       1280         *       1300         *       1320
LpCSa : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 1320

                       *       1340         *       1360         *       1380
LpCSa : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 1380

                       *       1400         *       1420         *       1440
LpCSa : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 1440

                       *       1460         *       1480         *       1500
LpCSa : TATCTTGAAAGTCTTAATCATGTGGACCAATGAAGACATAGATCAAGTTCTTTGCATGGG : 1500

                       *       1520         *       1540         *
LpCSa : CGGCGGCTGTTTCTTTGGGAAAAAACTTTTTATGGGAGTCTTTTTTTACC : 1550
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FIGURE 1 (cont.)

```
                    *        20         *        40         *        60
LpCSa : YIDGDEGILRYRGYPIEEVAESSSFVEVAYLLMYGNLPTQSQLAGWEFAISQHSAVPQGL :  60

                    *        80         *       100         *       120
LpCSa : LDIIQSMPHDAHPMGVLASAMSTLSVFHPDANPALRGQDLYKSKQVRDKQIVRVLGKAPV : 120

                    *       140         *       160         *       180
LpCSa : IAAAAYLRLAGRPFVLPSNNLSYSENFLYMLDSMGDKDYKPNPRLARVLDVLFILHAEHE : 180

                    *       200         *       220         *       240
LpCSa : MNCSTAAVRHLASSGVDVFTALSGAVGALYGPLHGGANEAVLKMLNEIGSVENIPEFIEG : 240

                    *       260         *       280         *       300
LpCSa : VKNRKRKMSGFGHRVYKNYDPRAKVIRKLAEEVFTIVGRDPLIEVAVALEKAALSDEYFI : 300

                    *       320         *       340         *       360
LpCSa : KRKLYPNVDFYSGLIYRAMGFPTEFFPVLFAVPRMAGWLAHWKESLDDPDNKIMRPQQVY : 360

                    *       380         *       400
LpCSa : TGTWLRHYTPVRERVPSSDSEQLGQIATSNATRRRRAGSAL : 401
```

FIGURE 2

```
                   *        20         *        40         *        60
LpCSa1 : GNNTTATATTGACGGGGATGAGGGAATTCTTCGCTACAGAGGCTATCCAATTGAGGAGGT :  60
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                   *        80         *       100         *       120
LpCSa1 : GGCTGAAAGCAGCTCGTTTGTTGAGGTCGCCTACCTCTTAATGTATGGGAATTTGCCCAC : 120
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                   *       140         *       160         *       180
LpCSa1 : CCAGAGTCAACTGGCAGGCTGGGAGTTTGCAATTTCGCAGCACTCTGCTGTTCCTCAAGG : 180
LpCSa2 : -------------GCAGGCTGGGAGTTTGCAATTTCGCA-CACTCTGCTGTTCCTCANGN :  46
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                   *       200         *       220         *       240
LpCSa1 : ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG : 240
LpCSa2 : ACTCTTGGATATAATACAATCAATGCCTCATGATGCCCACCCCATGGGTGTCCTTGCCAG : 106
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                   *       260         *       280         *       300
LpCSa1 : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 300
LpCSa2 : TGCAATGAGCACACTTTCAGTCTTCCATCCAGATGCAAACCCTGCTCTTAGAGGTCAAGA : 166
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -
```

FIGURE 3

```
                 *       320         *       340         *       360
LpCSa1 : TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC : 360
LpCSa2 : TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTTGGGAAGGCACC : 226
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *       380         *       400         *       420
LpCSa1 : AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCTTTTGTCCTTCCTTCAAA : 420
LpCSa2 : AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTTGTCCTTCCTTCAAA : 286
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *       440         *       460         *       480
LpCSa1 : TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA : 480
LpCSa2 : TAATCTCTCTTATTCAGAAAATTTCTTGTATATGCTGGACTCTATGGGTGACAAAGATTA : 346
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *       500         *       520         *       540
LpCSa1 : TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA : 540
LpCSa2 : TAAGCCAAATCCCAGACTTGCCCGGGTTCTGGATGTCCTTTTTATTCTTCATGCTGAACA : 406
LpCSa3 : -----------------------------------------------NTTNTGCTG-ACA :  12
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *       560         *       580         *       600
LpCSa1 : CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT : 600
LpCSa2 : CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT : 466
LpCSa3 : CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGTCGATGTCTT :  72
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -
```

FIGURE 3 (cont.)

```
                 *        620         *        640         *        660
LpCSa1 : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGNGGCGCAAATGA : 660
LpCSa2 : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA : 526
LpCSa3 : CACTGCTCTTTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA : 132
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *        680         *        700         *        720
LpCSa1 : NGCGGTACTT-AAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA : 719
LpCSa2 : GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA : 586
LpCSa3 : GGCGGTACTTAAAATGTTAAATGAGATTGGAAGTGTAGAGAATATTCCGGAATTCATTGA : 192
LpCSa4 : ------------------------------------------------------------ :   -
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *        740         *        760         *        780
LpCSa1 : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGNTTTGGGCACN---------------- : 763
LpCSa2 : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGTTTTGGGCACCGTGTGTATAAGAATTA : 646
LpCSa3 : GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGGCTTTGGGCACCGTGTGTATAAGAATTA : 252
LpCSa4 : ----------------------------------------------------------GA :   2
LpCSa5 : ------------------------------------------------------------ :   -
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *        800         *        820         *        840
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGN------------------------ : 682
LpCSa3 : TGATCCTCGTGCTAAAGTCATCCGGAAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG : 312
LpCSa4 : TTATCCTCGCGCTAAAGTCAT-CCGGAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG :  61
LpCSa5 : -----------------------GGAAGTTAGCGGAGGAGGTTTTCACGATTGTGGGACG :  37
LpCSa6 : ------------------------------------------------------------ :   -
LpCSa7 : ------------------------------------------------------------ :   -
LpCSa8 : ------------------------------------------------------------ :   -

                 *        860         *        880         *        900
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGTAGCACTGTCAGACGAGTATTT : 372
LpCSa4 : GGATCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT : 121
LpCSa5 : GGNTCCTCTTATCGAGGTAGCTGTTGCTTTGGAGAAGGCAGCACTGTCAGACGAGTATTT :  97
LpCSa6 : --------------------------------------------TNNCAGACGAGTATTT :  16
LpCSa7 : ---------------------------------------------GTCAGACGAGTATTT :  15
LpCSa8 : ------------------------------------------------------------ :   -
```

FIGURE 3 (cont.)

7/241

```
                       *       920         *       940         *       960
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT : 432
LpCSa4 : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT : 181
LpCSa5 : TATCGAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT : 157
LpCSa6 : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT :  76
LpCSa7 : TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTTATTCTGGCCTAATATATAGGGCAAT :  75
LpCSa8 : ------------------------------------------------------------ :   -

                       *       980         *      1000         *      1020
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 492
LpCSa4 : GGGATTCCCTGCAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 241
LpCSa5 : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 217
LpCSa6 : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 136
LpCSa7 : GGGATTCCCTACAGAGTTTTTCCCTGTTCTGTTTGCAGTTCCTCGCATGGCTGGTTGGTT : 135
LpCSa8 : ------------------------------------------------------------ :   -

                       *      1040         *      1060         *      1080
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 552
LpCSa4 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 301
LpCSa5 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 277
LpCSa6 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 196
LpCSa7 : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCCCAACAGGT : 195
LpCSa8 : ------------------------------------------------------------ :   -

                       *      1100         *      1120         *      1140
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 612
LpCSa4 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 361
LpCSa5 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 337
LpCSa6 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 256
LpCSa7 : ATACACCGGTACTTGGCTAAGGCATTACACCCCAGTGAGAGAACGGGTGCCATCAAGCGA : 255
LpCSa8 : ------------------------------------------------------------ :   -

                              1160         *      1180         *      1200
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : CAGTGAGCAGCTTGGGCAGATCACTACATCAAACGCGACGAGGCGTCGGCGTGCTGGTTC : 672
LpCSa4 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 421
LpCSa5 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 397
LpCSa6 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 316
LpCSa7 : CAGTGAGCAGCTTGGGCAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGCTGGCTC : 315
LpCSa8 : --------------GGCAGATCGCT-CATCAAACGCGTCGAGGCGTCGGCGTGCTGGCTC :  45
```

FIGURE 3 (cont.)

```
                   *      1220         *      1240         *      1260
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 732
LpCSa4 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 481
LpCSa5 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 457
LpCSa6 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 376
LpCSa7 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 375
LpCSa8 : TGCCCTGTAGAACAGTCTGCATGATACAGCATACAGTCCACACAATAAACCAAGCTGCCA : 105

                   *      1280         *      1300         *      1320
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : AGGGCCACGGCTGCTTAAATN--------------------------------------- : 753
LpCSa4 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATGTAGGC : 541
LpCSa5 : AGGGCCACAGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 517
LpCSa6 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 436
LpCSa7 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 435
LpCSa8 : AGGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCACGTATATATAGGC : 165

                   *      1340         *      1360         *      1380
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 601
LpCSa5 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 577
LpCSa6 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 496
LpCSa7 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 495
LpCSa8 : AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAAGTTGGTAGTAGAA : 225

                   *      1400         *      1420         *      1440
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 661
LpCSa5 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 637
LpCSa6 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 556
LpCSa7 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 555
LpCSa8 : TGCACTTGTAACGTGTTGTTAATTTGTTATCCTGCAATGTACGCTCTATAAACTGTTCAG : 285

                   *      1460         *      1480         *      1500
LpCSa1 : ------------------------------------------------------------ :   -
LpCSa2 : ------------------------------------------------------------ :   -
LpCSa3 : ------------------------------------------------------------ :   -
LpCSa4 : TGTCTTGAAAGTCTTAATCATGTGGACCAA-GAAGACATAGATCAAGTTCTTTGCATGGG : 720
LpCSa5 : TATCTTGAAAGTCTTANTCCNNNNAAAAA------------------------------- : 666
LpCSa6 : TATCTTGAAAGTCTTAATCATGTGGACCAA-GAAGACATAGATCAAGTTCTTTGCATGGG : 615
LpCSa7 : TATCTTGAAAGTCTTAATCATGTGGACCAATCAAAAAAAAAA------------------ : 597
LpCSa8 : TATCTTGAAAGTCTTAAAAAAAAAA----------------------------------- : 310
```

FIGURE 3 (cont.)

```
                      *       1520          *       1540          *
LpCSa1  : ---------------------------------------------------- :   -
LpCSa2  : ---------------------------------------------------- :   -
LpCSa3  : ---------------------------------------------------- :   -
LpCSa4  : CGGCGGCTGTTTCTTTGGNAAAAAA--------------------------- : 745
LpCSa5  : ---------------------------------------------------- :   -
LpCSa6  : CGGCGGCTGTTTCTTTGTGTTTCCTCTTTTTATGGGAGTCTTTTTTTACC : 665
LpCSa7  : ---------------------------------------------------- :   -
LpCSa8  : ---------------------------------------------------- :   -
```

FIGURE 3 (cont.)

```
                 *        20         *        40         *        60
LpCSb : CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG :  60

                 *        80         *       100         *       120
LpCSb : TTGAGAGTGAATTTGCAAAGGCTTATGAGAAGGGAATTCATAAATCAAAGTTCTGGGAGC : 120

                 *       140         *       160         *       180
LpCSb : CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT : 180

                 *       200         *       220         *       240
LpCSb : ACCGGAGAATTTTCAAGGACGGGAAAACTATTGCAGCTGATAATACACTGGACTACGCAG : 240

                 *       260         *       280         *       300
LpCSb : CTAATTTTTCACACATGCTTGGTTTTGATGACCCCAAAATGCTGGAGTTGATGCGCCTAT : 300

                 *       320         *       340         *       360
LpCSb : ACATAACAATTCACACTGATCACGAAGGAGGGAATGTTAGTGCTCATGCTGGGCATCTGG : 360

                 *       380         *       400         *       420
LpCSb : TTGGAAGTGCTCTGTCAGATCCTTATCTTTCTTTTGCAGCGGCACTGAACGGTTTAGCTG : 420

                 *       440         *       460         *       480
LpCSb : GACCACTGCACGGCTTGGCTAATCAGGAAGTGTTGTNATGGATCAAATCTGTGATGGAAG : 480

                 *       500         *       520         *       540
LpCSb : AAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA : 540

                 *       560         *       580         *       600
LpCSb : GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 600

                 *       620         *       640         *       660
LpCSb : CGTGCCAAAGGGAGTTTGCACTGAAGTATTTACCCGAAGACCCACTTTTCCAACTGGTCT : 660

                 *       680         *       700         *       720
LpCSb : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT : 720

                 *       740         *       760         *       780
LpCSb : GGCCTAATGTTGATGCTCACAGTGGAGTTTTGCTCAACCACTTCGGATTAGTTGAAGCAC : 780

                 *       800         *       820         *       840
LpCSb : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCTCATTT : 840
```

FIGURE 4

```
                    *       860         *       880         *       900
LpCSb : GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG :  900

                    *       920         *       940         *       960
LpCSb : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTTACAAATCAG :  960

                    *       980         *      1000         *      1020
LpCSb : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 1020

                    *      1040         *      1060         *      1080
LpCSb : ATCTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTCACAGACGGTAGAATTTTGTAA : 1080

                    *      1100         *      1120         *      1140
LpCSb : CCACCGNTACTTGAACACCGAATCANTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 1140

                    *      1160
LpCSb : GACACATAAGTTTTATGTGTCGCTCGG : 1167
```

FIGURE 4 (cont.)

```
                  *        20         *        40         *        60
LpCSb : SPCXCSPMTQFTTGVMALQVESEFAKAYEKGIHKSKFWEPTYEDSLNLIARLPQVASYVY :  60

                  *        80         *       100         *       120
LpCSb : RRIFKDGKTIAADNTLDYAANFSHMLGFDDPKMLELMRLYITIHTDHEGGNVSAHAGHLV : 120

                  *       140         *       160         *       180
LpCSb : GSALSDPYLSFAAALNGLAGPLHGLANQEVLXWIKSVMEETGSNITTDQLKEYVWKTLKS : 180

                  *       200         *       220         *       240
LpCSb : GKVVPGYGHGVLRNTDPRYSCQREFALKYLPEDPLFQLVSKLYEVVPPILTELGKVKNPW : 240

                  *       260         *       280         *       300
LpCSb : PNVDAHSGVLLNHFGLVEARYYTVLFGVSRSMGIGSQLIWDRALGLPLERPKSVTMEWLE : 300

LpCSb : NHCKKAAA : 308
```

FIGURE 5

```
                    *        20         *        40         *        60
LpCSb1 : CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTTACCACTGGAGTGATGGCACTCCAAG :  60
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                    *        80         *       100         *       120
LpCSb1 : TTGAGAGTGAATTTGCAAAGGCTTATGAGAAGGGAATTCATAAATCAAAGTTCTGGGAGC : 120
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                    *       140         *       160         *       180
LpCSb1 : CTACATATGAAGATAGCTTAAATTTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT : 180
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                    *       200         *       220         *       240
LpCSb1 : ACCGGAGAATTTTCAAGGACGGAAAACTATTGCAGCTGATAATACACTGGACTACGCAG : 240
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                    *       260         *       280         *       300
LpCSb1 : CTAATTTTTCACACATGCTTGGTTTTGATGACCCCAAAATGCTGGAGTTGATGCGCCTAT : 300
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                    *       320         *       340         *       360
LpCSb1 : ACATAACAATTCACACTGATCACGAAGGAGGGAATGTTAGTGCTCATGCTGGGCATCTGG : 360
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                    *       380         *       400         *       420
LpCSb1 : TTGGAAGTGCTCTGTCAGATCCTTATCTTTCTTTTGCAGCGGCACTGAACGGTTTAGCTG : 420
LpCSb2 : ------------------------------------------------------------ :   -
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -

                    *       440         *       460         *       480
LpCSb1 : GACCACTGCACGGCTTGGCTAATCAGGAAGTGTTGTTATGGATCAAATCTGTGATGGAAG : 480
LpCSb2 : -----------------------------------TNATGGAT-NAATCTGTGATGGAAG :  24
LpCSb3 : ------------------------------------------------------------ :   -
LpCSb4 : ------------------------------------------------------------ :   -
```

FIGURE 6

```
                  *       500         *       520         *       540
LpCSb1 : AAACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA : 540
LpCSb2 : -AACCGGGAGTAACATTACAACTGATCAGCTTAAAGAATATGTTTGGAAGACACTGAAGA :  83
LpCSb3 : -----------------------------------------------------CTGAAGA :   7
LpCSb4 : ------------------------------------------------------------ :   -

                  *       560         *       580         *       600
LpCSb1 : GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 600
LpCSb2 : GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT : 143
LpCSb3 : GTGGAAAGGTTGTTCCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT :  67
LpCSb4 : ------------------------------------------------------------ :   -

                  *       620         *       640         *       660
LpCSb1 : CGTGCCAAAGGGAGTTTGCACTGAAGTATTTACCTGAAGACCCACTTTTCCAACTGGTCT : 660
LpCSb2 : CGTGCCAAAGGGAGTTTGCACTGAAGTATTTACCCGAAGACCCACTTTTCCAACTGGTCT : 203
LpCSb3 : CGTGCCAAAGGGAGTNGGNACTGAAGTATTTACCCGAAGACCCACTTTTCCAACTGGTCT : 127
LpCSb4 : ------------------------------------------------------------ :   -

                  *       680         *       700         *       720
LpCSb1 : CCAAGTTGTATGAAGTTGTGCCTCCTATCCTCACTGAGTTAGGCAAGGTAAAAAACCCAT : 720
LpCSb2 : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT : 263
LpCSb3 : CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT : 187
LpCSb4 : ------------------------------------------------------------ :   -

                  *       740         *       760         *       780
LpCSb1 : GGCCTAATGTTGATGCTCACAGNGGAGTTTTGCTCAACCACTTCGGATTAGTTGAA-CAC : 779
LpCSb2 : GCCCTAATGTTGATGCTCACAGTGGAGTTTTGCTCAACCACTTCGGATTAGTTGAAGCAC : 323
LpCSb3 : GGCCTAATGTTGATGCTCACAGTGGAGTTTTGCTCAACCACTTCGGATTAGTTGAAGCAC : 247
LpCSb4 : ------------------------------------------------------------ :   -

                  *       800         *       820         *       840
LpCSb1 : GGNACTACACTGNCTTGNTCGGN------------------------------------- : 802
LpCSb2 : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCCCATTT : 383
LpCSb3 : GGTACTACACTGTCTTGTTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCTCATTT : 307
LpCSb4 : --------------------------------------GTTTTTGGATCCCAGCTCATTT :  22

                  *       860         *       880         *       900
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG : 443
LpCSb3 : GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG : 367
LpCSb4 : GGGTCCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCACCATGGAGTGGCTGG :  82

                  *       920         *       940         *       960
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTTACAAATCAG : 503
LpCSb3 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTNGTTTTACAAATCAN : 427
LpCSb4 : AAAACCACTGCAAGAAGGCTGCGGCCTGAAGCTACACCAATGCTTCGTTTTACAAATCAG : 142
```

FIGURE 6 (cont.)

```
                 *       980         *       1000         *       1020
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 563
LpCSb3 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGGTAGCCTTGTTTTACC : 487
LpCSb4 : GCCGTCTTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTTAGCCTTGTTTTACC : 202

                 *      1040         *       1060         *       1080
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : ATCTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTTACAGACGGTAGAATTTTGTAA : 623
LpCSb3 : ATNTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTCACAGACGGTAGAATTTTGTAA : 547
LpCSb4 : ATCTTCGTTTTCCTGGCCAATAACTGGAGCAAGAGGCTCACAGACGGTAGAATTTTGTAA : 262

                 *      1100         *       1120         *       1140
LpCSb1 : ------------------------------------------------------------ :   -
LpCSb2 : CCACCGNTACTTGAACACCGAATCANTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 683
LpCSb3 : CCACCGGTACTTG-ACACCGAATNANNTAAATGGNATTTGGCATAAAGAGATTAGGACAT : 606
LpCSb4 : CCACCGTTACTTGAACACCGAATCAGTTAAATGTCATTTGGCATAAAGAGATTAGGACAT : 322

                 *      1160
LpCSb1 : -------------------------- :   -
LpCSb2 : GACACATAAGTTTTATGTGNCGNTCGG : 710
LpCSb3 : GACACATAAGTTTTATGTGTCGCTCGG : 633
LpCSb4 : GACACATAAGTTTTATGTGTCGCTCGA : 349
```

FIGURE 6 (cont.)

```
                 *        20         *        40         *        60
LpCSc : TCNCCGTGGCCANAATNCCCCANCATTCAAATACCGCCCGTCAGCCACCAATCCTCCTAC :  60

                 *        80         *       100         *       120
LpCSc : CTTCTTATTTCCACCCCAACCGCCCAACATGTGTCCTCCCACCGAANAAACACCTGCTAC : 120

                 *       140         *       160         *       180
LpCSc : CAACGGCCATAGCAACGGCACCAACGGCGCCAATGGCTCCAAGGAAGGCTTCACAGGCGT : 180

                 *       200         *       220         *       240
LpCSc : CACGACCAGACAGAACCCTCACCCTACACACAAGAGCCCATATGCACCTGTTGGCGACTT : 240

                 *       260         *       280         *       300
LpCSc : TTTGTCAAATGTCGGCCGCTTCAAGATTATCGAGAGCACATTAAGAGAGGGCGAGCAATT : 300

                 *       320         *       340         *       360
LpCSc : CGCCAACGCCTACTTCGACCTTGAGGCTAAAATCAAGATCGCCAGAGCTCTCGACAACTT : 360

                 *       380         *       400         *       420
LpCSc : TGGTGTTGACTACATTGAAGTTACCAGCCCTGCTGCCTCTGAGCAGTCAAGAAGGGACTG : 420

                 *       440         *       460         *       480
LpCSc : CGAAGCCCTCTGCAAGCTCGGATTGAAAGCCAAGATCCTTACCCACGTACGATGCCACAT : 480

                 *       500         *       520         *       540
LpCSc : GGACGATGCCAGAATCGCTGTCGAGACTGGTGTTGACGGCCTCGATGTCGTCATTGGAAC : 540

                 *       560         *       580         *       600
LpCSc : CTCTGCGTACCTCCGCGAGCACAGCCATGGCAAGGACATGACATACATCAAAAACACAGC : 600

                 *       620         *
LpCSc : GCTGGAGGTGATTGAGTTTGTCAAGAGCAAGGGAN : 635
```

FIGURE 7

```
                    *        20         *        40         *        60
LpCSc : XRGXNXPXFKYRPSATNPPTFLFPPQPPNMCPPTEXTPATNGHSNGTNGANGSKEGFTGV :  60

                    *        80         *       100         *       120
LpCSc : TTRQNPHPTHKSPYAPVGDFLSNVGRFKIIESTLREGEQFANAYFDLEAKIKIARALDNF : 120

                    *       140         *       160         *       180
LpCSc : GVDYIEVTSPAASEQSRRDCEALCKLGLKAKILTHVRCHMDDARIAVETGVDGLDVVIGT : 180

                    *       200         *
LpCSc : SAYLREHSHGKDMTYIKNTALEVIEFVKSKG : 211
```

FIGURE 8

```
                 *        20         *        40         *        60
LpCSd : GTGNTATGGCNCANCCAGNANTCCTNCGTNCTGGCTNCCANANNAGNAANAAGCTATCGG :  60

                 *        80         *       100         *       120
LpCSd : CAACGACCTCAGCGATCAGGCCATCAAGGACTACCTGTGGTCCACCCTCAAGGCTGGCCA : 120

                 *       140         *       160         *       180
LpCSd : AGTCGTTCCCGGTTACGGACACGCCGTTCTCCGCAAGACCGACCCCCGCTACGTCTCCCA : 180

                 *       200         *       220         *       240
LpCSd : GCGCGAGTTCGCCCAGAAGCACCTTCCCGACGACCCAATGTTCAAGCTCGTCAGTCAGGT : 240

                 *       260         *       280         *       300
LpCSd : CTACAAGATCGCCCCTGGTGTTCTCACCGAGCACGGCAAGACCAAGAACCCCTACCCCAA : 300

                 *       320         *       340         *       360
LpCSd : CGTCGACGCCCACTCCGGTGTCCTCCTCCAGTACTACGGCCTCACTGAGCAGAACTACTA : 360

                 *       380         *       400         *       420
LpCSd : CACCGTTCTCTTCGGTGTATCCCGTGCGCTCGGTGTCCTTCCCCAGCTTATCATTGACCG : 420

                 *       440         *       460         *       480
LpCSd : TGCCGTCGGTGCCCCCATTGAGAGGCCCAAGTCTTTCAGCACTGAGGCTTACGCCAAGTT : 480

                 *       500         *       520         *       540
LpCSd : GGTTGGTGCTAAGTTGTAAGCGCGTTACTGCAACGTGCTCTACAGCCAGGAGAATGTGGA : 540

                 *       560         *       580         *       600
LpCSd : GGAATTTGTTTAACATTCAGAGATACCTTGTCCTGTGTAGAATTGCAATGTAAGGATAGG : 600

                 *       620         *
LpCSd : GAATGGGAGCGTTACGGCGCTACATCACTACATTTN : 636
```

FIGURE 9

```
                    *        20         *        40         *        60
LpCSd : XYGXXXXPXXWXPXXXXAIGNDLSDQAIKDYLWSTLKAGQVVPGYGHAVLRKTDPRYVSQ :  60

                    *        80         *       100         *       120
LpCSd : REFAQKHLPDDPMFKLVSQVYKIAPGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTEQNYY : 120

                    *       140         *       160
LpCSd : TVLFGVSRALGVLPQLIIDRAVGAPIERPKSFSTEAYAKLVGAKL : 165
```

FIGURE 10

```
                 *        20         *        40         *        60
LpMDHa : GGTTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  60

                 *        80         *       100         *       120
LpMDHa : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 120

                 *       140         *       160         *       180
LpMDHa : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 180

                 *       200         *       220         *       240
LpMDHa : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 240

                 *       260         *       280         *       300
LpMDHa : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 300

                 *       320         *       340         *       360
LpMDHa : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA : 360

                 *       380         *       400         *       420
LpMDHa : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG : 420

                 *       440         *       460         *       480
LpMDHa : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTGTTTTTGACTTT : 480

                 *       500         *       520         *       540
LpMDHa : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA : 540

                 *       560         *       580         *       600
LpMDHa : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG : 600

                 *       620         *       640         *       660
LpMDHa : TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAAATTGGGG : 660

                 *       680         *
LpMDHa : GTGANTCCATTGGCCTCAAGCCAAAAAAAAAAAAAAA : 696
```

FIGURE 11

```
                   *        20         *        40         *        60
LpMDHa : VGCWYHHSALFSQATPSTNALSSEDIKALTKRTQEGGTEVVEAKAGKGSATLSMAYAGAV :  60

                   *        80         *       100         *       120
LpMDHa : FGDACLKGLNGVPDIVECSYVQSTITELPFFASKVRLGKNGVEEVLGLGELSAFEKEGLE : 120

                   *       140
LpMDHa : SLKGELKSSIDKGIAFANAS : 140
```

FIGURE 12

```
                   *      320       *      340       *      360
LpMDHa1 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA :360
LpMDHa2 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA :359
LpMDHa3 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA :359
LpMDHa4 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA :356
LpMDHa5 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGANAAGGAAGGTTTGGA :257
LpMDHa6 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA : 77
LpMDHa7 : TGGAGTCGAGGAAGTGCTTGGTTTGGGTGAGCTGTCGGCCTTTGAGAAGGAAGGTTTGGA : 62

          *      380       *      400       *      420
LpMDHa1 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG :420
LpMDHa2 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG :419
LpMDHa3 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG :419
LpMDHa4 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG :416
LpMDHa5 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG :317
LpMDHa6 : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG :137
LpMDHa7 : AAGTCTCAAGGGTGAGNTCAAGTCTTCAATTGACAAGGGCATCGCGTTCGCCAATGCGAG :122

                   *      440       *      460       *      480
LpMDHa1 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG--TTT :475
LpMDHa2 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG--TTT :474
LpMDHa3 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG--TTT :474
LpMDHa4 : TTAATTAATTTTGCAGATTATAGCAAACCAGGTCTAGTTAAGGGGTCTG---TTG--NTT :471
LpMDHa5 : TTGATTAANTTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT :377
LpMDHa6 : TTGATTAAATTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT :197
LpMDHa7 : TTGATTAAATTTGCAGATTATAGCAATCCAGGTCTAGTTGAGGGGTCTGTTTTTGACTTT :182

                   *      500       *      520       *      540
LpMDHa1 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA :535
LpMDHa2 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA :534
LpMDHa3 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA :534
LpMDHa4 : TTGNTCANNGCTTTTTCTGCCCATCACGTGNGCATGNAAGATTTGAGCTTNACANTANNT :531
LpMDHa5 : TTGTTCAGNGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA :437
LpMDHa6 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA :257
LpMDHa7 : TTGTTCAGTGCTTTTTCTGCCCATCACGTGGGCATGGAAGATTTGAGCTTCACAATAAAA :242

                   *      560       *      580       *      600
LpMDHa1 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG :595
LpMDHa2 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG :594
LpMDHa3 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG :594
LpMDHa4 : ATNCCNGCGCGNN----------------------------------------------- :544
LpMDHa5 : ATCCGGCGGCGTAATGCCACANAACATTACTTGGACAAGAGGGAACTAGTTCGGGTNAAG :497
LpMDHa6 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG :317
LpMDHa7 : ATCCGGCGGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTTCGTGTCAAG :302
```

FIGURE 13 (cont.)

```
                   *        20         *        40         *        60
LpMDHa1 : GTTTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  60
LpMDHa2 : -CGTGGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  59
LpMDHa3 : -GTGGTGTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  59
LpMDHa4 : ----GGTTGCTGGTATCACCATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC :  56
LpMDHa5 : ------------------------------------------------------------ :   -
LpMDHa6 : ------------------------------------------------------------ :   -
LpMDHa7 : ------------------------------------------------------------ :   -

                   *        80         *       100         *       120
LpMDHa1 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 120
LpMDHa2 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 119
LpMDHa3 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 119
LpMDHa4 : ATTGTCTAGTGAAGACATCAAGGCTCTCACCAAGAGGACACAGGAGGGTGGGACAGAAGT : 116
LpMDHa5 : -------------------------------------------GAGGGTGGGACAGAAGT :  17
LpMDHa6 : ------------------------------------------------------------ :   -
LpMDHa7 : ------------------------------------------------------------ :   -

                   *       140         *       160         *       180
LpMDHa1 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 180
LpMDHa2 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 179
LpMDHa3 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 179
LpMDHa4 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 176
LpMDHa5 : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT :  77
LpMDHa6 : ------------------------------------------------------------ :   -
LpMDHa7 : ------------------------------------------------------------ :   -

                   *       200         *       220         *       240
LpMDHa1 : TTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 240
LpMDHa2 : TTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 239
LpMDHa3 : TTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 239
LpMDHa4 : TTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 236
LpMDHa5 : TTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCTGACATTGTTGAATGCTCCTA : 137
LpMDHa6 : ------------------------------------------------------------ :   -
LpMDHa7 : ------------------------------------------------------------ :   -

                   *       260         *       280         *       300
LpMDHa1 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 300
LpMDHa2 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 299
LpMDHa3 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 299
LpMDHa4 : CGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 296
LpMDHa5 : TGTGCAATCAACTATCACAGAACTGCCATTCTTTGCCTCCAAGGTGAGGCTCGGGAAGAA : 197
LpMDHa6 : -------------------------------------------GTNANGCTCGGNNAGAA :  17
LpMDHa7 : ----------------------------------------------------------AA :   2
```

FIGURE 13

```
                    *        620         *        640         *        660
LpMDHa1 : TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAAAAN----- :650
LpMDHa2 : TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAAAAA----- :649
LpMDHa3 : TTTTGAACTGGTACATTAAACGAACAATTGCTGATGCACTTTGAGAAAAAAAAAAA----- :649
LpMDHa4 : ------------------------------------------------------------- :  -
LpMDHa5 : TTTTGAACTGGNACATTAAACAAGCAATTGTTGTGCCCCTTTGNGAACCGCCCTTTGGGG :557
LpMDHa6 : TTTTGAACTGGTACATTAAACGAACAATTGTTGATGCACTTTGTGAACCGTCCTTTGGTG :377
LpMDHa7 : TTTTGAACTGGTACATTAAACGAACAATTGTTGAAAAAAAAAA------------------ :345

                    *        680         *
LpMDHa1 : ------------------------------------ :   -
LpMDHa2 : ------------------------------------ :   -
LpMDHa3 : ------------------------------------ :   -
LpMDHa4 : ------------------------------------ :   -
LpMDHa5 : GTGANTCCATTGGNCTNAAGCCNAAAAAAAAAA---- : 589
LpMDHa6 : TTGATTCCATTGTCTTCAAGTTAACGAANAANAAAA : 413
LpMDHa7 : ------------------------------------ :   -
```

FIGURE 13 (cont.)

```
                  *        20         *        40         *        60
LpMDHb : TTTGGTNCTTTTGCCGAGCGAGAAAGCTGTTCGGTGTCACCACCCTTGNGTTGTTCGTGC :  60

                  *        80         *       100         *       120
LpMDHb : TAAAACTTTCTACGCTGGGAAGGCAAACGTGCCAGTCACTGGGGTGAATGTTCCTGTTGT : 120

                  *       140         *       160         *       180
LpMDHb : TGGTGGCCATGCTGGTGTTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAA : 180

                  *       200         *       220         *       240
LpMDHb : TGCATTGTCCCATGAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGA : 240

                  *       260         *       280         *       300
LpMDHb : AGTTGTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCAATGGCATATGCTGGTGC : 300

                  *       320         *       340         *       360
LpMDHb : AGTATTTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTC : 360

                  *       380         *       400         *       420
LpMDHb : CTTTGTGCAATCAACCGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAA : 420

                  *       440         *       460         *       480
LpMDHb : GAACGGAGTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCT : 480

                  *       500         *       520         *       540
LpMDHb : GGAGAGCCTCAAGGGCGAGCTGNTGNCCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGA : 540

                  *       560         *       580         *       600
LpMDHb : GAGCTAGTCAACCTGCTCAGATTCTAACACTCCGCACATGAACTCGGTGGGATCTGATGA : 600

                  *       620         *       640         *       660
LpMDHb : ATTTTTGGTACGACTCCTTTCACTGCCCCCTTCTCCTGGGGACATTGAGGCGTCGNGCTC : 660

                  *       680         *       700         *       720
LpMDHb : CACAATAAAATGGCGTGNCTTGTTGCCATACTGAACTGAACTTGTAATACCAGAAAGAGT : 720

                  *       740         *       760         *       780
LpMDHb : GAAACCCTGTGCCTTATGTACCACAGTACGGTGAACCCGAAAATCATGAAGGTAGCAGAA : 780

                  *       800
LpMDHb : GATTCTGTGGAAGCTTTTTTCTTTTAN : 807
```

FIGURE 14

```
                    *        20         *        40         *        60
LpMDHb : LXLLPSEKAVRCHHPXVVRAKTFYAGKANVPVTGVNVPVVGGHAGVTILPQFSQATPASN :  60

                    *        80         *       100         *       120
LpMDHb : ALSHEDLKALTKRTQDGGTEVVEAKAGKGSATLSMAYAGAVFGDACLKGLNGVPDIVECS : 120

                    *       140         *       160         *       180
LpMDHb : FVQSTVTELPFFASKVRLGKNGVEEVIGLGELSAFEKEGLESLKGELXXSIEKGIKFAQE : 180

LpMDHb : S : 181
```

FIGURE 15

```
                    *        20         *        40         *        60
LpMDHb1 : TTTGGTNCTTTTGCCGAG-NANTAATCTGTTCGGTGTCACCACCCTTGNGTTGTTCGTGCT :  60
LpMDHb2 : -----------------GCGAGAGAGCTGTTTGGTGTCACCACCCTTGTGTTGTTCGTGCT :  44

                  *        80         *       100         *       120
LpMDHb1 : AAAACTTTCTACGCTGGGAAGGCAAACGTGCCAGTCACTGGGGTGAATGTTCCTGTTGTTG : 121
LpMDHb2 : AAAACTTTCTACGCTGGGAAGGCAAACGTGCCGGTCACTGGGGTGAATGTTCCTGTTGTTG : 105

                 *       140         *       160         *       180
LpMDHb1 : GTGGCCATGCTGGTGTTACTATCCTGCCACTGTTCTCACAGGCTACTCCTGCAAGTAATGC : 182
LpMDHb2 : GTGGCCATGCTGGTGTTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAATGC : 166

                *       200         *       220         *       240
LpMDHb1 : ATTGTCCCATGAGGATCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT : 243
LpMDHb2 : ATTGTCCCATGAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAGTT : 227

               *       260         *       280         *       300
LpMDHb1 : GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCAATGGCATATGCTGGTGCAGTAT : 304
LpMDHb2 : GTTGAAGCAAAGGCTGGAAAGGGCTCAGCAACATTGTCGATGGCATATGCTGGTGCAGTTT : 288

              *       320         *       340         *       360
LpMDHb1 : TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT : 365
LpMDHb2 : TTGGAGATGCATGCTTGAAGGGGCTCAATGGAGTTCCTGACATTGTAGAGTGCTCCTTTGT : 349

             *       380         *       400         *       420
LpMDHb1 : GCAATCAACTGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA : 426
LpMDHb2 : GCAATCAACCGTAACAGAGCTGCCATTCTTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA : 410

            *       440         *       460         *       480
LpMDHb1 : GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC : 487
LpMDHb2 : GTGGAGGAAGTGATTGGGCTGGGCGAGCTGTCTGCCTTCGAGAAGGAGGGTCTGGAGAGCC : 471

           *       500         *       520         *       540
LpMDHb1 : TCAAGGGCGAGCTGNTGNCCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGAGAGCTAGTC : 548
LpMDHb2 : TCAAGGGCGAGCTGTTGTCCTCCATTGAGAAGGGTATCAAGTTCGCTCAGGAGAGCTAGTC : 532

          *       560         *       580         *       600         *
LpMDHb1 : AACCTGCTCAGATTCTGACACTCCGTACATGAACTCGGTGGGATCTGATGAATTTTTGGTA : 609
LpMDHb2 : AACCTGCTCAGATTCTAACACTCCGCACATGAACTCGGTGGGATCTGATGAATTTTTGGTT : 593

                620         *       640         *       660         *
LpMDHb1 : CGACTCCTTTCTCTGCCCCTTTTTCGTGGGGACATTGAGGCGTTGNGCTTCACATTAAAAT : 670
LpMDHb2 : CGACTCCTTTCACTGCCCCCTTCTCCTGGGGACATTGAGGCGTCGTGCTCCACAATAAAAT : 654
```

FIGURE 16

```
                 680         *        700         *        720         *
LpMDHb1 : GGCGTGNNTTGTTG-CATACTGANCTGACCTTNTATTCN---------------------- : 708
LpMDHb2 : GGCGTGTCTTGTTGCCATACTGAACTGAACTTGTAATACCAGAAAGAGTGAAACCCTGTGC : 715

               740         *        760         *        780         *
LpMDHb1 : ------------------------------------------------------------- :   -
LpMDHb2 : CTTATGTACCACAGTACGGTGAACCCGAAAATCATGAAGGTAGCAGAAGATTCTGTGGAAG : 776

                 800
LpMDHb1 : -------------- :   -
LpMDHb2 : CTTTTTTCTTTTAN : 790
```

FIGURE 16 (cont.)

```
                   *        20         *        40         *        60
LpMDHc : GNNGGTNTACCGAGCGCNCATACTTTNGTGGGTGAGGTTCTTGGACTNGACCCAAGAGAT :  60

                   *        80         *       100         *       120
LpMDHc : GTCAATGTTCCTGTNGNTGGCGGGCATGCCGGAGTTACNATATTGCCACTCCTTTCGCAG : 120

                   *       140         *       160         *       180
LpMDHc : GTTAATCCTCCCTGCTCATTCACCATGAGGAAATTAGTATCTCACCTTCACAGCATACAG : 180

                   *       200         *       220         *       240
LpMDHc : AATGGTGGGACAGAAGTNGTCGAGGCGAAAGCTGGAGCAGGATCGGNNACTNTTTCTATG : 240

                   *       260         *       280         *       300
LpMDHc : GCGNATGCGGCAGCTAAATTTGCAGATGCTTGCTNGAGAGGATTGCATGGTGATGCTGGG : 300

                   *       320         *       340         *       360
LpMDHc : ATAGNGGANTGCTCTTATGTGGATTCTCAGGTGACGGANCTNTCTTTNTTTGCATCCAAA : 360

                   *       380         *       400         *
LpMDHc : GTTCGCCTTGGTTGTTCTGGCGTCNAGGAGATCTTGCCACTTGGTCCACTCAACGAGTN : 419
```

FIGURE 17

```
                        *        20         *        40         *        60
LpMDHc : XGXPSXHTXVGEVLGXDPRDVNVPXXGGHAGVXILPLLSQVNPPCSFTMRKLVSHLHSIQ :  60

                        *        80         *       100         *       120
LpMDHc : NGGTEXVEAKAGAGSXTXSMAXAAAKFADACXRGLHGDAGIXXCSYVDSQVTXXSXFASK : 120

                        *
LpMDHc : VRLGCSGVXEILPLGPLNE : 139
```

FIGURE 18

```
                         *        20          *        40          *        60
LpMDHd : GNGNTTCCGCCAACACAACACCACCGCTCCCCCGTCCGCATCTCTCCCTTTCGCCTCCAT :  60

                         *        80          *       100          *       120
LpMDHd : CGATCCAGATCCCACACACCGCCGCAGCCAGCAACGATGAGGCCGTCGGCGATGAGATCC : 120

                         *       140          *       160          *       180
LpMDHd : GCCGCGCAGCTCCTCCGCCGCCGCAGCTACTCGTCCGCGTCCGGCCAGCCGGAGCGGAAG : 180

                         *       200          *       220          *       240
LpMDHd : GTGGCCATCCTCGGCGCGGCCGGCGGGATCGGGCAGCCGCTGGCGCTCCTCATGAAGCTG : 240

                         *       260          *       280          *       300
LpMDHd : AACCCGCTCGTCTCCTCCCTCTCCCTCTACGACATCGCCGCCACCCCCGGCGTCGCCGCC : 300

                         *       320          *       340          *       360
LpMDHd : GACGTCTCCCACATCAACTCCCCGGCCCTGGTGAAGGGGTTCATGGGCGACGATCAGCTC : 360

                         *       380          *       400          *       420
LpMDHd : GCGGAGGCGTTGGAGGGGGCCGACCTCGTCATCATCCCGGCCGGCGTTCCGAGGAAGCCC : 420

                         *       440          *       460          *       480
LpMDHd : GGCATGACCAGGGACGATCTCTTCAACATCAACGCCGGCATCGTTAAGAACCTCTGCACC : 480

                         *       500          *       520          *       540
LpMDHd : GCCATCGCCAAGTACTGCCCCAACGCTCTTATCAACATGATCAGCAACCCTGTGAACTCA : 540

                         *       560          *       580          *       600
LpMDHd : ACTGTTCCAATTGCTGCTGAAGTTTTCAAGAAGGCTGGAACCTATGATGAGAAGAAGTTG : 600

                         *       620          *       640          *       660
LpMDHd : TTTGGTGTGACCACTCTTGATGTTGTTCGTGCCAGGACTTTCTATGCTGGGAAGGCTAAT : 660

                         *       680          *       700          *       720
LpMDHd : GTACCTGTTACTGGTGTGAACGTTCCTGTTGTTGGTGGTCATGCTGGTATCACCATTCTG : 720

                         *       740          *       760          *
LpMDHd : CCACTGTTCTCACAGGCAACTCCTTCGACTAATGCATTGTCTAGTGAAGACATN : 774
```

FIGURE 19

```
                  *        20         *        40         *        60
LpMDHd : XXPPTQHHRSPVRISPFRLHRSRSHTPPQPATMRPSAMRSAAQLLRRRSYSSASGQPERK :  60

                  *        80         *       100         *       120
LpMDHd : VAILGAAGGIGQPLALLMKLNPLVSSLSLYDIAATPGVAADVSHINSPALVKGFMGDDQL : 120

                  *       140         *       160         *       180
LpMDHd : AEALEGADLVIIPAGVPRKPGMTRDDLFNINAGIVKNLCTAIAKYCPNALINMISNPVNS : 180

                  *       200         *       220         *       240
LpMDHd : TVPIAAEVFKKAGTYDEKKLFGVTTLDVVRARTFYAGKANVPVTGVNVPVVGGHAGITIL : 240

                  *
LpMDHd : PLFSQATPSTNALSSEDX : 258
```

FIGURE 20

```
                        *        20        *        40        *        60
LpMDHe  :  TCCGTACNATTGCTGCTGAAGTATTTAAAAAAGCTGGGACATACAATCCTAAGAGATTGT  :   60

                        *        80        *       100        *       120
LpMDHe  :  TGGGGGTGACAACACTTGATGTAGTGAGAGCCAATACTTTTGTGGGTGAGGTTCTTGGAC  :  120

                        *       140        *       160        *       180
LpMDHe  :  TTGACCCCAGAGATGTCAATGTTCCTGTTGTTGGCGGCATGCCGGAGTTACGATATTAC  :  180

                        *       200        *       220        *       240
LpMDHe  :  CACTCCTTTCGCAGGTTAGTCCTCCCTGCTCGTTCACCCCTGAGGAAATTAGTTATCTCA  :  240

                        *       260        *       280        *       300
LpMDHe  :  CCTCACGCATACAGAATGGTGGGACAGAAGTTGTGGAGGCGAAAGCAGGAGCAGGATCGG  :  300

                        *       320        *       340        *       360
LpMDHe  :  CAACTCTTTCTATGGCGTATGCGGCAGCTAAATTTGCAGATGCTTGCTTGAGAGGATTGC  :  360

                        *       380        *       400        *       420
LpMDHe  :  ATGGTGATGCTGGGATAGTGGAGTGCTCTTATGTGGATTCTCAGGTGACCGGAACTGCCT  :  420

                        *       440        *       460        *       480
LpMDHe  :  TCTTTGCATCCAAAGTTCGCCTAGGTCGTTCTGGCGTCGAGGAGATCTTGCAACTTGGGT  :  480

                        *       500        *       520        *       540
LpMDHe  :  CCACTGAACCAGGTTTTGAAAGANCTGGACTGGAANAAGGCGAAANAANGAGCTATCCCG  :  540

                        *       560        *       580        *       600
LpMDHe  :  AGAGCCTTCCAGAAAGGNTGTGTCATTTCGTNCAACAAAGTGAGTTACATGCCATCATCT  :  600

                        *       620        *       640        *       660
LpMDHe  :  TTGTTGGATGTGCTTCCCCAAAGTTCCAACACACCGTCGNAATTGGCATATANATATTGC  :  660

                        *       680        *       700        *       720
LpMDHe  :  TGGTTTGGGGCCTTTTGCNTTNATGCAAACAGGCTACCTTNTGGGTGGGGGGGGTCCGTT  :  720

                        *       740        *       760        *       780
LpMDHe  :  NTGAAAAACTCTTAACATTTTTTTTTACGGTTGGNAACAAAATNTNTGAAAAGCCTGAGA  :  780

                        *       800        *
LpMDHe  :  ANTATATGATAANTGAANAAAGTTTNNAAAAAAAAN  :  816
```

FIGURE 21

```
                  *        20         *        40         *        60
LpMDHe : RXIAAEVFKKAGTYNPKRLLGVTTLDVVRANTFVGEVLGLDPRDVNVPVVGGHAGVTILP :  60

                  *        80         *       100         *       120
LpMDHe : LLSQVSPPCSFTPEEISYLTSRIQNGGTEVVEAKAGAGSATLSMAYAAAKFADACLRGLH : 120

                  *       140         *       160         *       180
LpMDHe : GDAGIVECSYVDSQVTGTAFFASKVRLGRSGVEEILQLGSTEPGFERXGLEXGEXXSYPE : 180

                  *       200         *       220         *       240
LpMDHe : SLPERXCHFXQQSELHAIIFVGCASPKFQHTVXIGIXILLVWGLLXXCKQATXWVGGVRX : 240

                  *       260         *
LpMDHe : EKLLTFFFTVXNKXXEKPEXYMIXEXSXXKK : 271
```

FIGURE 22

```
                    *        20         *        40         *        60
LpMDHf  :  GGGATGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC  :   60

                    *        80         *       100         *       120
LpMDHf  :  AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC  :  120

                    *       140         *       160         *       180
LpMDHf  :  ATTGCGGCAGAAGNTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG  :  180

                    *       200         *       220         *       240
LpMDHf  :  ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGNTGATCCT  :  240

                    *       260         *       280         *       300
LpMDHf  :  AGAGAAGNCAGTGTTCCGGNTGTTGGCGGGCATGCAGGGATCACTATATTGCCCCTCCTG  :  300

                    *       320         *       340         *       360
LpMDHf  :  NCCCAGGTCAGCCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC  :  360

                    *       380         *       400         *       420
LpMDHf  :  ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG  :  420

                    *       440         *       460         *       480
LpMDHf  :  TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT  :  480

                    *       500         *       520         *       540
LpMDHf  :  GCTGGCATTGTGGAATGTNCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTCTTTGCA  :  540

                    *       560         *       580         *       600
LpMDHf  :  ACAAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTCTTGGCCACTGAAT  :  600

                    *       620         *       640         *       660
LpMDHf  :  GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAG  :  660

                    *       680         *       700         *       720
LpMDHf  :  GGTGTGGCGTTCATGAACAAGTGAGATCATATGAATGGATGGATACCCCGCAACCTATAC  :  720

                    *       740         *       760         *       780
LpMDHf  :  ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCTCCTATATACCTGTAAAAT  :  780

                    *
LpMDHf  :  CTCTCCTGCCTGTAAGAA  :  798
```

FIGURE 23

```
                    *        20         *        40         *        60
LpMDHf : MLGIVRSICEGVAKSCPNAIVNLISNPVNSTVPIAAEXFKRAGTYCPKRLLGVTTLDVAR :  60

                    *        80         *       100         *       120
LpMDHf : ANTFVAEVLGXDPREXSVPXVGGHAGITILPLLXQVSPPCSFTPDEISYLTNRIQNGGTE : 120

                    *       140         *       160         *       180
LpMDHf : VVEAKAGAGSATLSMAFAAAKFADACLRGMRGDAGIVECXYVASEVTELPFFATKVRLGR : 180

                    *       200         *       220
LpMDHf : GGAEEILPLGPLNDFERAGLEKAXKELSESIQKGVAFMNK : 220
```

FIGURE 24

```
                 *        20         *        40         *        60
LpMDHf1 : GNNNTGATTNATNCAACAAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC :  60
LpMDHf2 : -GGATGATTNATNCAACAAAAATGCTGGG-ATTGTCCGATCAATCTGTGAGGGCGTTGCC :  58

                 *        80         *       100         *       120
LpMDHf1 : AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 120
LpMDHf2 : AAGAGCTGTCCTAATGCAATAGTGAATTTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 118

                 *       140         *       160         *       180
LpMDHf1 : ATTGCGGCANAAGNTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG : 180
LpMDHf2 : ATTGCGGCAGAAGNTTTCAAGAGGGCTGGAACTTACTGCCCCAAACGTCTCCTTGGAGTG : 178

                 *       200         *       220         *       240
LpMDHf1 : ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGNAGNTGATCCT : 240
LpMDHf2 : ACAACTCTTGATGTAGCGAGGGCTAACACCTTTGTGGCTGAAGTGCTTGGAGTTGATCCT : 238

                 *       260         *       280         *       300
LpMDHf1 : AGAGAAGNCAGTGTTCCGGNTGTTGGCGGGCATGCNGGGATCACTATATTGCCCCTCCTG : 300
LpMDHf2 : AGAGAAGNCAGTGTTCCGGTTGTTGGCGGGCATGCAGGGATCACTATATTGCCCCTCCTG : 298

                 *       320         *       340         *       360
LpMDHf1 : NCCCAGGTCAGCCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 360
LpMDHf2 : NCCCAGGTCAGCCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTTGACTAACCGC : 358

                 *       380         *       400         *       420
LpMDHf1 : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : 420
LpMDHf2 : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : 418

                 *       440         *       460         *       480
LpMDHf1 : TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT : 480
LpMDHf2 : TCAATGGCTTTTGCTGCTGCAAAATTCGCCGATGCATGCTTGCGTGGAATGCGTGGTGAT : 478

                 *       500         *       520         *       540
LpMDHf1 : GCTGGCATTGTGGAATGTNCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTCTTTGCA : 540
LpMDHf2 : GCTGGNATTGTGGAATGTN----------------------------------------- : 497

                 *       560         *       580         *       600
LpMDHf1 : ACAAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTCTTGGGCCACTGAAT : 600
LpMDHf2 : ------------------------------------------------------------ :   -

                 *       620         *       640         *       660
LpMDHf1 : GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAG : 660
LpMDHf2 : ------------------------------------------------------------ :   -
```

FIGURE 25

```
                    *        680         *        700         *        720
LpMDHf1 : GGTGTGGCGTTCATGAACAAGTGAGATCATATGAATGGATGGATACCCCGCAACCTATAC : 720
LpMDHf2 : ------------------------------------------------------------ :   -

                    *        740         *        760         *        780
LpMDHf1 : ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCTCCTATATACCTGTAAAAT : 780
LpMDHf2 : ------------------------------------------------------------ :   -

                    *
LpMDHf1 : CTCTCCTGCCTGTAAGAA : 798
LpMDHf2 : ------------------ :   -
```

FIGURE 25 (cont.)

```
                             *        20         *        40         *        60
LpMDHg : CAATTGCACGTTCTTGCTCACTTCAGCATCACCCTCACGCTTCTCCTACACAACCCCTCC :  60

                             *        80         *       100         *       120
LpMDHg : CAACCGTCACTATGGTCAAGGCTGTCGTCGCAGGTGCTGCTGGTGGTATCGGCCAGCCCC : 120

                             *       140         *       160         *       180
LpMDHg : TCTCTCTTCTACTCAAGACGAGCCCCCTCATCGATGAGCTTGCCCTCTACGATGTTGTCA : 180

                             *       200         *       220         *       240
LpMDHg : ACACTCCCGGTGTTGCCGCTGATCTTTCCCACATCTCATCCCGCGCTCAAATCGCCGGCT : 240

                             *       260         *       280         *       300
LpMDHg : ACCTCCCCAAGGATGATGGCGCAAAGGCTGCATTCAAAGATGCCGACATTATCGTCATCC : 300

                             *       320         *       340         *       360
LpMDHg : CCGCCGGCATTCCTCGCAAGCCTGGCATGACCCGTGATGACCTCTTCAACATCAACGCCG : 360

                             *       380         *       400         *       420
LpMDHg : GAATTGTCAAGGGTCTGATTGAGGTTGCCGCCGAAGTTGCCCCCAAGGCCTTCATTCTGG : 420

                             *       440         *       460         *       480
LpMDHg : TCATCTCCAACCCTGTCAACTCTACCGTCCCTATCTCTGCCGAGGTCCTCAAGGCCAAGG : 480

                             *       500         *       520         *       540
LpMDHg : GCGTCTTCAACCCTCAGCGTCTTTTCGGTGTCACCACCCTCGACATCGTCCGTGCCGAGA : 540

                             *       560         *       580         *       600
LpMDHg : CTTTCGTCGCCAGCATCACCGGCGAGAAGCAGCCCCAGAACTTGACCGTCCCCGTCATTG : 600

                             *       620         *       640         *       660
LpMDHg : GCGGCCACTCCGGCGAGACCATCGTCCCGCTTTTCAGCAAGGNTCAGCCCTCTGCTTNCA : 660

LpMDHg : TTCCCGC : 667
```

FIGURE 26

```
                    *        20         *        40         *        60
LpMDHg : IARSCSLQHHPHASPTQPLPTVTMVKAVVAGAAGGIGQPLSLLLKTSPLIDELALYDVVN :  60

                    *        80         *       100         *       120
LpMDHg : TPGVAADLSHISSRAQIAGYLPKDDGAKAAFKDADIIVIPAGIPRKPGMTRDDLFNINAG : 120

                    *       140         *       160         *       180
LpMDHg : IVKGLIEVAAEVAPKAFILVISNPVNSTVPISAEVLKAKGVFNPQRLFGVTTLDIVRAET : 180

                    *       200         *       220
LpMDHg : FVASITGEKQPQNLTVPVIGGHSGETIVPLFSKXQPSAXIP : 221
```

FIGURE 27

```
                            *        20         *        40         *        60
LpMDHh : TNACGGAGCTGCTTAAATCAGCCCCCATTCCGCCTCGTCTATAGCGATCCTTCATCCCGT :  60

                            *        80         *       100         *       120
LpMDHh : TGTCGTCGCCTCCTCCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGCTCCAATG : 120

                            *       140         *       160         *       180
LpMDHh : GCGGCGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCT : 180

                            *       200         *       220         *       240
LpMDHh : CTTGTTCCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCAT : 240

                            *       260         *       280         *       300
LpMDHh : ATGCTGGATATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGAT : 300

                            *       320         *       340         *       360
LpMDHh : GCCGCATTTCCACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACT : 360

                            *       380         *       400         *       420
LpMDHh : GGTGTGAATGTTGCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAG : 420

                            *       440         *       460         *       480
LpMDHh : GATGTTATGTCTAAGAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCAT : 480

                            *       500         *       520         *       540
LpMDHh : GCAGCCCCGAATTGCAAGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATC : 540

                            *       560         *       580         *       600
LpMDHh : TTAAAGGAGTTTGCTCCATCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGAC : 600

                            *       620         *       640         *       660
LpMDHh : CATAACAGGGCACTTGGTCAGATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAG : 660

                            *       680         *       700         *       720
LpMDHh : AATGTTATCATCTGGGGCAATCACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACC : 720

                            *       740         *       760         *       780
LpMDHh : GTGAAGACTTCCAGTGGCGAGAAGCCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTA : 780

                            *       800         *       820         *       840
LpMDHh : AATGCAGGGTTCATTGCCACTGTCCAGCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAG : 840
```

FIGURE 28

```
                  *       860        *       880        *       900
LpMDHh : CTCTCCAGTGCTCTCTCTGCTGCCAGCTCTGCTTGTGACCACATCCGTGATTGGGTTCTC :  900

                  *       920        *       940        *       960
LpMDHh : GGAACCCCTGAGGGAACATTTGTTTCCATGGGTGTGTATTCTGATGGTTCATACGGTGTG :  960

                  *       980        *      1000        *      1020
LpMDHh : CCTGCTGGGCTTATCTACTCCTTCCCAGTAACTTGCTGCGGTGGTGAATGGACAATTGTT : 1020

                  *      1040        *      1060        *      1080
LpMDHh : CAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGAAGATGGATGCCACAGCCCAGGAGCTC : 1080

                  *      1100        *      1120        *      1140
LpMDHh : TCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAGTAACTGCATACCAGGGAGCAGCTG : 1140

                  *      1160        *      1180        *      1200
LpMDHh : CCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTCCATGAAACTCATCTCCACTCAG : 1200

                  *      1220        *      1240        *      1260
LpMDHh : AACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAGTGTGTATGAATGAGGCTTTT : 1260

                  *      1280        *      1300        *      1320
LpMDHh : GTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTGGCAGGAAGATTGGAACAA : 1320

                  *      1340        *      1360        *      1380
LpMDHh : TTTGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTATGAATGAGGCTTTTGT : 1380

                  *      1400        *      1420        *      1440
LpMDHh : AGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGGAGGATTGGAACAATT : 1440

                  *      1460        *      1480
LpMDHh : TGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAAAAAA :  1484
```

FIGURE 28 (cont.)

```
                   *        20         *        40         *        60
LpMDHh : MAAKEPMRVLVTGAAGQIGYALVPMIARGIMLGADQPVILHMLDIPPAAEALNGVKMELV :  60

                   *        80         *       100         *       120
LpMDHh : DAAFPLLKGVVATTDVVEACTGVNVAVMVGGFPRKEGMERKDVMSKNVSIYKSQASALEA : 120

                   *       140         *       160         *       180
LpMDHh : HAAPNCKVLVVANPANTNALILKEFAPSIPEKNISCLTRLDHNRALGQISERLDVQVSDV : 180

                   *       200         *       220         *       240
LpMDHh : KNVIIWGNHSSSQYPDVNHATVKTSSGEKPVRELVKDDEWLNAGFIATVQQRGAAIIKAR : 240

                   *       260         *       280         *       300
LpMDHh : KLSSALSAASSACDHIRDWVLGTPEGTFVSMGVYSDGSYGVPAGLIYSFPVTCCGGEWTI : 300

                   *       320         *
LpMDHh : VQGLPIDEFSRKKMDATAQELSEEKALAYSCLE : 333
```

FIGURE 29

```
                        *        20         *        40         *        60
LpMDHh1  : TNACGGAGCTGCTTAAATCAGCCCCCATTCCGCCTCGTCT-C-ACTATCCTTCATCCCGTTG : 60
LpMDHh2  : -----------------------------CCGNTTTACCTGT-NCNAN-CG-CGTGNCGTT- : 29
LpMDHh3  : ------------------------------------GNGTAT-CCTNTGNTACA-CGNTGTN : 24
LpMDHh4  : --------------------------------------GTTTACCGTTNCTAC--CNNTGTN : 22
LpMDHh5  : ------------------------------------------NNNTACCTTNCTNCCCGTTG : 20
LpMDHh6  : -------------------------------------------GNNTNCCTTNGTCCCGTTG : 19
LpMDHh7  : -------------------------------------------GCTTT-CTTTATCCCGTTG : 18
LpMDHh8  : -------------------------------------------GCTATCCTTCATCCCGTTG : 19
LpMDHh9  : -------------------------------------------GCTATCCTTCATCCCGTTG : 19
LpMDHh10 : --------------------------------------------NTACCTTNCTNCCCGTTG : 18
LpMDHh11 : --------------------------------------------GNNTNCTTNCTCCCCGTG : 18
LpMDHh12 : --------------------------------------------CTATCCTT-ATCCCGTTG : 17
LpMDHh13 : ---------------------------------------------GATCCTT-ATCCCGTTG : 16
LpMDHh14 : ---------------------------------------------GNNACCTTGTCCCGTTG : 17
LpMDHh15 : ---------------------------------------------GATCCTTCATCCCGTTG : 17
LpMDHh16 : ---------------------------------------------GNTCCTTCATCCCGTTG : 17
LpMDHh17 : ---------------------------------------------GATCCTT-ATCCCGTTG : 16
LpMDHh18 : ---------------------------------------------GNTCCNTCATCCCGTTG : 17
LpMDHh19 : ---------------------------------------------GNNCCTTCATCCCGTTG : 17
LpMDHh20 : ---------------------------------------------GTTCCTT-NTCCCGTTG : 16
LpMDHh21 : ---------------------------------------------GNTCCTTCATCCCGTTG : 17
LpMDHh22 : ---------------------------------------------GATCCTTCATCCCGTTG : 17
LpMDHh23 : ----------------------------------------------GNCCTTNATCCCNTTG : 16
LpMDHh24 : ----------------------------------------------GNTCNTNATCCCGTTG : 16
LpMDHh25 : ----------------------------------------------TTCCTTNGTCCCGTTG : 16
LpMDHh26 : -----------------------------------------------TCCTTNATCCCGTTG : 15
LpMDHh27 : -----------------------------------------------ACCTTCTNCCCGTTG : 15
LpMDHh28 : -----------------------------------------------TCCTT-NTCCCGTTG : 14
LpMDHh29 : -----------------------------------------------TCCTT-ATCCCGTTG : 14
LpMDHh30 : -----------------------------------------------TCCTTCNTCCCGTTG : 15
LpMDHh31 : ------------------------------------------------CCTTCATCCCGTTG : 14
LpMDHh32 : ------------------------------------------------NCCTNNTCCCNTTG : 14
LpMDHh34 : ------------------------------------------------NCGTNATCCCGTTG : 14
LpMDHh35 : -------------------------------------------------CTTNGTCCCGTTG : 13
LpMDHh36 : -------------------------------------------------NTNCTNCCGNGTG : 13
LpMDHh37 : -------------------------------------------------NTNCTNCCCCNNG : 13
LpMDHh38 : -------------------------------------------------NTTCATCCCGTTG : 13
LpMDHh39 : --------------------------------------------------TTCATCCCNTTG : 12
LpMDHh40 : --------------------------------------------------TTGATCCCGTTG : 12
LpMDHh41 : --------------------------------------------------NTTATCCCGGTG : 12
LpMDHh42 : --------------------------------------------------NTTATCCCGTTG : 12
LpMDHh43 : --------------------------------------------------GTCNTCCCGTTG : 12
LpMDHh44 : --------------------------------------------------TT-NTCCCGTTG : 11
LpMDHh45 : ---------------------------------------------------TTGTCCCGTTG : 11
LpMDHh46 : ---------------------------------------------------TTGTCCCGTTG : 11
LpMDHh47 : ------------------------------------------------------TCCCGTTG : 8
LpMDHh48 : --------------------------------------------------------CG-TTG : 5
LpMDHh49 : --------------------------------------------------------CCGTTG : 6
LpMDHh50 : -------------------------------------------------------------- : -
LpMDHh51 : -------------------------------------------------------------- : -
LpMDHh52 : -------------------------------------------------------------- : -
LpMDHh53 : -------------------------------------------------------------- : -
LpMDHh54 : -------------------------------------------------------------- : -
LpMDHh55 : -------------------------------------------------------------- : -
LpMDHh56 : -------------------------------------------------------------- : -
LpMDHh57 : -------------------------------------------------------------- : -
LpMDHh58 : -------------------------------------------------------------- : -
LpMDHh59 : -------------------------------------------------------------- : -
LpMDHh60 : -------------------------------------------------------------- : -
LpMDHh61 : -------------------------------------------------------------- : -
LpMDHh62 : -------------------------------------------------------------- : -
LpMDHh63 : -------------------------------------------------------------- : -
LpMDHh64 : -------------------------------------------------------------- : -
```

FIGURE 30

```
                        *        80         *        100         *        120
LpMDHh1  : TCGTCGCCTCCTCCCGAACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG : 122
LpMDHh2  : T-G-CTNCTGCGCGN-AACCACTCTCCCANCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  88
LpMDHh3  : GGTTCGCCTCCTCCCGAGCCACTCTCCCATCCCCCAACTCCAGAACCGGCTCCAATGGCGG :  86
LpMDHh4  : GGTTCGCCTCCTCCCG-AAAACNCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  83
LpMDHh5  : TCGTCGCCTCCTCCCGAACCACTCTNCCCNNCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  82
LpMDHh6  : TCGTCGCCTCCTCCCGANCCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  80
LpMDHh7  : TCG-CTNCTCCTCCC-GACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh8  : TCGTCGCCTCCTCCCGAACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  81
LpMDHh9  : TCGTCGCCTCCTCCCGAACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  81
LpMDHh10 : TCGTCGCCTCCTCCCGAACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  79
LpMDHh11 : TCGTCACCTCCTCCCGAACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  80
LpMDHh12 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh13 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh14 : TCGTCGCCTCCTCCCGNACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh15 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh16 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh17 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh18 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh19 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh20 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh21 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh22 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  78
LpMDHh23 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh24 : TCGTCGNCTNCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh25 : TCGTCGCCTCCTCCCGAACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh26 : TCGTCGCCTCCTCCCGAACC-CTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  76
LpMDHh27 : TCGTCGCCTCCTCCCGAACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  77
LpMDHh28 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh29 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh30 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  76
LpMDHh31 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh32 : TCGTCGCCTCCTCCCGAACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  76
LpMDHh34 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAAGGGCGG :  75
LpMDHh35 : TCGTCGCCTCCTCCCGAACCACTCTCCCTNCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh36 : TCGTCGCCTCCTCCCGAACCACTCTCCCTNCCCCGAACTCCA-AACCGGCTCCAATGGCGG :  74
LpMDHh37 : TCGTCGCCTCCTCCCGAACCACTCTCCCNNCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  75
LpMDHh38 : TCGTCGCCTCCTCCCG-AACNCTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  74
LpMDHh39 : TCGTNGCCTNCTCCCGAACCACTCTCCCNTCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  74
LpMDHh40 : TCGTCGCCTCCTCCCG-AACCCTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  73
LpMDHh41 : TCGTCGCCTCCTCCCGAACN-CTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  73
LpMDHh42 : TCGTCGCCTCCTCCCGAACC-CTCTCCCATCCCCGAACTCC-GAACCGGCTCCAATGGCGG :  72
LpMDHh43 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  73
LpMDHh44 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  72
LpMDHh45 : TCGTCGCCTCCTCCCG-ACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  71
LpMDHh46 : TCGTCGCCTCCTCCCGAACCACTCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  72
LpMDHh47 : TCGTCGCCTCCTCCCG-ACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  69
LpMDHh48 : TCGTCGCCTCCTCCCG-ACCCTNCTCCCC-TCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  65
LpMDHh49 : TCGTCGCCTCCTCCCGAACCACTCTCCCATCCCCGAACTCCAGAACCGGCTCCAATGGCGG :  68
LpMDHh50 : ---------------GGACC-CTCTCCCATCCCCGAACTCCAGNACCGGCTCCAATGGCGG :  46
LpMDHh51 : -----------------------------NCCCCGNANTCCA-NACCGGCTCCAA-GGCGG :  30
LpMDHh52 : ------------------------------------------------------------- :   -
LpMDHh53 : ------------------------------------------------------------- :   -
LpMDHh54 : ------------------------------------------------------------- :   -
LpMDHh55 : ------------------------------------------------------------- :   -
LpMDHh56 : ------------------------------------------------------------- :   -
LpMDHh57 : ------------------------------------------------------------- :   -
LpMDHh58 : ------------------------------------------------------------- :   -
LpMDHh59 : ------------------------------------------------------------- :   -
LpMDHh60 : ------------------------------------------------------------- :   -
LpMDHh61 : ------------------------------------------------------------- :   -
LpMDHh62 : ------------------------------------------------------------- :   -
LpMDHh63 : ------------------------------------------------------------- :   -
LpMDHh64 : ------------------------------------------------------------- :   -
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FIGURE 30 (cont)

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                        *       140         *       160         *       180
LpMDHh1  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 184
LpMDHh2  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGNAGGACAAATTGGATATGCTCTTGTT : 150
LpMDHh3  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 148
LpMDHh4  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 145
LpMDHh5  : CGAAGNAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 144
LpMDHh6  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 142
LpMDHh7  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh8  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 143
LpMDHh9  : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 143
LpMDHh10 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 141
LpMDHh11 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 142
LpMDHh12 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh13 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh14 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh15 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh16 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh17 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh18 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh19 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh20 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh21 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh22 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 140
LpMDHh23 : CCAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh24 : NGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh25 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh26 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138
LpMDHh27 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 139
LpMDHh28 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh29 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh30 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 138
LpMDHh31 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh32 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACANATTGGATATGCTCTTGTT : 138
LpMDHh34 : CNAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh35 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh36 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136
LpMDHh37 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 137
LpMDHh38 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136
LpMDHh39 : CGAAGGAACCGATGCGCGTGCTCNTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 136
LpMDHh40 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135
LpMDHh41 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135
LpMDHh42 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134
LpMDHh43 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 135
LpMDHh44 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134
LpMDHh45 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 133
LpMDHh46 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 134
LpMDHh47 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 131
LpMDHh48 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 127
LpMDHh49 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 130
LpMDHh50 : CGAAGGAACCGATGCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT : 108
LpMDHh51 : CGAAGNAACCGA-GCGCGTGCTCGTCACCGGCGCCGCAGGACAAATTGGATATGCTCTTGTT :  91
LpMDHh52 : -----GGACCGATGCCCGTGCTCGTCACCGGCGCCGCAGGNCAAATTGGATATGCTCTTGTT :  57
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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FIGURE 30 (cont.)

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                         *       200         *       220         *       240
LpMDHh1  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 246
LpMDHh2  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 212
LpMDHh3  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 210
LpMDHh4  : CCGATGATTGCTAGGCNAATTATGCTTGGNGTGCACTAGCCTGTTATTNTGCATATC----- : 202
LpMDHh5  : CCGATGATTGCTAGGGGAATTATGCTTGGTGTGGACCAGCCTGTTATTCTGCATATGCTGGA : 206
LpMDHh6  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 204
LpMDHh7  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh8  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 205
LpMDHh9  : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 205
LpMDHh10 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 203
LpMDHh11 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 204
LpMDHh12 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh13 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh14 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh15 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh16 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh17 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh18 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh19 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh20 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh21 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh22 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 202
LpMDHh23 : CCGATGATTGCTANGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh24 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh25 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh26 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 200
LpMDHh27 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 201
LpMDHh28 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh29 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh30 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 200
LpMDHh31 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh32 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 200
LpMDHh34 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh35 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh36 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 198
LpMDHh37 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 199
LpMDHh38 : CCGATGATTGCTAGGGGAATTATGCTGGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 198
LpMDHh39 : CCGATGATTGCTANGGGAATTATGCTTGGTGCGGACCANCCTGTTATTCTGCATATGCTGGA : 198
LpMDHh40 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCAGGA : 197
LpMDHh41 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCGGTTATTCTGCATATGCTGGA : 197
LpMDHh42 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 196
LpMDHh43 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 197
LpMDHh44 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 196
LpMDHh45 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 195
LpMDHh46 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 196
LpMDHh47 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 193
LpMDHh48 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 189
LpMDHh49 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 192
LpMDHh50 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 170
LpMDHh51 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 153
LpMDHh52 : CCGATGATTGCTAGGGGAATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCATATGCTGGA : 119
LpMDHh53 : --------------------TATGCTTGGTGCGG-CCAGCCTGTTATTCTGCATATGCTGGA :  41
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

48/241

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                 *       260         *       280         *       300         *
LpMDHh1  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 308
LpMDHh2  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGNATTTN : 274
LpMDHh3  : TATTGCACCAGCTGCTGAAGCTCTTAATGGCGTTAACATGGAAGTGNNT-NGGCGGCNTAGN : 271
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 268
LpMDHh6  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 266
LpMDHh7  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh8  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 267
LpMDHh9  : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 267
LpMDHh10 : TATTCCACCAGCGGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 265
LpMDHh11 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 266
LpMDHh12 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh13 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh14 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh15 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh16 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh17 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh18 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh19 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh20 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh21 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh22 : TATTCCACCAGCTGCTGAANCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 264
LpMDHh23 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCNCATTTC : 263
LpMDHh24 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh25 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh26 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 262
LpMDHh27 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 263
LpMDHh28 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh29 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh30 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 262
LpMDHh31 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh32 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 262
LpMDHh34 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh35 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh36 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 260
LpMDHh37 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 261
LpMDHh38 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 260
LpMDHh39 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 260
LpMDHh40 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGNTGATGCCGCATTTC : 259
LpMDHh41 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 259
LpMDHh42 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 258
LpMDHh43 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 259
LpMDHh44 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 258
LpMDHh45 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 257
LpMDHh46 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 258
LpMDHh47 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 255
LpMDHh48 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 251
LpMDHh49 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 254
LpMDHh50 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 232
LpMDHh51 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 215
LpMDHh52 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 181
LpMDHh53 : TATTCCACCAGCTGCTGAAGCTCTTAATGGTGTTAAGATGGAGTTGGTTGATGCCGCATTTC : 103
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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FIGURE 30 (cont.)

```
                     320         *        340         *        360         *
LpMDHh1  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 370
LpMDHh2  : CACTTTTNAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGNGNGAATGT- : 335
LpMDHh3  : NCTTTNTCGCN--------------------------------------------------- : 282
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 330
LpMDHh6  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 328
LpMDHh7  : CACTTCTCAAGGGAGTTGTTGCAACAACTGACGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh8  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 329
LpMDHh9  : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 329
LpMDHh10 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 327
LpMDHh11 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 328
LpMDHh12 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh13 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh14 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh15 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh16 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh17 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh18 : CACTTCTCAAGGGAGTTGTTGCGACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh19 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh20 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh21 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh22 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 326
LpMDHh23 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTNAGGCTTGCACTGG---------- : 315
LpMDHh24 : CACTTNTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh25 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh26 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 324
LpMDHh27 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 325
LpMDHh28 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh29 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh30 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 324
LpMDHh31 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh32 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 324
LpMDHh34 : CACTTCTCAAGGGAGTTGTTGCAACGACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh35 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 323
LpMDHh36 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322
LpMDHh37 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGCT : 323
LpMDHh38 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 322
LpMDHh39 : CACTTCTCAAGGGAGNTGNTGCAACAACTGATGTTGNTGAGGCTNGCACTGGTGTGAATGTT : 322
LpMDHh40 : CACTTNTCAAGGGAGTTGNTGCAACAACTGATGTNGTTGANGCTTGCACTGGNGTGAATGTT : 321
LpMDHh41 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321
LpMDHh42 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320
LpMDHh43 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 321
LpMDHh44 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320
LpMDHh45 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 319
LpMDHh46 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 320
LpMDHh47 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 317
LpMDHh48 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 313
LpMDHh49 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 316
LpMDHh50 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 294
LpMDHh51 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 277
LpMDHh52 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 243
LpMDHh53 : CACTTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACTGGTGTGAATGTT : 165
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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FIGURE 30 (cont.)

50/241

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                  380       *       400       *       420       *
LpMDHh1  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 432
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 392
LpMDHh6  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 390
LpMDHh7  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh8  : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 391
LpMDHh9  : GCGTTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 391
LpMDHh10 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 389
LpMDHh11 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 390
LpMDHh12 : GCGTTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh13 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh14 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh15 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh16 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh17 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh18 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh19 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh20 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh21 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh22 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 388
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh25 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh26 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 386
LpMDHh27 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 387
LpMDHh28 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh29 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh30 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 386
LpMDHh31 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh32 : GCGGTTATGGNTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 386
LpMDHh34 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh35 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh36 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 384
LpMDHh37 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 385
LpMDHh38 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 384
LpMDHh39 : GCGGTTATGGATGGTGGAT------------------------------------------- : 341
LpMDHh40 : GCGGNNNTGNCNNGCCCANGTAANATNN---------------------------------- : 349
LpMDHh41 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 383
LpMDHh42 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 382
LpMDHh43 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 383
LpMDHh44 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 382
LpMDHh45 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 381
LpMDHh46 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 382
LpMDHh47 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 379
LpMDHh48 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 375
LpMDHh49 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 378
LpMDHh50 : GCGGTTATGGTTGGTGGATCCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 356
LpMDHh51 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 339
LpMDHh52 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA : 305
LpMDHh53 : GCGGTTATGGTTGGTGGATTCCCCAGGAAGGAGGGAGTGGAAAGGAAGGATGTTATGTCTAA : 227
LpMDHh54 : ------TNGGTTGGTGGATTCCCCAGGAAGGAGGGAATGGAAAGGAAGGATGTTATGTCTAA :  56
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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FIGURE 30 (cont.)

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                 440         *        460         *        480         *
LpMDHh1  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 494
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 454
LpMDHh6  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 452
LpMDHh7  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCNAATTGCA : 450
LpMDHh8  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 453
LpMDHh9  : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 453
LpMDHh10 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 451
LpMDHh11 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 452
LpMDHh12 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh13 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh14 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh15 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh16 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh17 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh18 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh19 : GAATGTTTCAATCTACAAATCTCAAGCATCCGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh20 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh21 : GAATGTTTCAATCTACAAATCTCAAGCATCCGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh22 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 450
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh25 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh26 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 448
LpMDHh27 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 449
LpMDHh28 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh29 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh30 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 448
LpMDHh31 : NAATGTTTCAATCTACAAATCTTAAGCATCTGCCCTTGAAGCCCATGCA-CCCCNAATTGCA : 446
LpMDHh32 : NAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 448
LpMDHh34 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh35 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh36 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 446
LpMDHh37 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 447
LpMDHh38 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAG-CCATGCAGCCCCGAATTGCA : 445
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 445
LpMDHh42 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 444
LpMDHh43 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 445
LpMDHh44 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 444
LpMDHh45 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 443
LpMDHh46 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 444
LpMDHh47 : AAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 441
LpMDHh48 : GAATGTTTCAATCTACAAATCTCAAGTATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 437
LpMDHh49 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 440
LpMDHh50 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 418
LpMDHh51 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGNA : 401
LpMDHh52 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 367
LpMDHh53 : GAATGTTTCAATCTACAAATCTCAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 289
LpMDHh54 : GAATGTTTCAATCTACAAATCTCAAGNGNNTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA : 118
LpMDHh55 : ----------------------TAAGCATCTGCCCTTGAAGCCCATGCAGCCCCGAATTGCA :  40
LpMDHh56 : -----------------------------------------CCATGCAA-CCCCGNANTGCA :  20
LpMDHh57 : ---------------------------------------------TGCAGCCCCG-ATTGCA :  16
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
               500         *        520         *        540         *        5
LpMDHh1  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 556
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 516
LpMDHh6  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 514
LpMDHh7  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh8  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 515
LpMDHh9  : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 515
LpMDHh10 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 513
LpMDHh11 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 514
LpMDHh12 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh13 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh14 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh15 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTCGCTCCA : 512
LpMDHh16 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh17 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh18 : AGGTTCTGGTTGTTGCCAATCCAGTAAACACCAATGCTCTTATCGTAAAGGAGTTTGCTCCA : 512
LpMDHh19 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh20 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh21 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTNTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh22 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 512
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATNTTAAAGGAGTTTGCTCCA : 511
LpMDHh25 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh26 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 510
LpMDHh27 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 511
LpMDHh28 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 509
LpMDHh29 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 509
LpMDHh30 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 510
LpMDHh31 : AGGGTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTTTTATTTTAAANGAGTTTGCTCCA : 508
LpMDHh32 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCANTGCTCTTATCTTAAAGGAGTTTGCTCCA : 510
LpMDHh34 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 509
LpMDHh35 : AGGTTCTGGTTGTTGCCAATCCA--------------------------------------- : 470
LpMDHh36 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 508
LpMDHh37 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 509
LpMDHh38 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 507
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGNTTGCTCCA : 507
LpMDHh42 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 506
LpMDHh43 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 507
LpMDHh44 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 506
LpMDHh45 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 505
LpMDHh46 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 506
LpMDHh47 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTTTTATCTTAAAGGAGTTTGCTCCA : 503
LpMDHh48 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 499
LpMDHh49 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 502
LpMDHh50 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 480
LpMDHh51 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 463
LpMDHh52 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 429
LpMDHh53 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 351
LpMDHh54 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 180
LpMDHh55 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA : 102
LpMDHh56 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA :  82
LpMDHh57 : AGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATCTTAAAGGAGTTTGCTCCA :  78
LpMDHh58 : -------------------------------------------------------------- :   -
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
             60        *       580        *       600        *       620
LpMDHh1  : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 618
LpMDHh2  : ------------------------------------------------------------- :   -
LpMDHh3  : ------------------------------------------------------------- :   -
LpMDHh4  : ------------------------------------------------------------- :   -
LpMDHh5  : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 578
LpMDHh6  : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 576
LpMDHh7  : TCTATTCCTGANAAGAACATNAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTNGGTCA : 574
LpMDHh8  : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 577
LpMDHh9  : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 577
LpMDHh10 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 575
LpMDHh11 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 576
LpMDHh12 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 574
LpMDHh13 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGC---------- : 563
LpMDHh14 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 574
LpMDHh15 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 574
LpMDHh16 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 574
LpMDHh17 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 573
LpMDHh18 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 574
LpMDHh19 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 574
LpMDHh20 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 573
LpMDHh21 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 574
LpMDHh22 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 574
LpMDHh23 : ------------------------------------------------------------- :   -
LpMDHh24 : TCTNTTCCTGAGAA----------------------------------------------- : 525
LpMDHh25 : TCTATTCCTGAGAAGAACATCAGATGTTTGACCCGNCTAGACCATAACAGGGCACTCGGTCA : 573
LpMDHh26 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 572
LpMDHh27 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 573
LpMDHh28 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 571
LpMDHh29 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 571
LpMDHh30 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 572
LpMDHh31 : TNTATTCCTGANAAGAACATNANTTGTTTGACCCGCCTAGACCATAACANGGNNCTTGNCAA : 570
LpMDHh32 : TCTATCCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 572
LpMDHh34 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 571
LpMDHh35 : ------------------------------------------------------------- :   -
LpMDHh36 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 570
LpMDHh37 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGNCTAGACCATAACAGGGCACTCGGNCA : 571
LpMDHh38 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 569
LpMDHh39 : ------------------------------------------------------------- :   -
LpMDHh40 : ------------------------------------------------------------- :   -
LpMDHh41 : TCTATTCCTGAGAANAACATCAGNTGTTTGACCCGCCTAGACCATAACAGGNCACTCGGNCA : 569
LpMDHh42 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 568
LpMDHh43 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 569
LpMDHh44 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 568
LpMDHh45 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 567
LpMDHh46 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 568
LpMDHh47 : TCTATTCCTGANAAGAACATNANTTGTTTGACCCGCCTANACCATAACAGGGCACTTGGTCA : 565
LpMDHh48 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 561
LpMDHh49 : TCTATTCCTGAGAAGAACATCAGTTATTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 564
LpMDHh50 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 542
LpMDHh51 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 525
LpMDHh52 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 491
LpMDHh53 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 413
LpMDHh54 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTNA : 242
LpMDHh55 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTCGGTCA : 164
LpMDHh56 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 144
LpMDHh57 : TCTATTCCTGAGAAGAACATCAGTTGTTTGACCCGCCTAGACCATAACAGGGCACTTGGTCA : 140
LpMDHh58 : ------------------------------------------------------------- :   -
LpMDHh59 : ------------------------------------------------------------- :   -
LpMDHh60 : ------------------------------------------------------------- :   -
LpMDHh61 : ------------------------------------------------------------- :   -
LpMDHh62 : ------------------------------------------------------------- :   -
LpMDHh63 : ------------------------------------------------------------- :   -
LpMDHh64 : ------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
                     *       640         *       660         *       680
LpMDHh1  : GATCTCTGAGAGACTTGATGNCCAAGTTAGTGATGTGAANAATGTTATCATCTGGGGCAATC : 680
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : GATCTCTGAGAGACTTGATGGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 640
LpMDHh6  : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 638
LpMDHh7  : GATCTCTGAGAGACTTNATGTCCAANTTAGTGATGTGAANAATGTTATCATCTGGGGTAATC : 636
LpMDHh8  : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 639
LpMDHh9  : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 639
LpMDHh10 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 637
LpMDHh11 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 638
LpMDHh12 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 636
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC : 636
LpMDHh15 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 636
LpMDHh16 : GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC : 636
LpMDHh17 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 635
LpMDHh18 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC : 636
LpMDHh19 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 636
LpMDHh20 : GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC : 635
LpMDHh21 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 636
LpMDHh22 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 636
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : GATCTCTGAGAGACTTGATGTGCAAGTTANCGATGTGAANAATGCTATCATCTGGGGANATC : 635
LpMDHh26 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAAAATGTTATCATCTGGGGCAATC : 634
LpMDHh27 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC : 635
LpMDHh28 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 633
LpMDHh29 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 633
LpMDHh30 : GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC : 634
LpMDHh31 : AATCTTTNANAGACTTGNTNTCAAN------------------------------------- : 595
LpMDHh32 : GATCTCTGAGAGACTTGATGTCCAAGTTAGNGATGNGAANAATGTTATCATCTGGGGCAATC : 634
LpMDHh34 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 633
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : GATCTCTGANAGACTTGATGTCCAAGTTA--------------------------------- : 599
LpMDHh37 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATG--------------------------- : 606
LpMDHh38 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 631
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : GANCTCTGAGAGACNTGATGCCCAAGNTNGNGNTGN-------------------------- : 605
LpMDHh42 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGCAAATC : 630
LpMDHh43 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 631
LpMDHh44 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 630
LpMDHh45 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC ; 629
LpMDHh46 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC ; 630
LpMDHh47 : GATCTNTGANAGACTTGATGGCCAAGTTAGNGATGTGAAAAATGTTATCATNTGGGGCAATN : 627
LpMDHh48 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 623
LpMDHh49 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 626
LpMDHh50 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 604
LpMDHh51 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC : 587
LpMDHh52 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 553
LpMDHh53 : GATCTCTGAGAGACTTGATGTNCAAGTTAGTGATGTGAANAATGNTATCATCTGGNCANCTC : 475
LpMDHh54 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 304
LpMDHh55 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC : 226
LpMDHh56 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 206
LpMDHh57 : GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC : 202
LpMDHh58 : --------------------------------------------------------GCAATC :   6
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : -------------------------------------------------------------- :   -
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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FIGURE 30 (cont.)

55/241

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                   *       700         *       720         *       740
LpMDHh1  : ACTCTTNCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGCCGAGAAG : 742
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : ACTCTTCCAG---------------------------------------------------- : 650
LpMDHh6  : ACTCTTCCAGTCAGTACCCTGA---------------------------------------- : 660
LpMDHh7  : ACCCTTCCAGTCAATACCCTGATNTGAACCACCCCGCCNNAAANACTTCCAG-GGCGA---- : 693
LpMDHh8  : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 701
LpMDHh9  : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGCGGCGAGAAG : 701
LpMDHh10 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAANACT--------------- : 684
LpMDHh11 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 700
LpMDHh12 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG : 698
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGN------ : 692
LpMDHh15 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh16 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh17 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 697
LpMDHh18 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh19 : ACTCTTNCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh20 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 697
LpMDHh21 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 698
LpMDHh22 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG : 698
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : ACTCTTNCAGNC-ATACCCTGATGTGAACCACGCCACCGNGAACACNTNCACTGCCNACAAG : 696
LpMDHh26 : ACTCTTCCAGTC-------------------------------------------------- : 646
LpMDHh27 : ACTCTTNCAGTCAATACCCTGATGTGAACCACGCCACCGTGAANACTTTCAGTGGCGAGAAG : 697
LpMDHh28 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh29 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh30 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 696
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGNGAAGACTTCCAGTGNCGAGANN : 696
LpMDHh34 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 695
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTTCAGTGG------- : 686
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGG------- : 685
LpMDHh43 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 693
LpMDHh44 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 692
LpMDHh45 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAA- : 690
LpMDHh46 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG : 692
LpMDHh47 : ACTNTTCCAGTCAGTNCCCTGATGTGAACCACNCCGCCGGAAANACTTCCAG---------- : 679
LpMDHh48 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGN--------- : 676
LpMDHh49 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 688
LpMDHh50 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAGGACTTCCAGTGGCGAGAAG : 666
LpMDHh51 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 649
LpMDHh52 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 615
LpMDHh53 : ACTCTTNCANNCNTTNCCCTGATGNNANCCNCGCCNCG------------------------ : 513
LpMDHh54 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 366
LpMDHh55 : ACTCTTCCAGTCAATACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 288
LpMDHh56 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 268
LpMDHh57 : ACTCTTCCAGTCAGTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG : 264
LpMDHh58 : ACTCTTCCAGTCAGTACCCTG-NGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG :  67
LpMDHh59 : -------------GTACCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG :  49
LpMDHh60 : -----------------------------------------------TTCNGTGGCAAG-AG :  14
LpMDHh61 : ------------------------------------------------------GCGAGAAG :   8
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
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FIGURE 30 (cont.)

56/241

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                   *       760         *       780         *       800
LpMDHh1  : CCTGTTCGCGAACTTGTTAAAGACGATG---------------------------------- : 770
LpMDHh2  : -------------------------------------------------------------- :  -
LpMDHh3  : -------------------------------------------------------------- :  -
LpMDHh4  : -------------------------------------------------------------- :  -
LpMDHh5  : -------------------------------------------------------------- :  -
LpMDHh6  : -------------------------------------------------------------- :  -
LpMDHh7  : -------------------------------------------------------------- :  -
LpMDHh8  : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGNTCATTGCCACTGTCCA : 763
LpMDHh9  : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCANGGGTCATTGCCACTGTCCA : 763
LpMDHh10 : -------------------------------------------------------------- :  -
LpMDHh11 : CCTGTTC------------------------------------------------------- : 707
LpMDHh12 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh13 : -------------------------------------------------------------- :  -
LpMDHh14 : -------------------------------------------------------------- :  -
LpMDHh15 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh16 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh17 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 759
LpMDHh18 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh19 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh20 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 759
LpMDHh21 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTNAATGCAGGGTTCATTGCCACTGNCCA : 760
LpMDHh22 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 760
LpMDHh23 : -------------------------------------------------------------- :  -
LpMDHh24 : -------------------------------------------------------------- :  -
LpMDHh25 : -------------------------------------------------------------- :  -
LpMDHh26 : -------------------------------------------------------------- :  -
LpMDHh27 : CCTGTTCGCGAACT------------------------------------------------ : 711
LpMDHh28 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 757
LpMDHh29 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 757
LpMDHh30 : CCTGTTCGCGAACTTGNTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 758
LpMDHh31 : -------------------------------------------------------------- :  -
LpMDHh32 : -------------------------------------------------------------- :  -
LpMDHh34 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 757
LpMDHh35 : -------------------------------------------------------------- :  -
LpMDHh36 : -------------------------------------------------------------- :  -
LpMDHh37 : -------------------------------------------------------------- :  -
LpMDHh38 : -------------------------------------------------------------- :  -
LpMDHh39 : -------------------------------------------------------------- :  -
LpMDHh40 : -------------------------------------------------------------- :  -
LpMDHh41 : -------------------------------------------------------------- :  -
LpMDHh42 : -------------------------------------------------------------- :  -
LpMDHh43 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 755
LpMDHh44 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 754
LpMDHh45 : -------------------------------------------------------------- :  -
LpMDHh46 : CCTGTTCG------------------------------------------------------ : 700
LpMDHh47 : -------------------------------------------------------------- :  -
LpMDHh48 : -------------------------------------------------------------- :  -
LpMDHh49 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 750
LpMDHh50 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 728
LpMDHh51 : CCTGTTCGCGAACTTGTTAAAGACGAT----------------------------------- : 676
LpMDHh52 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 677
LpMDHh53 : -------------------------------------------------------------- :  -
LpMDHh54 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 428
LpMDHh55 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 350
LpMDHh56 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 330
LpMDHh57 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 326
LpMDHh58 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 129
LpMDHh59 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA : 111
LpMDHh60 : CCTGTTCGCG-ACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA :  75
LpMDHh61 : CCTGTTCGCGAACTTGTTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA :  70
LpMDHh62 : -------------------------------------------------------------- :  -
LpMDHh63 : -------------------------------------------------------------- :  -
LpMDHh64 : -------------------------------------------------------------- :  -
```

FIGURE 30 (cont.)

```
                   *       820         *       840         *       860
LpMDHh1  : -------------------------------------------------------------- :   -
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : -------------------------------------------------------------- :   -
LpMDHh6  : -------------------------------------------------------------- :   -
LpMDHh7  : -------------------------------------------------------------- :   -
LpMDHh8  : GCAGCGTGGTGCTGCAATCATCAAAGCGAG-------------------------------- : 793
LpMDHh9  : GCAGCGTGGNGCTGCAATCATCAAAGNGAGGAAC---------------------------- : 797
LpMDHh10 : -------------------------------------------------------------- :   -
LpMDHh11 : -------------------------------------------------------------- :   -
LpMDHh12 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTNCA-------------------- : 801
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : -------------------------------------------------------------- :   -
LpMDHh15 : GCAG---------------------------------------------------------- : 764
LpMDHh16 : GCAGCGTGG----------------------------------------------------- : 769
LpMDHh17 : GCANCGTGGTG--------------------------------------------------- : 770
LpMDHh18 : GCAGCGTGGTGCTGCAATC------------------------------------------- : 779
LpMDHh19 : ACAGCGTGGTGCTGCAATCATCAAAGCG---------------------------------- : 788
LpMDHh20 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGC--------------------------- : 794
LpMDHh21 : GCAGCGTGGTGCTGCNATCATCAAAGCGAGGAAGCTT------------------------- : 797
LpMDHh22 : GCAGCGTGGNGCTGC-ATCATCAAAGCGAGGAAGCTCTTCAGT------------------ : 802
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : -------------------------------------------------------------- :   -
LpMDHh26 : -------------------------------------------------------------- :   -
LpMDHh27 : -------------------------------------------------------------- :   -
LpMDHh28 : GCAGCGTGGTG--------------------------------------------------- : 768
LpMDHh29 : GCAGCGTGGTGCTGCAATCATCAAAG------------------------------------ : 783
LpMDHh30 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTNCAGTGC---------------- : 803
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : -------------------------------------------------------------- :   -
LpMDHh34 : GCAGCGTGGTGCTGCAATCATA---------------------------------------- : 779
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : -------------------------------------------------------------- :   -
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : -------------------------------------------------------------- :   -
LpMDHh43 : GCAGCGTG------------------------------------------------------ : 763
LpMDHh44 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT-------------------------- : 790
LpMDHh45 : -------------------------------------------------------------- :   -
LpMDHh46 : -------------------------------------------------------------- :   -
LpMDHh47 : -------------------------------------------------------------- :   -
LpMDHh48 : -------------------------------------------------------------- :   -
LpMDHh49 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT-------------------------- : 786
LpMDHh50 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTG------------------ : 772
LpMDHh51 : -------------------------------------------------------------- :   -
LpMDHh52 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 739
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTTTCCAGTGCTCTTTTTGCTGCCAGCT : 490
LpMDHh55 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 412
LpMDHh56 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 392
LpMDHh57 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 388
LpMDHh58 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 191
LpMDHh59 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 173
LpMDHh60 : GCAGCGNGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 137
LpMDHh61 : GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTCTGCTGCCAGCT : 132
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
                *      880       *       900       *       920       *
LpMDHh1   : -------------------------------------------------------------- :   -
LpMDHh2   : -------------------------------------------------------------- :   -
LpMDHh3   : -------------------------------------------------------------- :   -
LpMDHh4   : -------------------------------------------------------------- :   -
LpMDHh5   : -------------------------------------------------------------- :   -
LpMDHh6   : -------------------------------------------------------------- :   -
LpMDHh7   : -------------------------------------------------------------- :   -
LpMDHh8   : -------------------------------------------------------------- :   -
LpMDHh9   : -------------------------------------------------------------- :   -
LpMDHh10  : -------------------------------------------------------------- :   -
LpMDHh11  : -------------------------------------------------------------- :   -
LpMDHh12  : -------------------------------------------------------------- :   -
LpMDHh13  : -------------------------------------------------------------- :   -
LpMDHh14  : -------------------------------------------------------------- :   -
LpMDHh15  : -------------------------------------------------------------- :   -
LpMDHh16  : -------------------------------------------------------------- :   -
LpMDHh17  : -------------------------------------------------------------- :   -
LpMDHh18  : -------------------------------------------------------------- :   -
LpMDHh19  : -------------------------------------------------------------- :   -
LpMDHh20  : -------------------------------------------------------------- :   -
LpMDHh21  : -------------------------------------------------------------- :   -
LpMDHh22  : -------------------------------------------------------------- :   -
LpMDHh23  : -------------------------------------------------------------- :   -
LpMDHh24  : -------------------------------------------------------------- :   -
LpMDHh25  : -------------------------------------------------------------- :   -
LpMDHh26  : -------------------------------------------------------------- :   -
LpMDHh27  : -------------------------------------------------------------- :   -
LpMDHh28  : -------------------------------------------------------------- :   -
LpMDHh29  : -------------------------------------------------------------- :   -
LpMDHh30  : -------------------------------------------------------------- :   -
LpMDHh31  : -------------------------------------------------------------- :   -
LpMDHh32  : -------------------------------------------------------------- :   -
LpMDHh34  : -------------------------------------------------------------- :   -
LpMDHh35  : -------------------------------------------------------------- :   -
LpMDHh36  : -------------------------------------------------------------- :   -
LpMDHh37  : -------------------------------------------------------------- :   -
LpMDHh38  : -------------------------------------------------------------- :   -
LpMDHh39  : -------------------------------------------------------------- :   -
LpMDHh40  : -------------------------------------------------------------- :   -
LpMDHh41  : -------------------------------------------------------------- :   -
LpMDHh42  : -------------------------------------------------------------- :   -
LpMDHh43  : -------------------------------------------------------------- :   -
LpMDHh44  : -------------------------------------------------------------- :   -
LpMDHh45  : -------------------------------------------------------------- :   -
LpMDHh46  : -------------------------------------------------------------- :   -
LpMDHh47  : -------------------------------------------------------------- :   -
LpMDHh48  : -------------------------------------------------------------- :   -
LpMDHh49  : -------------------------------------------------------------- :   -
LpMDHh50  : -------------------------------------------------------------- :   -
LpMDHh51  : -------------------------------------------------------------- :   -
LpMDHh52  : CTGCTTGTGACCACATCCGTGATT-------------------------------------- : 763
LpMDHh53  : -------------------------------------------------------------- :   -
LpMDHh54  : CTGCTTGTGACCACATCCGGGATTGGGTTCTCGGAACCCCTGANGGAACATTTGTTTCCATG : 552
LpMDHh55  : CTGCTTGTGACCACATCCGTGATTGGGTTCTTGGAACCCCTGAGGGAACATTTGTTTCCATG : 474
LpMDHh56  : CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG : 454
LpMDHh57  : CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG : 450
LpMDHh58  : CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG : 253
LpMDHh59  : CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG : 235
LpMDHh60  : CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG : 199
LpMDHh61  : CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGGAACATTTGTTTCCATG : 194
LpMDHh62  : -------------------------------------------------------------- :   -
LpMDHh63  : -------------------------------------------------------------- :   -
LpMDHh64  : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
                    940         *       960         *       980         *
LpMDHh1  : -------------------------------------------------------------- :   -
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : -------------------------------------------------------------- :   -
LpMDHh6  : -------------------------------------------------------------- :   -
LpMDHh7  : -------------------------------------------------------------- :   -
LpMDHh8  : -------------------------------------------------------------- :   -
LpMDHh9  : -------------------------------------------------------------- :   -
LpMDHh10 : -------------------------------------------------------------- :   -
LpMDHh11 : -------------------------------------------------------------- :   -
LpMDHh12 : -------------------------------------------------------------- :   -
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : -------------------------------------------------------------- :   -
LpMDHh15 : -------------------------------------------------------------- :   -
LpMDHh16 : -------------------------------------------------------------- :   -
LpMDHh17 : -------------------------------------------------------------- :   -
LpMDHh18 : -------------------------------------------------------------- :   -
LpMDHh19 : -------------------------------------------------------------- :   -
LpMDHh20 : -------------------------------------------------------------- :   -
LpMDHh21 : -------------------------------------------------------------- :   -
LpMDHh22 : -------------------------------------------------------------- :   -
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : -------------------------------------------------------------- :   -
LpMDHh26 : -------------------------------------------------------------- :   -
LpMDHh27 : -------------------------------------------------------------- :   -
LpMDHh28 : -------------------------------------------------------------- :   -
LpMDHh29 : -------------------------------------------------------------- :   -
LpMDHh30 : -------------------------------------------------------------- :   -
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : -------------------------------------------------------------- :   -
LpMDHh34 : -------------------------------------------------------------- :   -
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : -------------------------------------------------------------- :   -
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : -------------------------------------------------------------- :   -
LpMDHh43 : -------------------------------------------------------------- :   -
LpMDHh44 : -------------------------------------------------------------- :   -
LpMDHh45 : -------------------------------------------------------------- :   -
LpMDHh46 : -------------------------------------------------------------- :   -
LpMDHh47 : -------------------------------------------------------------- :   -
LpMDHh48 : -------------------------------------------------------------- :   -
LpMDHh49 : -------------------------------------------------------------- :   -
LpMDHh50 : -------------------------------------------------------------- :   -
LpMDHh51 : -------------------------------------------------------------- :   -
LpMDHh52 : -------------------------------------------------------------- :   -
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : GGTGTGTATTCTGATGGNT-ATACNGGGTGCCTGGTGGGCTTATCTACTCCTTNCCAGNAAC : 613
LpMDHh55 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 536
LpMDHh56 : GNTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 516
LpMDHh57 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 512
LpMDHh58 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 315
LpMDHh59 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 297
LpMDHh60 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 261
LpMDHh61 : GGTGTGTATTCTGATGGTTCATACGGTGTGCCTGCTGGGCTTATCTACTCCTTCCCAGTAAC : 256
LpMDHh62 : -------------------------------------------------------------- :   -
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
                1000         *         1020          *         1040          *
LpMDHh1   : -------------------------------------------------------------- :   -
LpMDHh2   : -------------------------------------------------------------- :   -
LpMDHh3   : -------------------------------------------------------------- :   -
LpMDHh4   : -------------------------------------------------------------- :   -
LpMDHh5   : -------------------------------------------------------------- :   -
LpMDHh6   : -------------------------------------------------------------- :   -
LpMDHh7   : -------------------------------------------------------------- :   -
LpMDHh8   : -------------------------------------------------------------- :   -
LpMDHh9   : -------------------------------------------------------------- :   -
LpMDHh10  : -------------------------------------------------------------- :   -
LpMDHh11  : -------------------------------------------------------------- :   -
LpMDHh12  : -------------------------------------------------------------- :   -
LpMDHh13  : -------------------------------------------------------------- :   -
LpMDHh14  : -------------------------------------------------------------- :   -
LpMDHh15  : -------------------------------------------------------------- :   -
LpMDHh16  : -------------------------------------------------------------- :   -
LpMDHh17  : -------------------------------------------------------------- :   -
LpMDHh18  : -------------------------------------------------------------- :   -
LpMDHh19  : -------------------------------------------------------------- :   -
LpMDHh20  : -------------------------------------------------------------- :   -
LpMDHh21  : -------------------------------------------------------------- :   -
LpMDHh22  : -------------------------------------------------------------- :   -
LpMDHh23  : -------------------------------------------------------------- :   -
LpMDHh24  : -------------------------------------------------------------- :   -
LpMDHh25  : -------------------------------------------------------------- :   -
LpMDHh26  : -------------------------------------------------------------- :   -
LpMDHh27  : -------------------------------------------------------------- :   -
LpMDHh28  : -------------------------------------------------------------- :   -
LpMDHh29  : -------------------------------------------------------------- :   -
LpMDHh30  : -------------------------------------------------------------- :   -
LpMDHh31  : -------------------------------------------------------------- :   -
LpMDHh32  : -------------------------------------------------------------- :   -
LpMDHh34  : -------------------------------------------------------------- :   -
LpMDHh35  : -------------------------------------------------------------- :   -
LpMDHh36  : -------------------------------------------------------------- :   -
LpMDHh37  : -------------------------------------------------------------- :   -
LpMDHh38  : -------------------------------------------------------------- :   -
LpMDHh39  : -------------------------------------------------------------- :   -
LpMDHh40  : -------------------------------------------------------------- :   -
LpMDHh41  : -------------------------------------------------------------- :   -
LpMDHh42  : -------------------------------------------------------------- :   -
LpMDHh43  : -------------------------------------------------------------- :   -
LpMDHh44  : -------------------------------------------------------------- :   -
LpMDHh45  : -------------------------------------------------------------- :   -
LpMDHh46  : -------------------------------------------------------------- :   -
LpMDHh47  : -------------------------------------------------------------- :   -
LpMDHh48  : -------------------------------------------------------------- :   -
LpMDHh49  : -------------------------------------------------------------- :   -
LpMDHh50  : -------------------------------------------------------------- :   -
LpMDHh51  : -------------------------------------------------------------- :   -
LpMDHh52  : -------------------------------------------------------------- :   -
LpMDHh53  : -------------------------------------------------------------- :   -
LpMDHh54  : TTGCTGNGGGGGGGAATGGACAATTGNTCAAAGGCTNCCNATCNACNAGTT----------- : 664
LpMDHh55  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 598
LpMDHh56  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 578
LpMDHh57  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 574
LpMDHh58  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 377
LpMDHh59  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGGTCGACGAGTTCTCAAGAAAGA : 359
LpMDHh60  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 323
LpMDHh61  : TTGCTGCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA : 318
LpMDHh62  : --------------------------------CCTTCCCGAAACCCGAGTTCTC-TTTTAG- :  28
LpMDHh63  : -------------------------------------------------------------- :   -
LpMDHh64  : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
                1060          *         1080          *         1100          *
LpMDHh1   : -------------------------------------------------------------- :   -
LpMDHh2   : -------------------------------------------------------------- :   -
LpMDHh3   : -------------------------------------------------------------- :   -
LpMDHh4   : -------------------------------------------------------------- :   -
LpMDHh5   : -------------------------------------------------------------- :   -
LpMDHh6   : -------------------------------------------------------------- :   -
LpMDHh7   : -------------------------------------------------------------- :   -
LpMDHh8   : -------------------------------------------------------------- :   -
LpMDHh9   : -------------------------------------------------------------- :   -
LpMDHh10  : -------------------------------------------------------------- :   -
LpMDHh11  : -------------------------------------------------------------- :   -
LpMDHh12  : -------------------------------------------------------------- :   -
LpMDHh13  : -------------------------------------------------------------- :   -
LpMDHh14  : -------------------------------------------------------------- :   -
LpMDHh15  : -------------------------------------------------------------- :   -
LpMDHh16  : -------------------------------------------------------------- :   -
LpMDHh17  : -------------------------------------------------------------- :   -
LpMDHh18  : -------------------------------------------------------------- :   -
LpMDHh19  : -------------------------------------------------------------- :   -
LpMDHh20  : -------------------------------------------------------------- :   -
LpMDHh21  : -------------------------------------------------------------- :   -
LpMDHh22  : -------------------------------------------------------------- :   -
LpMDHh23  : -------------------------------------------------------------- :   -
LpMDHh24  : -------------------------------------------------------------- :   -
LpMDHh25  : -------------------------------------------------------------- :   -
LpMDHh26  : -------------------------------------------------------------- :   -
LpMDHh27  : -------------------------------------------------------------- :   -
LpMDHh28  : -------------------------------------------------------------- :   -
LpMDHh29  : -------------------------------------------------------------- :   -
LpMDHh30  : -------------------------------------------------------------- :   -
LpMDHh31  : -------------------------------------------------------------- :   -
LpMDHh32  : -------------------------------------------------------------- :   -
LpMDHh34  : -------------------------------------------------------------- :   -
LpMDHh35  : -------------------------------------------------------------- :   -
LpMDHh36  : -------------------------------------------------------------- :   -
LpMDHh37  : -------------------------------------------------------------- :   -
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LpMDHh39  : -------------------------------------------------------------- :   -
LpMDHh40  : -------------------------------------------------------------- :   -
LpMDHh41  : -------------------------------------------------------------- :   -
LpMDHh42  : -------------------------------------------------------------- :   -
LpMDHh43  : -------------------------------------------------------------- :   -
LpMDHh44  : -------------------------------------------------------------- :   -
LpMDHh45  : -------------------------------------------------------------- :   -
LpMDHh46  : -------------------------------------------------------------- :   -
LpMDHh47  : -------------------------------------------------------------- :   -
LpMDHh48  : -------------------------------------------------------------- :   -
LpMDHh49  : -------------------------------------------------------------- :   -
LpMDHh50  : -------------------------------------------------------------- :   -
LpMDHh51  : -------------------------------------------------------------- :   -
LpMDHh52  : -------------------------------------------------------------- :   -
LpMDHh53  : -------------------------------------------------------------- :   -
LpMDHh54  : -------------------------------------------------------------- :   -
LpMDHh55  : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 660
LpMDHh56  : AGATGGATGCCACAGCCCAGGAGCTCTCGNAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 640
LpMDHh57  : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 636
LpMDHh58  : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 439
LpMDHh59  : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTTGCCTACTCGTGCCTCGAG : 421
LpMDHh60  : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 385
LpMDHh61  : AGATGGATGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG : 380
LpMDHh62  : AGA-GGACGCCACAGCCCAGGAGCTCTCGGAGGAGAAGGTTNTCGCCTACTCGGGCCTCGAG :  89
LpMDHh63  : ------------------------CCTCGGAGGAGAAGGCTCTCGCCTACTCGTGCCTCGAG :  38
LpMDHh64  : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
                  1120         *      1140         *      1160         *      11
LpMDHh1  : -------------------------------------------------------------- :   -
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : -------------------------------------------------------------- :   -
LpMDHh6  : -------------------------------------------------------------- :   -
LpMDHh7  : -------------------------------------------------------------- :   -
LpMDHh8  : -------------------------------------------------------------- :   -
LpMDHh9  : -------------------------------------------------------------- :   -
LpMDHh10 : -------------------------------------------------------------- :   -
LpMDHh11 : -------------------------------------------------------------- :   -
LpMDHh12 : -------------------------------------------------------------- :   -
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : -------------------------------------------------------------- :   -
LpMDHh15 : -------------------------------------------------------------- :   -
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LpMDHh19 : -------------------------------------------------------------- :   -
LpMDHh20 : -------------------------------------------------------------- :   -
LpMDHh21 : -------------------------------------------------------------- :   -
LpMDHh22 : -------------------------------------------------------------- :   -
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : -------------------------------------------------------------- :   -
LpMDHh26 : -------------------------------------------------------------- :   -
LpMDHh27 : -------------------------------------------------------------- :   -
LpMDHh28 : -------------------------------------------------------------- :   -
LpMDHh29 : -------------------------------------------------------------- :   -
LpMDHh30 : -------------------------------------------------------------- :   -
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : -------------------------------------------------------------- :   -
LpMDHh34 : -------------------------------------------------------------- :   -
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : -------------------------------------------------------------- :   -
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : -------------------------------------------------------------- :   -
LpMDHh43 : -------------------------------------------------------------- :   -
LpMDHh44 : -------------------------------------------------------------- :   -
LpMDHh45 : -------------------------------------------------------------- :   -
LpMDHh46 : -------------------------------------------------------------- :   -
LpMDHh47 : -------------------------------------------------------------- :   -
LpMDHh48 : -------------------------------------------------------------- :   -
LpMDHh49 : -------------------------------------------------------------- :   -
LpMDHh50 : -------------------------------------------------------------- :   -
LpMDHh51 : -------------------------------------------------------------- :   -
LpMDHh52 : -------------------------------------------------------------- :   -
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTN : 722
LpMDHh56 : TAACTGCATACCAGGGAGCAGCTGTCGCTCTGATGTTTTGAATAAAA-GNACATTTTGNCTN : 701
LpMDHh57 : TAACTGCATACCAGGGAGCAGCTGCCGCTCT------------------------------- : 667
LpMDHh58 : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 501
LpMDHh59 : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 483
LpMDHh60 : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 447
LpMDHh61 : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 442
LpMDHh62 : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 151
LpMDHh63 : TAACTGCATACCAGGGAGCAGCTGCCGCTCTGATGTTTTGAATAAAAGGAACATTTTGGCTC : 100
LpMDHh64 : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
             80         *        1200         *        1220         *        1240
LpMDHh1   : -------------------------------------------------------------- :   -
LpMDHh2   : -------------------------------------------------------------- :   -
LpMDHh3   : -------------------------------------------------------------- :   -
LpMDHh4   : -------------------------------------------------------------- :   -
LpMDHh5   : -------------------------------------------------------------- :   -
LpMDHh6   : -------------------------------------------------------------- :   -
LpMDHh7   : -------------------------------------------------------------- :   -
LpMDHh8   : -------------------------------------------------------------- :   -
LpMDHh9   : -------------------------------------------------------------- :   -
LpMDHh10  : -------------------------------------------------------------- :   -
LpMDHh11  : -------------------------------------------------------------- :   -
LpMDHh12  : -------------------------------------------------------------- :   -
LpMDHh13  : -------------------------------------------------------------- :   -
LpMDHh14  : -------------------------------------------------------------- :   -
LpMDHh15  : -------------------------------------------------------------- :   -
LpMDHh16  : -------------------------------------------------------------- :   -
LpMDHh17  : -------------------------------------------------------------- :   -
LpMDHh18  : -------------------------------------------------------------- :   -
LpMDHh19  : -------------------------------------------------------------- :   -
LpMDHh20  : -------------------------------------------------------------- :   -
LpMDHh21  : -------------------------------------------------------------- :   -
LpMDHh22  : -------------------------------------------------------------- :   -
LpMDHh23  : -------------------------------------------------------------- :   -
LpMDHh24  : -------------------------------------------------------------- :   -
LpMDHh25  : -------------------------------------------------------------- :   -
LpMDHh26  : -------------------------------------------------------------- :   -
LpMDHh27  : -------------------------------------------------------------- :   -
LpMDHh28  : -------------------------------------------------------------- :   -
LpMDHh29  : -------------------------------------------------------------- :   -
LpMDHh30  : -------------------------------------------------------------- :   -
LpMDHh31  : -------------------------------------------------------------- :   -
LpMDHh32  : -------------------------------------------------------------- :   -
LpMDHh34  : -------------------------------------------------------------- :   -
LpMDHh35  : -------------------------------------------------------------- :   -
LpMDHh36  : -------------------------------------------------------------- :   -
LpMDHh37  : -------------------------------------------------------------- :   -
LpMDHh38  : -------------------------------------------------------------- :   -
LpMDHh39  : -------------------------------------------------------------- :   -
LpMDHh40  : -------------------------------------------------------------- :   -
LpMDHh41  : -------------------------------------------------------------- :   -
LpMDHh42  : -------------------------------------------------------------- :   -
LpMDHh43  : -------------------------------------------------------------- :   -
LpMDHh44  : -------------------------------------------------------------- :   -
LpMDHh45  : -------------------------------------------------------------- :   -
LpMDHh46  : -------------------------------------------------------------- :   -
LpMDHh47  : -------------------------------------------------------------- :   -
LpMDHh48  : -------------------------------------------------------------- :   -
LpMDHh49  : -------------------------------------------------------------- :   -
LpMDHh50  : -------------------------------------------------------------- :   -
LpMDHh51  : -------------------------------------------------------------- :   -
LpMDHh52  : -------------------------------------------------------------- :   -
LpMDHh53  : -------------------------------------------------------------- :   -
LpMDHh54  : -------------------------------------------------------------- :   -
LpMDHh55  : CATGAAACTCAT-------------------------------------------------- : 734
LpMDHh56  : CATG---------------------------------------------------------- : 705
LpMDHh57  : -------------------------------------------------------------- :   -
LpMDHh58  : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG : 563
LpMDHh59  : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG : 545
LpMDHh60  : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTCAGCTGGTTTTTCCAG : 509
LpMDHh61  : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG : 504
LpMDHh62  : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG : 213
LpMDHh63  : CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTTTAGCTGGTTTTTCCAG : 162
LpMDHh64  : -------------------------------------------------------------- :   -
```

FIGURE 30 (cont.)

```
                     *        1260         *        1280         *        1300
LpMDHh1  : -------------------------------------------------------------- :   -
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : -------------------------------------------------------------- :   -
LpMDHh6  : -------------------------------------------------------------- :   -
LpMDHh7  : -------------------------------------------------------------- :   -
LpMDHh8  : -------------------------------------------------------------- :   -
LpMDHh9  : -------------------------------------------------------------- :   -
LpMDHh10 : -------------------------------------------------------------- :   -
LpMDHh11 : -------------------------------------------------------------- :   -
LpMDHh12 : -------------------------------------------------------------- :   -
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : -------------------------------------------------------------- :   -
LpMDHh15 : -------------------------------------------------------------- :   -
LpMDHh16 : -------------------------------------------------------------- :   -
LpMDHh17 : -------------------------------------------------------------- :   -
LpMDHh18 : -------------------------------------------------------------- :   -
LpMDHh19 : -------------------------------------------------------------- :   -
LpMDHh20 : -------------------------------------------------------------- :   -
LpMDHh21 : -------------------------------------------------------------- :   -
LpMDHh22 : -------------------------------------------------------------- :   -
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : -------------------------------------------------------------- :   -
LpMDHh26 : -------------------------------------------------------------- :   -
LpMDHh27 : -------------------------------------------------------------- :   -
LpMDHh28 : -------------------------------------------------------------- :   -
LpMDHh29 : -------------------------------------------------------------- :   -
LpMDHh30 : -------------------------------------------------------------- :   -
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : -------------------------------------------------------------- :   -
LpMDHh34 : -------------------------------------------------------------- :   -
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : -------------------------------------------------------------- :   -
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : -------------------------------------------------------------- :   -
LpMDHh43 : -------------------------------------------------------------- :   -
LpMDHh44 : -------------------------------------------------------------- :   -
LpMDHh45 : -------------------------------------------------------------- :   -
LpMDHh46 : -------------------------------------------------------------- :   -
LpMDHh47 : -------------------------------------------------------------- :   -
LpMDHh48 : -------------------------------------------------------------- :   -
LpMDHh49 : -------------------------------------------------------------- :   -
LpMDHh50 : -------------------------------------------------------------- :   -
LpMDHh51 : -------------------------------------------------------------- :   -
LpMDHh52 : -------------------------------------------------------------- :   -
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 625
LpMDHh59 : TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 607
LpMDHh60 : TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 571
LpMDHh61 : TGTGTATGAATGAGGCTTTTGTAGCGCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 566
LpMDHh62 : TGTGTATGANTGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 275
LpMDHh63 : TGTGTATGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACAGGATATTG : 224
LpMDHh64 : -------GNAAGNAGCTTTTGTAGCTCTATTTTCGCCTGNAGATTTACAGGACAGGATATTG :  55
```

FIGURE 30 (cont.)

```
                       *       1320         *       1340         *       1360
LpMDHh1   : -------------------------------------------------------------- :   -
LpMDHh2   : -------------------------------------------------------------- :   -
LpMDHh3   : -------------------------------------------------------------- :   -
LpMDHh4   : -------------------------------------------------------------- :   -
LpMDHh5   : -------------------------------------------------------------- :   -
LpMDHh6   : -------------------------------------------------------------- :   -
LpMDHh7   : -------------------------------------------------------------- :   -
LpMDHh8   : -------------------------------------------------------------- :   -
LpMDHh9   : -------------------------------------------------------------- :   -
LpMDHh10  : -------------------------------------------------------------- :   -
LpMDHh11  : -------------------------------------------------------------- :   -
LpMDHh12  : -------------------------------------------------------------- :   -
LpMDHh13  : -------------------------------------------------------------- :   -
LpMDHh14  : -------------------------------------------------------------- :   -
LpMDHh15  : -------------------------------------------------------------- :   -
LpMDHh16  : -------------------------------------------------------------- :   -
LpMDHh17  : -------------------------------------------------------------- :   -
LpMDHh18  : -------------------------------------------------------------- :   -
LpMDHh19  : -------------------------------------------------------------- :   -
LpMDHh20  : -------------------------------------------------------------- :   -
LpMDHh21  : -------------------------------------------------------------- :   -
LpMDHh22  : -------------------------------------------------------------- :   -
LpMDHh23  : -------------------------------------------------------------- :   -
LpMDHh24  : -------------------------------------------------------------- :   -
LpMDHh25  : -------------------------------------------------------------- :   -
LpMDHh26  : -------------------------------------------------------------- :   -
LpMDHh27  : -------------------------------------------------------------- :   -
LpMDHh28  : -------------------------------------------------------------- :   -
LpMDHh29  : -------------------------------------------------------------- :   -
LpMDHh30  : -------------------------------------------------------------- :   -
LpMDHh31  : -------------------------------------------------------------- :   -
LpMDHh32  : -------------------------------------------------------------- :   -
LpMDHh34  : -------------------------------------------------------------- :   -
LpMDHh35  : -------------------------------------------------------------- :   -
LpMDHh36  : -------------------------------------------------------------- :   -
LpMDHh37  : -------------------------------------------------------------- :   -
LpMDHh38  : -------------------------------------------------------------- :   -
LpMDHh39  : -------------------------------------------------------------- :   -
LpMDHh40  : -------------------------------------------------------------- :   -
LpMDHh41  : -------------------------------------------------------------- :   -
LpMDHh42  : -------------------------------------------------------------- :   -
LpMDHh43  : -------------------------------------------------------------- :   -
LpMDHh44  : -------------------------------------------------------------- :   -
LpMDHh45  : -------------------------------------------------------------- :   -
LpMDHh46  : -------------------------------------------------------------- :   -
LpMDHh47  : -------------------------------------------------------------- :   -
LpMDHh48  : -------------------------------------------------------------- :   -
LpMDHh49  : -------------------------------------------------------------- :   -
LpMDHh50  : -------------------------------------------------------------- :   -
LpMDHh51  : -------------------------------------------------------------- :   -
LpMDHh52  : -------------------------------------------------------------- :   -
LpMDHh53  : -------------------------------------------------------------- :   -
LpMDHh54  : -------------------------------------------------------------- :   -
LpMDHh55  : -------------------------------------------------------------- :   -
LpMDHh56  : -------------------------------------------------------------- :   -
LpMDHh57  : -------------------------------------------------------------- :   -
LpMDHh58  : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCCGTGTGTA : 687
LpMDHh59  : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCA------------------------ : 646
LpMDHh60  : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTA : 633
LpMDHh61  : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTA------------ : 616
LpMDHh62  : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTATTATTCCTGTGTGTA : 337
LpMDHh63  : GCAGGAAGATTGGAACAATTTGACGTCTGACAAAAAAAAAA--------------------- : 265
LpMDHh64  : GCAGGAAGATTGGAACAATTTGACGTCTGATTAAAACCAACCTCTTA-TATTCCTGTGTGTA : 116
```

FIGURE 30 (cont.)

```
                   *       1380         *        1400         *        1420
LpMDHh1  : -------------------------------------------------------------- :   -
LpMDHh2  : -------------------------------------------------------------- :   -
LpMDHh3  : -------------------------------------------------------------- :   -
LpMDHh4  : -------------------------------------------------------------- :   -
LpMDHh5  : -------------------------------------------------------------- :   -
LpMDHh6  : -------------------------------------------------------------- :   -
LpMDHh7  : -------------------------------------------------------------- :   -
LpMDHh8  : -------------------------------------------------------------- :   -
LpMDHh9  : -------------------------------------------------------------- :   -
LpMDHh10 : -------------------------------------------------------------- :   -
LpMDHh11 : -------------------------------------------------------------- :   -
LpMDHh12 : -------------------------------------------------------------- :   -
LpMDHh13 : -------------------------------------------------------------- :   -
LpMDHh14 : -------------------------------------------------------------- :   -
LpMDHh15 : -------------------------------------------------------------- :   -
LpMDHh16 : -------------------------------------------------------------- :   -
LpMDHh17 : -------------------------------------------------------------- :   -
LpMDHh18 : -------------------------------------------------------------- :   -
LpMDHh19 : -------------------------------------------------------------- :   -
LpMDHh20 : -------------------------------------------------------------- :   -
LpMDHh21 : -------------------------------------------------------------- :   -
LpMDHh22 : -------------------------------------------------------------- :   -
LpMDHh23 : -------------------------------------------------------------- :   -
LpMDHh24 : -------------------------------------------------------------- :   -
LpMDHh25 : -------------------------------------------------------------- :   -
LpMDHh26 : -------------------------------------------------------------- :   -
LpMDHh27 : -------------------------------------------------------------- :   -
LpMDHh28 : -------------------------------------------------------------- :   -
LpMDHh29 : -------------------------------------------------------------- :   -
LpMDHh30 : -------------------------------------------------------------- :   -
LpMDHh31 : -------------------------------------------------------------- :   -
LpMDHh32 : -------------------------------------------------------------- :   -
LpMDHh34 : -------------------------------------------------------------- :   -
LpMDHh35 : -------------------------------------------------------------- :   -
LpMDHh36 : -------------------------------------------------------------- :   -
LpMDHh37 : -------------------------------------------------------------- :   -
LpMDHh38 : -------------------------------------------------------------- :   -
LpMDHh39 : -------------------------------------------------------------- :   -
LpMDHh40 : -------------------------------------------------------------- :   -
LpMDHh41 : -------------------------------------------------------------- :   -
LpMDHh42 : -------------------------------------------------------------- :   -
LpMDHh43 : -------------------------------------------------------------- :   -
LpMDHh44 : -------------------------------------------------------------- :   -
LpMDHh45 : -------------------------------------------------------------- :   -
LpMDHh46 : -------------------------------------------------------------- :   -
LpMDHh47 : -------------------------------------------------------------- :   -
LpMDHh48 : -------------------------------------------------------------- :   -
LpMDHh49 : -------------------------------------------------------------- :   -
LpMDHh50 : -------------------------------------------------------------- :   -
LpMDHh51 : -------------------------------------------------------------- :   -
LpMDHh52 : -------------------------------------------------------------- :   -
LpMDHh53 : -------------------------------------------------------------- :   -
LpMDHh54 : -------------------------------------------------------------- :   -
LpMDHh55 : -------------------------------------------------------------- :   -
LpMDHh56 : -------------------------------------------------------------- :   -
LpMDHh57 : -------------------------------------------------------------- :   -
LpMDHh58 : TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGG- : 748
LpMDHh59 : -------------------------------------------------------------- :   -
LpMDHh60 : TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCATGATATTGGCAGGA : 695
LpMDHh61 : -------------------------------------------------------------- :   -
LpMDHh62 : TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGACATGATATTGGCAGGA : 399
LpMDHh63 : -------------------------------------------------------------- :   -
LpMDHh64 : TGAATGAGGCTTTTGTAGCTCTATTTTCGCCTGATGATTTACAGGCCACGATATTGGCAGGA : 178
```

FIGURE 30 (cont.)

```
                 *       1440         *       1460         *       1480
LpMDHh1   : ------------------------------------------------------------ :   -
LpMDHh2   : ------------------------------------------------------------ :   -
LpMDHh3   : ------------------------------------------------------------ :   -
LpMDHh4   : ------------------------------------------------------------ :   -
LpMDHh5   : ------------------------------------------------------------ :   -
LpMDHh6   : ------------------------------------------------------------ :   -
LpMDHh7   : ------------------------------------------------------------ :   -
LpMDHh8   : ------------------------------------------------------------ :   -
LpMDHh9   : ------------------------------------------------------------ :   -
LpMDHh10  : ------------------------------------------------------------ :   -
LpMDHh11  : ------------------------------------------------------------ :   -
LpMDHh12  : ------------------------------------------------------------ :   -
LpMDHh13  : ------------------------------------------------------------ :   -
LpMDHh14  : ------------------------------------------------------------ :   -
LpMDHh15  : ------------------------------------------------------------ :   -
LpMDHh16  : ------------------------------------------------------------ :   -
LpMDHh17  : ------------------------------------------------------------ :   -
LpMDHh18  : ------------------------------------------------------------ :   -
LpMDHh19  : ------------------------------------------------------------ :   -
LpMDHh20  : ------------------------------------------------------------ :   -
LpMDHh21  : ------------------------------------------------------------ :   -
LpMDHh22  : ------------------------------------------------------------ :   -
LpMDHh23  : ------------------------------------------------------------ :   -
LpMDHh24  : ------------------------------------------------------------ :   -
LpMDHh25  : ------------------------------------------------------------ :   -
LpMDHh26  : ------------------------------------------------------------ :   -
LpMDHh27  : ------------------------------------------------------------ :   -
LpMDHh28  : ------------------------------------------------------------ :   -
LpMDHh29  : ------------------------------------------------------------ :   -
LpMDHh30  : ------------------------------------------------------------ :   -
LpMDHh31  : ------------------------------------------------------------ :   -
LpMDHh32  : ------------------------------------------------------------ :   -
LpMDHh34  : ------------------------------------------------------------ :   -
LpMDHh35  : ------------------------------------------------------------ :   -
LpMDHh36  : ------------------------------------------------------------ :   -
LpMDHh37  : ------------------------------------------------------------ :   -
LpMDHh38  : ------------------------------------------------------------ :   -
LpMDHh39  : ------------------------------------------------------------ :   -
LpMDHh40  : ------------------------------------------------------------ :   -
LpMDHh41  : ------------------------------------------------------------ :   -
LpMDHh42  : ------------------------------------------------------------ :   -
LpMDHh43  : ------------------------------------------------------------ :   -
LpMDHh44  : ------------------------------------------------------------ :   -
LpMDHh45  : ------------------------------------------------------------ :   -
LpMDHh46  : ------------------------------------------------------------ :   -
LpMDHh47  : ------------------------------------------------------------ :   -
LpMDHh48  : ------------------------------------------------------------ :   -
LpMDHh49  : ------------------------------------------------------------ :   -
LpMDHh50  : ------------------------------------------------------------ :   -
LpMDHh51  : ------------------------------------------------------------ :   -
LpMDHh52  : ------------------------------------------------------------ :   -
LpMDHh53  : ------------------------------------------------------------ :   -
LpMDHh54  : ------------------------------------------------------------ :   -
LpMDHh55  : ------------------------------------------------------------ :   -
LpMDHh56  : ------------------------------------------------------------ :   -
LpMDHh57  : ------------------------------------------------------------ :   -
LpMDHh58  : ------------------------------------------------------------ :   -
LpMDHh59  : ------------------------------------------------------------ :   -
LpMDHh60  : GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTACTAAAAAAAAAAA--- : 750
LpMDHh61  : ------------------------------------------------------------ :   -
LpMDHh62  : GGATTGGAACAANNANANN----------------------------------------- : 418
LpMDHh63  : ------------------------------------------------------------ :   -
LpMDHh64  : GGATTGGAACAATTTGACGCCTGATTAAAACCAACCTCTTATTATTCTAAAAAAAAAAAA : 236
```

FIGURE 30 (cont.)

```
                   *        20         *        40         *        60
LpMDHi  : GTNCATAAAGCTGCCCAAAGCAATNCGTGNAATATTATCAGTAACCCTGTCAATTCTACC :  60

                   *        80         *       100         *       120
LpMDHi  : GTACCAATTGCTGCTGAAGTATTTAAAAAAGCTGGGACATACAATNCTAAGAGATTGTTG : 120

                   *       140         *       160         *
LpMDHi  : GGGGTTGACAACNGTTNGATGNNANTGACAGACCNTGCTCTTNGNNGNCGAGGTNCN : 177
```

FIGURE 31

```
                  *        20         *        40         *
LpMDHi  : XHKAAQSNXXXNIISNPVNSTVPIAAEVFKKAGTYNXKRLLGVDNXXMXXTDXALXXRG : 58
```

FIGURE 32

```
                      *        20         *        40         *        60
LpMDHj : ANAAAGGAGCCGACGCAGGGGCGCAGAATTCCATCTGCTNACTCTGCCACCACCCAAGTT :  60

                      *        80         *       100         *       120
LpMDHj : GGACATGGCGTCAGCTGTTACAATCAGTTCAGTCAGCGCGCAGGCCGCTTTGGTTTCAAA : 120

                      *       140         *       160         *       180
LpMDHj : ACCAAGGAACCATGGCAGCACGAGCTACAGTGGCCTAAAGGCATCATCGTCGTCGATCAG : 180

                      *       200         *       220         *       240
LpMDHj : CTTCGAATCAGGAACATCATTCCTGGGCAAGACCGCCTCCCTCCGGGCAACTGTTACCAC : 240

                      *       260         *       280         *       300
LpMDHj : AAGGGTTGTGCCAAAGGCGAAGTCTGGGTCGCAGATATCGCCTCAGGCATCTTACAAGGT : 300

                      *       320         *       340         *       360
LpMDHj : GGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAGATGTC : 360

                      *       380         *       400         *       420
LpMDHj : TCCTCTGGTCTCGGAGCTGCGCCTGTATGATATCGCGAATGTCAAGGGCGTCGCTGCAGA : 420

                      *       440         *       460         *       480
LpMDHj : TCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCAGAGCTAGC : 480

                      *       500         *       520         *       540
LpMDHj : AGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAGCCAGG : 540

                      *       560         *       580         *       600
LpMDHj : CATGACCCGTGATGACCTTTTTAACATNAATGCGGGAATCGNCAAGTCGCTTATTGAGGC : 600

                      *       620         *       640         *       660
LpMDHj : TGTTGCAGACAATTGCCCTGAGGGCCTTATTCATATCATCAACAACCCCGGTCAAACTCC : 660

LpMDHj : CCCT : 664
```

FIGURE 33

```
                    *        20         *        40         *        60
LpMDHj : XRSRRRGAEFHLXTLPPPKLDMASAVTISSVSAQAALVSKPRNHGSTSYSGLKASSSSIS :  60

                    *        80         *       100         *       120
LpMDHj : FESGTSFLGKTASLRATVTTRVVPKAKSGSQISPQASYKVAVLGAAGGIGQPLGLLIKMS : 120

                    *       140         *       160         *       180
LpMDHj : PLVSELRLYDIANVKGVAADLSHCNTPAQVMDFTGPAELAECLKGVDVVVIPAGVPRKPG : 180

                    *       200         *       220
LpMDHj : MTRDDLFNXNAGIXKKSLIEAVADNCPEGLIHIINNPGQTPP : 221
```

FIGURE 34

```
                 *        20         *        40         *        60
LpMDHk : TNTTTANCCCNCCAANTATCCAGNANCCACCTGGCCCTACACANAANAAAAACAAAAANN :  60

                 *        80         *       100         *       120
LpMDHk : AACCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 120

                 *       140         *       160         *       180
LpMDHk : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 180

                 *       200         *       220         *       240
LpMDHk : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 240

                 *       260         *       280         *       300
LpMDHk : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 300

                 *       320         *       340         *       360
LpMDHk : ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC : 360

                 *       380         *       400         *       420
LpMDHk : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 420

                 *       440         *       460         *       480
LpMDHk : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 480

                 *       500         *       520         *       540
LpMDHk : GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA : 540

                 *       560         *       580         *       600
LpMDHk : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 600

                 *       620         *       640         *       660
LpMDHk : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 660

                 *       680         *       700         *       720
LpMDHk : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 720

                 *       740         *       760         *       780
LpMDHk : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 780

                 *       800         *       820         *       840
LpMDHk : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG : 840

                 *       860         *       880         *       900
LpMDHk : AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT : 900
```

FIGURE 35

```
                    *       920         *       940         *       960
LpMDHk : CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAACTGAACAG :  960

                    *       980         *      1000         *      1020
LpMDHk : CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCGGTGGAGGCGAAGGCTGGTGCTGGC : 1020

                    *      1040         *      1060         *      1080
LpMDHk : TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTTGTTGAGTCATCGCTCCGCGCA : 1080

                    *      1100         *      1120         *      1140
LpMDHk : ATGGCTGGTGATCCAGATGTTTACGAGTGCACGTATGTTCAGTCTGAGTTAACAGAGCTT : 1140

                    *      1160         *      1180         *      1200
LpMDHk : CCATTCTTCGCGTCCAGAGTTAAGCTTGGGAAGGACGGNGTTGAGTCCATCATTTCCTCC : 1200

                    *      1220         *      1240         *      1260
LpMDHk : GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG : 1260

LpMDHk : AAG : 1263
```

FIGURE 35 (cont.)

```
                   *        20         *        40         *        60
LpMDHk : XLXXQXSXXHLALHXXKTKXNQXARGEPGRTQQFPSAHQPKLEMASAVTISSVSAQAALV :  60

                   *        80         *       100         *       120
LpMDHk : SKPRNHGSTSYSGLKASSSSISFESGTSFLGKTASLRATITSRIVPKAKSGSQISPQASY : 120

                   *       140         *       160         *       180
LpMDHk : KVAVLGAAGGIGQPLGLLIKMSPLVSELRLYDIANVKGVAADLSHCNTPSQVMDFTGPAE : 180

                   *       200         *       220         *       240
LpMDHk : LADCLKGVDVVVIPAGVPRKPGMTRDDLFNINAGIVKSLIEAVADNCPEAFIHIISNPVN : 240

                   *       260         *       280         *       300
LpMDHk : STVPIAAEILKQKGVYNPKKLFGVSTLDVVRANTFVAQKKNLSLIDVDVPVVGGHAGITI : 300

                   *       320         *       340         *       360
LpMDHk : LPLLSKTRPSVSFTDEETEQLTKRIQNAGTEAVEAKAGAGSATLSMAYAAARFVESSLRA : 360

                   *       380         *       400         *       420
LpMDHk : MAGDPDVYECTYVQSELTELPFFASRVKLGKDXVESIISSDLEGVTEYEAKALXALKAEL : 420

LpMDHk : K : 421
```

FIGURE 36

```
                    *         20         *         40         *         60
LpMDHk1  : TNTTTANCCCNCCAANTATCCAGNANCCACCTGCCCCGAACCA-AN-AAAAANAAAAAGN : 58
LpMDHk2  : --------------------------------GNGCCGCCACGCAANAAAAANAAAAANN : 28
LpMDHk3  : --------------------------------GNCCCG-CAACGAAGAAAAAAGAAAAGC : 27
LpMDHk4  : ---------------------------------GNCCGCCANGCAANAAAANNAAAAANN : 27
LpMDHk5  : ---------------------------------GCCCGCANNGCAACAAAAANAAAAANN : 27
LpMDHk6  : ----------------------------------GCCN-CAAGCNAGAAAAAAGAAAAGC : 25
LpMDHk7  : -----------------------------------GTTTCNCAGAN-AAAAACCNAAANT : 24
LpMDHk8  : -----------------------------------GTTTCNCAGAN-AAAAACCNAAAGN : 24
LpMDHk9  : -----------------------------------GNNACACANANNAAAAACAAAAANN : 25
LpMDHk10 : -----------------------------------GTTACACANANNAAAAACAAAAANN : 25
LpMDHk11 : -----------------------------------CCT-CAAGG-A-ANAAAAGAAAAGC : 22
LpMDHk12 : ------------------------------------TTTCCCANANAACNAAAANTTTTN : 24
LpMDHk13 : -------------------------------------TTCCCCAAAANCAAAANTTTTTG : 23
LpMDHk14 : --------------------------------------ACACANANNAAAAANAAAAANN : 22
LpMDHk15 : --------------------------------------ACACANANNAAAAANAAAAANN : 22
LpMDHk16 : --------------------------------------ACACANNN-AA-AANNAAAAAG : 20
LpMDHk17 : ---------------------------------------CANNNNA-AA-AACAAAAAGN : 19
LpMDHk18 : ---------------------------------------GTTGCAACAAAANGAAAAAAG : 21
LpMDHk19 : ----------------------------------------GNAGCAGAAAAAGAAAAAAC : 20
LpMDHk20 : ----------------------------------------GNAGCAGAAAAAGAAAAAAC : 20
LpMDHk21 : ----------------------------------------GNAGCAGAAAAAGAAAAAAC : 20
LpMDHk22 : ----------------------------------------GNAGCAGAAAAAGAAAAAAG : 20
LpMDHk23 : -----------------------------------------CANANNAAAAANAAAAANN : 19
LpMDHk24 : -----------------------------------------CANANNAAAAANAAAAANN : 19
LpMDHk25 : -----------------------------------------CANANNAAAAACAAAAANN : 19
LpMDHk26 : -----------------------------------------CANANNAAAAACAAAAANN : 19
LpMDHk27 : -----------------------------------------GACCAGAAAAAGAAAAAAC : 19
LpMDHk28 : -----------------------------------------GTCCAGAAAAAGAAAAAAC : 19
LpMDHk29 : ------------------------------------------ANNA-AAAG-NAAAAAGN : 16
LpMDHk30 : ------------------------------------------ANANNAAAANCAAAAANN : 18
LpMDHk31 : -------------------------------------------AANNAAAANNAAAAANN : 17
LpMDHk32 : --------------------------------------------NNNAAAAANAAAAANN : 16
LpMDHk33 : --------------------------------------------ANNAAAANCAAAAANN : 16
LpMDHk34 : --------------------------------------------NAGAAAAACAAAAAAC : 16
LpMDHk35 : --------------------------------------------GAGAAAAAAGAAAAGC : 16
LpMDHk36 : ---------------------------------------------ANAAAANCAAAAANN : 15
LpMDHk37 : -----------------------------------------------NAACANNNAAA-- : 11
LpMDHk38 : -----------------------------------------------GNACAC-ANANN- : 11
LpMDHk39 : ------------------------------------------------AAACCAAAAANN : 12
LpMDHk40 : ------------------------------------------------GNCAC-ANANN- : 10
LpMDHk41 : ------------------------------------------------GANCCCANANN- : 11
LpMDHk42 : ------------------------------------------------GAGCAGAAAA-- : 10
LpMDHk43 : -------------------------------------------------AAANAAAAANN : 11
LpMDHk44 : -------------------------------------------------AANCCAAAAAN : 11
LpMDHk45 : -------------------------------------------------AAACAAAAAAN : 11
LpMDHk46 : --------------------------------------------------CACAANANN- : 9
LpMDHk47 : --------------------------------------------------AANNAAAAAN : 10
LpMDHk48 : ---------------------------------------------------GN-NNAAN- : 7
LpMDHk49 : ----------------------------------------------------C-ANANN- : 6
LpMDHk50 : ----------------------------------------------------GNACCAG- : 7
LpMDHk51 : -----------------------------------------------------CANNNN- : 6
LpMDHk52 : -----------------------------------------------------CANANN- : 6
LpMDHk53 : -----------------------------------------------------GACCAG- : 6
LpMDHk54 : ------------------------------------------------------ANANN- : 5
LpMDHk55 : --------------------------------------------------------CAG- : 3
LpMDHk56 : ------------------------------------------------------------ : -
LpMDHk57 : ------------------------------------------------------------ : -
LpMDHk58 : ------------------------------------------------------------ : -
LpMDHk59 : ------------------------------------------------------------ : -
LpMDHk60 : ------------------------------------------------------------ : -
LpMDHk61 : ------------------------------------------------------------ : -
LpMDHk62 : ------------------------------------------------------------ : -
LpMDHk63 : ------------------------------------------------------------ : -
LpMDHk64 : ------------------------------------------------------------ : -
LpMDHk65 : ------------------------------------------------------------ : -
LpMDHk66 : ------------------------------------------------------------ : -
```

FIGURE 37

```
                    *       80       *       100       *       120
LpMDHk1  : AGCCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 118
LpMDHk2  : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 85
LpMDHk3  : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACG-AGCAATTCCCATCTGCTCACCAACCC : 86
LpMDHk4  : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 84
LpMDHk5  : ANCCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 85
LpMDHk6  : AGCCAGNNCGCAAGGGGCGAGCCNGGGCGCACG-AGCAATTCCCATCTGCTCACCAACCC : 84
LpMDHk7  : ATCCAGNA-GC-AGGGGCGANCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 82
LpMDHk8  : NNCCAGNACGC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 83
LpMDHk9  : A-CCAGNA-GCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 83
LpMDHk10 : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 82
LpMDHk11 : AGCTCAGNCGCAAGGGGCGAGCCGGGGCGCACG-AGCAATTCCCATCTGCTCACCAACCC : 81
LpMDHk12 : NACCAGNN-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 82
LpMDHk13 : NACCAGNA-GC-AGNGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 81
LpMDHk14 : ACCAGNAC-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 80
LpMDHk15 : A-CCAGNA-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCGTCTGCTCACCAACCC : 79
LpMDHk16 : NACCAGNAG-CAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 79
LpMDHk17 : NNCCAGNNG-CAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 78
LpMDHk18 : AGCCAG-NCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 80
LpMDHk19 : AGCCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 80
LpMDHk20 : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 80
LpMDHk21 : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 80
LpMDHk22 : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 80
LpMDHk23 : ACCCAGNN-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 77
LpMDHk24 : ACCCAGNN-GC-AGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC ; 77
LpMDHk25 : A-CCAGNA-GCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 77
LpMDHk26 : ANCCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 79
LpMDHk27 : AGCCAG-NCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 78
LpMDHk28 : AGCCAGNNCGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 79
LpMDHk29 : NCCC-GNCG-CAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 74
LpMDHk30 : ANCCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 78
LpMDHk31 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 76
LpMDHk32 : ANCCAGNA-GCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 75
LpMDHk33 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 75
LpMDHk34 : AGCCAGNC-GCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 75
LpMDHk35 : AGCCAG-ACGCAAGGGGCGAGCCGGGGCGCACG-AGCAATTCCCATCTGCTCACCAACCC : 74
LpMDHk36 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 74
LpMDHk37 : A---A-CAAAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 67
LpMDHk38 : AAAAN-CAAAAAAGGGGCGAGCCGGGGCGCACNCAGCAATTCCCATCTGCGCACCAACCC : 70
LpMDHk39 : ACCCAGNAGCCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 72
LpMDHk40 : AAAAA-CAAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 69
LpMDHk41 : AAAAANAAAAAANGGG-CGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 70
LpMDHk42 : A---N-GAAAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 66
LpMDHk43 : ACCCAG-NNGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 70
LpMDHk44 : NACCAGNACGCAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 71
LpMDHk45 : A-CCAGNACGCAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 70
LpMDHk46 : AAAAA-NANAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 68
LpMDHk47 : NACCAGNACGCAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 70
LpMDHk48 : AAAAA-NAAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 66
LpMDHk49 : AAAAA-CAAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 65
LpMDHk50 : AAAAAGAAAAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 67
LpMDHk51 : AAAANCAAAAAAGGNACGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 66
LpMDHk52 : AAAAANANAAAANGGG-CGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 65
LpMDHk53 : AAAAAGAAAAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 66
LpMDHk54 : AAAAANAAAAAANGGG-CGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 64
LpMDHk55 : AAAAAGAAAAAAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 63
LpMDHk56 : --AAA-AAAANAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 57
LpMDHk57 : ---AANNAAAAAANGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCGCACCAACCC : 57
LpMDHk58 : ----------CAAGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC : 50
LpMDHk59 : ----------ANAGGGGCNNGCCGGGGCGC-CGC-G-AATT-CCATCTG-NCNCC-A-CC : 43
LpMDHk60 : -----------------GGAGCCGGGGCNC-CGCAGCAATTCCCATCTGCTCACCAACCC : 42
LpMDHk61 : ----------------------GGGGGCGCACGCA-CAATTCCCATCTGCTCACCAACCC : 37
LpMDHk62 : ----------------------------NCA-GCAGCAATTCCCTNCTGCCCACCAACCC : 31
LpMDHk63 : ----------------------------GNCACNACATTCCCCNNCTGCCCACCAACCC : 31
LpMDHk64 : ----------------------------------------------TCTGCCCACCAACCC : 15
LpMDHk65 : ------------------------------------------------------------ : -
LpMDHk66 : ------------------------------------------------------------ : -
```

FIGURE 37 (cont.)

```
                        *       140         *       160         *       180
LpMDHk1  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 178
LpMDHk2  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 145
LpMDHk3  : AAGTTGGACATGGCATCAGCTGTTACCATCAGTTCGGTCAGCGCGCAGTCCGCTGTGGTT : 146
LpMDHk4  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 144
LpMDHk5  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 145
LpMDHk6  : AAGTTGGACATGGCATCAGCTGTTACCATCAGTTCGGTCAGCGCGCAGTCCGCTGTGGTT : 144
LpMDHk7  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 142
LpMDHk8  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 143
LpMDHk9  : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 143
LpMDHk10 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 142
LpMDHk11 : AAGTTGGNGATGGCATCAGCTGTTACCATCAGTTCGGTCAGCGCGCAGTCCGCTGTGGTT : 141
LpMDHk12 : AAGTTGGGGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 142
LpMDHk13 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 141
LpMDHk14 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGTTCAGTCAGCGCGCAGGCCGCTTTGGTC : 140
LpMDHk15 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 139
LpMDHk16 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 139
LpMDHk17 : AAGTTGGGNATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 138
LpMDHk18 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCCTTGGTC : 140
LpMDHk19 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 140
LpMDHk20 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 140
LpMDHk21 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 140
LpMDHk22 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCCTTGGTC : 140
LpMDHk23 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 137
LpMDHk24 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 137
LpMDHk25 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 137
LpMDHk26 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGATC : 139
LpMDHk27 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 138
LpMDHk28 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 139
LpMDHk29 : AAGTTGCGGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 134
LpMDHk30 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 138
LpMDHk31 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 136
LpMDHk32 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 135
LpMDHk33 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAATCAGCGCGCAGGCCGCTTTGGTC : 135
LpMDHk34 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 135
LpMDHk35 : AAGTTGGACATGGCATCAGCTGTTACCATCAGTTCGGTCAGCGCGCAGTCCGCTGTGGTT : 134
LpMDHk36 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 134
LpMDHk37 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 127
LpMDHk38 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 130
LpMDHk39 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 132
LpMDHk40 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 129
LpMDHk41 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 130
LpMDHk42 : AAGTTGGACATGGCATCAGCTGNCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 126
LpMDHk43 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 130
LpMDHk44 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 131
LpMDHk45 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 130
LpMDHk46 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 128
LpMDHk47 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 130
LpMDHk48 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 126
LpMDHk49 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 125
LpMDHk50 : AAGTTGGACATGGCATCTGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 127
LpMDHk51 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 126
LpMDHk52 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 125
LpMDHk53 : AAGTTGGACATGGCATCAGCCGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 126
LpMDHk54 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 124
LpMDHk55 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 123
LpMDHk56 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 117
LpMDHk57 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG : 117
LpMDHk58 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 110
LpMDHk59 : AAGTTGGACATGGCATCAGCTGT-ACCATCAGTT-AGT-AGCGCCCAGGCCGCTCTGGTG : 100
LpMDHk60 : AAGTTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC : 102
LpMDHk61 : A--TTGGAGATGGCATCAGCTGTTACCATCAGCTCAGTCAGCGCGCAGGCCGCTTTGGTC :  95
LpMDHk62 : A-NTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG :  90
LpMDHk63 : -ANTTGGA-ATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG :  89
LpMDHk64 : AAGTTGGACATGGCATCAGCTGTCACCATCAGTTCAGTCAGCGCCCAGGCCGCTCTGGTG :  75
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : ------------------------------------------------------------ :   -
```

FIGURE 37 (cont.)

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                 *       200         *       220         *       240
LpMDHk1  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 238
LpMDHk2  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 205
LpMDHk3  : TCGAAACCAAGGAATCATGGCAGCACGAGCTTCGGTGGCCTAAAGGCATCATCGGCGTCG : 206
LpMDHk4  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 204
LpMDHk5  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 205
LpMDHk6  : TCGAAACCAAGGAATCATGGCAGCACGAGCTTCGGTGGCCTAAAGGCATCATCGGCGTCG : 204
LpMDHk7  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 202
LpMDHk8  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 203
LpMDHk9  : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 203
LpMDHk10 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 202
LpMDHk11 : TCGAAACCAAGGAATCATGGCAGCACGAGCTTCGGTGGCCTAAAGGCATCATCGGCGTCG : 201
LpMDHk12 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 202
LpMDHk13 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 201
LpMDHk14 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk15 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 199
LpMDHk16 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 199
LpMDHk17 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 198
LpMDHk18 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk19 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk20 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk21 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk22 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 200
LpMDHk23 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCAGCATCATCGTCG : 197
LpMDHk24 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 197
LpMDHk25 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 197
LpMDHk26 : TCGAAACCAAGGAATCGTGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 199
LpMDHk27 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 198
LpMDHk28 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 199
LpMDHk29 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 194
LpMDHk30 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 198
LpMDHk31 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 196
LpMDHk32 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 195
LpMDHk33 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 195
LpMDHk34 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 195
LpMDHk35 : TCGAAACCAAGGAATCATGGCAGCACGAGCTTCGGTGGCCTAAAGGCATCATCGGCGTCG : 194
LpMDHk36 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 194
LpMDHk37 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 187
LpMDHk38 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 190
LpMDHk39 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 192
LpMDHk40 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 189
LpMDHk41 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 190
LpMDHk42 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 186
LpMDHk43 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 190
LpMDHk44 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 191
LpMDHk45 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 190
LpMDHk46 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 188
LpMDHk47 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 190
LpMDHk48 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 186
LpMDHk49 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 185
LpMDHk50 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 187
LpMDHk51 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 186
LpMDHk52 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 185
LpMDHk53 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 186
LpMDHk54 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 184
LpMDHk55 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 183
LpMDHk56 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 177
LpMDHk57 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 177
LpMDHk58 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 170
LpMDHk59 : T-AAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 159
LpMDHk60 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 162
LpMDHk61 : TCGAAACCAAGGAATCATGGCAGCACAAGCTACAGTGGCCTAAAGGCATCATCATCGTCG : 155
LpMDHk62 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 150
LpMDHk63 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 149
LpMDHk64 : TCAAAACCAAGGAGTCATGGCAGCACGAGCTTCAGTGGCCTGAAGGCATCATCATCGTCG : 135
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : ------------------------------------------------------------ :   -
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FIGURE 37 (cont.)

79/241

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                  *       260         *       280         *       300
LpMDHk1  : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCACCTCTCTTCGGGCGACTATC : 298
LpMDHk2  : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 265
LpMDHk3  : ATCAGCTTTGAATCAGGGACATCGTTCCTGGGCAAGACTGCCTCGCTGCGGGCGACTGTT : 266
LpMDHk4  : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 264
LpMDHk5  : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 265
LpMDHk6  : ATCAGCTTTGAATCAGGGACATCGTTCCTGGGCAAGACTGCCTCGCTGCGGGCGACTGTT : 264
LpMDHk7  : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 262
LpMDHk8  : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 263
LpMDHk9  : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 263
LpMDHk10 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 262
LpMDHk11 : ATCAGCTTTGAATCAGGGACATCGTTCCTGGGCAAGACTGNCTCGCTGCGGGCGACTGTT : 261
LpMDHk12 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 262
LpMDHk13 : ATCAGCTTCGAATCANGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 261
LpMDHk14 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 260
LpMDHk15 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 259
LpMDHk16 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 259
LpMDHk17 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 258
LpMDHk18 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 260
LpMDHk19 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 260
LpMDHk20 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 260
LpMDHk21 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 260
LpMDHk22 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 260
LpMDHk23 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 257
LpMDHk24 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 257
LpMDHk25 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 257
LpMDHk26 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 259
LpMDHk27 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 258
LpMDHk28 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 259
LpMDHk29 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 254
LpMDHk30 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 258
LpMDHk31 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 256
LpMDHk32 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 255
LpMDHk33 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 255
LpMDHk34 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 255
LpMDHk35 : ATCAGCTTTGAATCAGGGACATCGTTCCTGGGCAAGACTGCCTCGCTGCGGGCGACTGTT : 254
LpMDHk36 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 254
LpMDHk37 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 247
LpMDHk38 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 250
LpMDHk39 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 252
LpMDHk40 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 249
LpMDHk41 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 250
LpMDHk42 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 246
LpMDHk43 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 250
LpMDHk44 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 251
LpMDHk45 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 250
LpMDHk46 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 248
LpMDHk47 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 250
LpMDHk48 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 246
LpMDHk49 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 245
LpMDHk50 : ATCAGCTTCGAATCTGGAGCATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 247
LpMDHk51 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 246
LpMDHk52 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGCC : 245
LpMDHk53 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 246
LpMDHk54 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 244
LpMDHk55 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 243
LpMDHk56 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 237
LpMDHk57 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 237
LpMDHk58 : ATCAGCTTCGAATCAGGGCCATCATTCCTGGACAAGACCGNCTCTCTTCGGGCGACTATC : 230
LpMDHk59 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 219
LpMDHk60 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 222
LpMDHk61 : ATCAGCTTCGAATCAGGGACATCATTCCTGGGCAAGACCGCCTCTCTTCGGGCGACTATC : 215
LpMDHk62 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 210
LpMDHk63 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 209
LpMDHk64 : ATCAGCTTCGAATCTGGAACATCATTCCTGGGCAAGACTGCCTCTCTTCGGGCGTCAGTC : 195
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : ------------------------------------------------------------ :   -
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FIGURE 37 (cont.)

		* 320 * 340 * 360		
LpMDHk1	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	358
LpMDHk2	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	325
LpMDHk3	:	ACCCCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	326
LpMDHk4	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	324
LpMDHk5	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	325
LpMDHk6	:	ACCCCAAGGATTGNGCCAAAGGCAAAGTCTGGGTCTCANATATCGCCTCAGGCATCTTAC	:	324
LpMDHk7	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	322
LpMDHk8	:	ACCTCAAGGATTGTGCCAAAGGCAAAGCCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	323
LpMDHk9	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	323
LpMDHk10	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	322
LpMDHk11	:	ACCCCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	321
LpMDHk12	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	322
LpMDHk13	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	321
LpMDHk14	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	320
LpMDHk15	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	319
LpMDHk16	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	319
LpMDHk17	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	318
LpMDHk18	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	320
LpMDHk19	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	320
LpMDHk20	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	320
LpMDHk21	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	320
LpMDHk22	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	320
LpMDHk23	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	317
LpMDHk24	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	317
LpMDHk25	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	317
LpMDHk26	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	319
LpMDHk27	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	318
LpMDHk28	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	319
LpMDHk29	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	314
LpMDHk30	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	318
LpMDHk31	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	316
LpMDHk32	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	315
LpMDHk33	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	315
LpMDHk34	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	315
LpMDHk35	:	ACCCCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	314
LpMDHk36	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	314
LpMDHk37	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	307
LpMDHk38	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	310
LpMDHk39	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	312
LpMDHk40	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	309
LpMDHk41	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	310
LpMDHk42	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	306
LpMDHk43	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	310
LpMDHk44	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	311
LpMDHk45	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	310
LpMDHk46	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	308
LpMDHk47	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	310
LpMDHk48	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	306
LpMDHk49	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	305
LpMDHk50	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTCAC	:	307
LpMDHk51	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	306
LpMDHk52	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	305
LpMDHk53	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	306
LpMDHk54	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	304
LpMDHk55	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	303
LpMDHk56	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	297
LpMDHk57	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	297
LpMDHk58	:	ACCTCAAGGATTGTGCCAAAGGCAAAGNCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	290
LpMDHk59	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	279
LpMDHk60	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCTCAGGCCTCGTAC	:	282
LpMDHk61	:	ACCTCAAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCACCCCAGGCCTCGTAC	:	275
LpMDHk62	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	270
LpMDHk63	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	269
LpMDHk64	:	ACCCCGAGGATTGTGCCAAAGGCAAAGTCTGGGTCTCAGATATCGCCTCAGGCATCTTAC	:	255
LpMDHk65	:	--	:	-
LpMDHk66	:	--	:	-

FIGURE 37 (cont.)

81/241

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                      *       380         *       400         *       420
LpMDHk1  : AAGGTGGCGGTGCTTGGTGCTGACGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 418
LpMDHk2  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 385
LpMDHk3  : AAGGTGGCGGTGCTTGGTGCTGCTGGTGGCATCGGCCAACCACTGGGCCTGCTGATCAAG : 386
LpMDHk4  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 384
LpMDHk5  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 385
LpMDHk6  : AAGGNGGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAN : 384
LpMDHk7  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 382
LpMDHk8  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 383
LpMDHk9  : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 383
LpMDHk10 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 382
LpMDHk11 : AAGGTGGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 381
LpMDHk12 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 382
LpMDHk13 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 381
LpMDHk14 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 380
LpMDHk15 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 379
LpMDHk16 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 379
LpMDHk17 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 378
LpMDHk18 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 380
LpMDHk19 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 380
LpMDHk20 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 380
LpMDHk21 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 380
LpMDHk22 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 380
LpMDHk23 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 377
LpMDHk24 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 377
LpMDHk25 : AAGGTGGCGGTGTTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 377
LpMDHk26 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 379
LpMDHk27 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGACCAAG : 378
LpMDHk28 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 379
LpMDHk29 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 374
LpMDHk30 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 378
LpMDHk31 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 376
LpMDHk32 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 375
LpMDHk33 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 375
LpMDHk34 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 375
LpMDHk35 : AAGGTGGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 374
LpMDHk36 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 374
LpMDHk37 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 367
LpMDHk38 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 370
LpMDHk39 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 372
LpMDHk40 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 369
LpMDHk41 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 370
LpMDHk42 : AAGGTGGTGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 366
LpMDHk43 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 370
LpMDHk44 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 371
LpMDHk45 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 370
LpMDHk46 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 368
LpMDHk47 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 370
LpMDHk48 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 366
LpMDHk49 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTTAACCACTGGGCCTGCTGATCAAG : 365
LpMDHk50 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 367
LpMDHk51 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 366
LpMDHk52 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 365
LpMDHk53 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 366
LpMDHk54 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 364
LpMDHk55 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 363
LpMDHk56 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 357
LpMDHk57 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 357
LpMDHk58 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 350
LpMDHk59 : AAGGTGGCGGTGCTTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 339
LpMDHk60 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 342
LpMDHk61 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 335
LpMDHk62 : AAGGTGGCGGNGCTTGGTGCTGNCGGNGGCATNGGCCAACCACTGGGCCTGCTGATNAAG : 330
LpMDHk63 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 329
LpMDHk64 : AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG : 315
LpMDHk65 : -------------TTGGTGCTGCTGGTGGCATCGGTCAACCACTGGGCCTGCTGATCAAG :  47
LpMDHk66 : ------------------------------------------------------------ :   -
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FIGURE 37 (cont.)

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                      *       440         *       460         *       480
LpMDHk1  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGACAATGTCAAGGGAGTCGCT : 478
LpMDHk2  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 445
LpMDHk3  : ATGTCTCCTCTAGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 446
LpMDHk4  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 444
LpMDHk5  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 445
LpMDHk6  : ATGTCTCCTCTGGTCTCAN------------------------------------------ : 403
LpMDHk7  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 442
LpMDHk8  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 443
LpMDHk9  : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 443
LpMDHk10 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 442
LpMDHk11 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 441
LpMDHk12 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 442
LpMDHk13 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 441
LpMDHk14 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk15 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 439
LpMDHk16 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 439
LpMDHk17 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 438
LpMDHk18 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk19 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk20 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk21 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk22 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 440
LpMDHk23 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 437
LpMDHk24 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 437
LpMDHk25 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 437
LpMDHk26 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 439
LpMDHk27 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 438
LpMDHk28 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 439
LpMDHk29 : ATGTCTCCTCTGGTCTCAGAACTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 434
LpMDHk30 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 438
LpMDHk31 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 436
LpMDHk32 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 435
LpMDHk33 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 435
LpMDHk34 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 435
LpMDHk35 : ATGTCTCCTCTGGTCTCANAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 434
LpMDHk36 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 434
LpMDHk37 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 427
LpMDHk38 : ATGTCGCCTCTGGCCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 430
LpMDHk39 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 432
LpMDHk40 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 429
LpMDHk41 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 430
LpMDHk42 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 426
LpMDHk43 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 430
LpMDHk44 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 431
LpMDHk45 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 430
LpMDHk46 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 428
LpMDHk47 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 430
LpMDHk48 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 426
LpMDHk49 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 425
LpMDHk50 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 427
LpMDHk51 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 426
LpMDHk52 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 425
LpMDHk53 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 426
LpMDHk54 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 424
LpMDHk55 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 423
LpMDHk56 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 417
LpMDHk57 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCCGTATGATAATGCGAATGTCAAGGGCGTCGCT : 417
LpMDHk58 : ATGNNTCCTCTGGTCTCANAGCTGCGCCTGTATGATATTGCCAATGNCAAGGGAGTCGCT : 410
LpMDHk59 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGCGTCGCT : 399
LpMDHk60 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 402
LpMDHk61 : ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTCAAGGGAGTCGCT : 395
LpMDHk62 : ATG--------------------------------------------------------- : 333
LpMDHk63 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 389
LpMDHk64 : ATGTCGCCTCTGGTCTCGGAGCTGCGCCTGTATGATATTGCGAATGTCAAGGGCGTCGCT : 375
LpMDHk65 : ATGTCTCCTCTCGTCTCGGAGCTGCGCCTGTATGATATCGCCAATGTCAAGGGAGTCGCT : 107
LpMDHk66 : ------------------------------------------------------------ :   -
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FIGURE 37 (cont.)

83/241

	* 500 * 520 * 540	
LpMDHk1 :	GCAGATCTCAGNCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 538
LpMDHk2 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 505
LpMDHk3 :	GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 506
LpMDHk4 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 504
LpMDHk5 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 505
LpMDHk6 :	--	: -
LpMDHk7 :	GCAGATCTCAGCCACTGGAACACGCCTTCTCAGGTCATGGACTTGACTGGCCCAGCAGAA	: 502
LpMDHk8 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 503
LpMDHk9 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 503
LpMDHk10 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 502
LpMDHk11 :	GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 501
LpMDHk12 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 502
LpMDHk13 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 501
LpMDHk14 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 500
LpMDHk15 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 499
LpMDHk16 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 499
LpMDHk17 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 498
LpMDHk18 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 500
LpMDHk19 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCTGAA	: 500
LpMDHk20 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 500
LpMDHk21 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 500
LpMDHk22 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 500
LpMDHk23 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 497
LpMDHk24 :	GCAGATCTCAGCCGCTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 497
LpMDHk25 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 497
LpMDHk26 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 499
LpMDHk27 :	GCAGGTCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGTCCAGCAGAA	: 498
LpMDHk28 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 499
LpMDHk29 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCGCTGGCCCAGCAGAA	: 494
LpMDHk30 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 498
LpMDHk31 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 496
LpMDHk32 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 495
LpMDHk33 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 495
LpMDHk34 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 495
LpMDHk35 :	GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 494
LpMDHk36 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 494
LpMDHk37 :	GCCGATCTCAGCCACCGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 487
LpMDHk38 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 490
LpMDHk39 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 492
LpMDHk40 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 489
LpMDHk41 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCTGGTCATGGACTTCACTGGCCCCGCGGAA	: 490
LpMDHk42 :	GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 486
LpMDHk43 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 490
LpMDHk44 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 491
LpMDHk45 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGCCTTCACTGGCCCAGCAGAA	: 490
LpMDHk46 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 488
LpMDHk47 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 490
LpMDHk48 :	GCCGACCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 486
LpMDHk49 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 485
LpMDHk50 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 487
LpMDHk51 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 486
LpMDHk52 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 485
LpMDHk53 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 486
LpMDHk54 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 484
LpMDHk55 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 483
LpMDHk56 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 477
LpMDHk57 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 477
LpMDHk58 :	GCAAATCTCANNCACTGCAACACGCCTTCTNAGGNCATGGACTTCACTGGNCCANCANAA	: 470
LpMDHk59 :	GCAGATCTTAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 459
LpMDHk60 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 462
LpMDHk61 :	GCAGATCTCAGCCACTGCAACACGCCTTCTCAGGTCATGGACTTCACTGGCCCAGCAGAA	: 455
LpMDHk62 :	--	: -
LpMDHk63 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 449
LpMDHk64 :	GCCGATCTCAGCCACTGCAACACGCCTGCTCAGGTCATGGACTTCACTGGCCCCGCGGAA	: 435
LpMDHk65 :	GCAGATCTCAGCCACTGCAACACGCCTGCTCAGGCCATGGACTTCACTGGCCCCGCGGAA	: 167
LpMDHk66 :	-----GATCAGCC:CTGCAACACGCCTGCTCAGGCCATGGACTTCACTGGCCCCGCGGAA	: 54

FIGURE 37 (cont.)

84/241

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                 *       560         *       580         *       600
LpMDHk1  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGNCATCCCTGCGGGTGTNCCAAGGAAG : 598
LpMDHk2  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 565
LpMDHk3  : CTAGCCGACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 566
LpMDHk4  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCTCAAGGAAG : 564
LpMDHk5  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 565
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : CTAGCTGACTGCTTGAAAGGTGGTGATGTTGNCNGCATCCCTGCGGNNGTCNCAAGGAA- : 561
LpMDHk8  : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 563
LpMDHk9  : CTAGCTGGCTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 563
LpMDHk10 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 562
LpMDHk11 : CTAGCCGACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 561
LpMDHk12 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 562
LpMDHk13 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCTCAAGGAAG : 561
LpMDHk14 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk15 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 559
LpMDHk16 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 559
LpMDHk17 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 558
LpMDHk18 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk19 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk20 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk21 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk22 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 560
LpMDHk23 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 557
LpMDHk24 : CTAGCTGACTGCTTGAGAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 557
LpMDHk25 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 557
LpMDHk26 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 559
LpMDHk27 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 558
LpMDHk28 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 559
LpMDHk29 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTNCCAAGGAAG : 554
LpMDHk30 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 558
LpMDHk31 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 556
LpMDHk32 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 555
LpMDHk33 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 555
LpMDHk34 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 555
LpMDHk35 : CTAGCCGACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 554
LpMDHk36 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 554
LpMDHk37 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTNCCAAGGAAG : 547
LpMDHk38 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCG-NATCCCTGCGGGTGTTCCAAGGAAG : 549
LpMDHk39 : CTAGCTGACTGCTTGAAAGG-GTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 551
LpMDHk40 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 549
LpMDHk41 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAN : 550
LpMDHk42 : CTAGCCGACTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 546
LpMDHk43 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 550
LpMDHk44 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 551
LpMDHk45 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 550
LpMDHk46 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 548
LpMDHk47 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 550
LpMDHk48 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 546
LpMDHk49 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 545
LpMDHk50 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 547
LpMDHk51 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 546
LpMDHk52 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 545
LpMDHk53 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 546
LpMDHk54 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 544
LpMDHk55 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 543
LpMDHk56 : CTAGCAGACTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 537
LpMDHk57 : CTAGCAGACTGCTTGAAAGGCGTGGATGCTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 537
LpMDHk58 : CTA--------------------------------------------------------- : 473
LpMDHk59 : CTAGCCGACTGCTTGAAANGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 519
LpMDHk60 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 522
LpMDHk61 : CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 515
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 509
LpMDHk64 : CTAGCAGAGTGCTTGAAAGGCGTGGATGTTGNCGTCATCCCTGCGGGTGTCCCAAGGAAG : 495
LpMDHk65 : CTAGCAGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 227
LpMDHk66 : CTAGCAGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCCAAGGAAG : 114
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FIGURE 37 (cont.)

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                *        620         *        640         *        660
LpMDHk1  : CCAGNCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGNNAAGTCGCTTATT : 658
LpMDHk2  : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 625
LpMDHk3  : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 626
LpMDHk4  : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 624
LpMDHk5  : CCAGGCACGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 625
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 623
LpMDHk9  : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 623
LpMDHk10 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 622
LpMDHk11 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 621
LpMDHk12 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 622
LpMDHk13 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 621
LpMDHk14 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk15 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619
LpMDHk16 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619
LpMDHk17 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 618
LpMDHk18 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk19 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGNCAAGTCGCTTATT : 620
LpMDHk20 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk21 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk22 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 620
LpMDHk23 : CCAGGCATGACCCATGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 617
LpMDHk24 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 617
LpMDHk25 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 617
LpMDHk26 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619
LpMDHk27 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 618
LpMDHk28 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 619
LpMDHk29 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 614
LpMDHk30 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 618
LpMDHk31 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 616
LpMDHk32 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 615
LpMDHk33 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 615
LpMDHk34 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 615
LpMDHk35 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 614
LpMDHk36 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 614
LpMDHk37 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGG-CATCGTC-AGTNGCTTATC : 605
LpMDHk38 : CCAGGCATGACCCGTGATGACCTTTNTAACATCAATGCGGGCATCGNCAAGNCGCTTATC : 609
LpMDHk39 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 611
LpMDHk40 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 609
LpMDHk41 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 610
LpMDHk42 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 606
LpMDHk43 : CCAGACAACGTGCCCTGAGCGCTTCATTCCATATCATCACGCACCCGCGTCAACTCCAGTCTC : 610
LpMDHk44 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 611
LpMDHk45 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 610
LpMDHk46 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 608
LpMDHk47 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 610
LpMDHk48 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 606
LpMDHk49 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 605
LpMDHk50 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 607
LpMDHk51 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 606
LpMDHk52 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 605
LpMDHk53 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 606
LpMDHk54 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 604
LpMDHk55 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 603
LpMDHk56 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 597
LpMDHk57 : CCAGGCATGACCCGTGATGACCTTTTTAACATCNATGCGGGCATCGTCAAGTCGCTTATC : 597
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGCCAAGTCGCTTATC : 579
LpMDHk60 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 582
LpMDHk61 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 575
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 569
LpMDHk64 : CCAGGCATGACCCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATC : 555
LpMDHk65 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 287
LpMDHk66 : CCTGGCATGACTCGTGATGACCTTTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT : 174
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FIGURE 37 (cont.)

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                      *       680         *       700         *       720
LpMDHk1  : GAGGCTGTTGCAGACAACTCCCCTGAGGCCTTCATCCATATCATCANCNACCC------- : 711
LpMDHk2  : GAGGCTGTTGCAGACAACTGCC-------------------------------------- : 647
LpMDHk3  : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 686
LpMDHk4  : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 684
LpMDHk5  : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 685
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : GAGGCTGTTGCAGACAACTCCCCTGAGGCCTTCATC------------------------- : 659
LpMDHk9  : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 683
LpMDHk10 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 682
LpMDHk11 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 681
LpMDHk12 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATNCATATCATCAGCAACCCGGTCAAC : 682
LpMDHk13 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 681
LpMDHk14 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATNCATATCATCAGCAACCCGGTCACN : 680
LpMDHk15 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 679
LpMDHk16 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 679
LpMDHk17 : GAGGCTGTTGCAGACA-------------------------------------------- : 634
LpMDHk18 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 680
LpMDHk19 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGNCAAC : 680
LpMDHk20 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 680
LpMDHk21 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 680
LpMDHk22 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 680
LpMDHk23 : GAGGCTGTTGC------------------------------------------------- : 628
LpMDHk24 : GAGGCTGTTGCAGACAACTGCCC------------------------------------- : 640
LpMDHk25 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 677
LpMDHk26 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATNCATATCATCAGCAACCCGGTCAAC : 679
LpMDHk27 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 678
LpMDHk28 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 679
LpMDHk29 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 674
LpMDHk30 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 678
LpMDHk31 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 676
LpMDHk32 : GAGGCTGTTGCAGACAACTGCC-------------------------------------- : 637
LpMDHk33 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 675
LpMDHk34 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 675
LpMDHk35 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 674
LpMDHk36 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 674
LpMDHk37 : GAGGCTGTTGCAGAC-ACT-GCCTGAGGCCTT-ATCCATATTATCA-NNACCCGG--GAC : 659
LpMDHk38 : GAGGCTGTTGCAGACAACTGCCCTGAGGNCTTCATCCATATTATGAGAACCCCGGNCAAC : 669
LpMDHk39 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTT--------------------------- : 644
LpMDHk40 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 669
LpMDHk41 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 670
LpMDHk42 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 666
LpMDHk43 : CCGANTGCTGCNGAGANCTAAACAGAA--------------------------------- : 637
LpMDHk44 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 671
LpMDHk45 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 670
LpMDHk46 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCAT--------------------- : 647
LpMDHk47 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAAC---------- : 661
LpMDHk48 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCA-------------------------- : 640
LpMDHk49 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 665
LpMDHk50 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 667
LpMDHk51 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCNA- : 665
LpMDHk52 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 665
LpMDHk53 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 666
LpMDHk54 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 664
LpMDHk55 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 663
LpMDHk56 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 657
LpMDHk57 : GAGGCTGNTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCNAC : 657
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : NAGGCTGTTGCAGACAACTCCCTTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 639
LpMDHk60 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 642
LpMDHk61 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 635
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 629
LpMDHk64 : GAGGCTGTTGCAGACAACTGCCCTGAGGCCTTCATCCATATTATCAGCAACCCGGTCAAC : 615
LpMDHk65 : GAGGCTGTTGCAGACAACTGCCCAGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 347
LpMDHk66 : GAGGCTGTTGCAGACAACTGCCCAGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC : 234
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FIGURE 37 (cont.)

87/241

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                    *        740         *        760         *        780
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 746
LpMDHk4  : TNCACTGT---------------------------------------------------- : 692
LpMDHk5  : TNCACTGTGA-------------------------------------------------- : 695
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : TNCACTGTGCCGATTGCTGCTGA------------------------------------- : 706
LpMDHk10 : TCCACTGTGCCGATTGCTGCTGAA------------------------------------ : 706
LpMDHk11 : TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTNTACAACCCCAAGAAG : 741
LpMDHk12 : TNCACTGTG--------------------------------------------------- : 691
LpMDHk13 : TNCACTGTGCCGATTGCTGCTGAG------------------------------------ : 705
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : TCCACTGTGCCGATTGCTGCTGAGAT---------------------------------- : 705
LpMDHk16 : TNCACTGTGCCGATTGCTGCTGAGATA--------------------------------- : 706
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 740
LpMDHk19 : TCCACTGNGCCGATTGCTGCTGANATTCTGAAACANAAGGGCGNNTACAACCCCAANAAG : 740
LpMDHk20 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 740
LpMDHk21 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 740
LpMDHk22 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 740
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : TCCACTGTGCCGATTGCTGCT--------------------------------------- : 698
LpMDHk26 : TNCACTGTGCCGATTGCTGCTGAGATTCTGAAAN-------------------------- : 713
LpMDHk27 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 738
LpMDHk28 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 739
LpMDHk29 : TTCACTGTGC-------------------------------------------------- : 684
LpMDHk30 : TNCACTGTGCCGATTGT------------------------------------------- : 695
LpMDHk31 : TNCACTGTGCCGATTGCTG----------------------------------------- : 695
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAACGGCGTNT-CCACCCCAAGAAG : 734
LpMDHk35 : TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 734
LpMDHk36 : TNCACTGTGCCGATTGCTGCTGAGATTCTGAA---------------------------- : 706
LpMDHk37 : TGCACGGTGCCGATTGCTGNAAT------------------------------------- : 682
LpMDHk38 : TCCACGGCGCCGATTGNTGCAGAGATTCTGAAACAGAA-GGCGT---------------- : 712
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : TNCACGGTGCCGAT---------------------------------------------- : 683
LpMDHk41 : TCCACGGTGCCGATTGCTGCAGAGA----------------------------------- : 695
LpMDHk42 : TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 726
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : TNCACTGTGCCGATT--------------------------------------------- : 686
LpMDHk45 : TNCACTGTGCCGATTGCTGCTGC------------------------------------- : 693
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : TCCACGGTGCCGATTG-------------------------------------------- : 681
LpMDHk50 : TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 727
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : TNCACGGTGCCGATN--------------------------------------------- : 680
LpMDHk53 : TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 726
LpMDHk54 : TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAG---------------------- : 702
LpMDHk55 : TCCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 723
LpMDHk56 : TNCACGGTGCCGATTGCTGCAGAGATTCTGAAACA-AAAGGCGTCTACAAC--------- : 707
LpMDHk57 : TCCACGGNGCCGATTGNTGCA:ANATTTTGC----------------------------- : 687
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : TNC--------------------------------------------------------- : 642
LpMDHk60 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG : 702
LpMDHk61 : TNCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAGCCCCAAGAAG : 695
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : T----------------------------------------------------------- : 630
LpMDHk64 : TNCACGGTGCCGATTGCTGCAGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAA---- : 671
LpMDHk65 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGTGTCTACAACCCCAAGAAG : 407
LpMDHk66 : TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGTGTCTACAACCCCAAGAAG : 294
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FIGURE 37 (cont.)

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                       *         800         *         820         *         840
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : CTCTTCGGGGTTTNCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANA----- : 801
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAAAANAAN : 801
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : CTCTTCGGGGTTTCCACC------------------------------------------ : 758
LpMDHk19 : CTCTTNGGGGNTTNCACCCTG--------------------------------------- : 761
LpMDHk20 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAA---------------------------- : 772
LpMDHk21 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAN---------------------------- : 772
LpMDHk22 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCANAAGAAG : 800
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGA--------------------------- : 771
LpMDHk28 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAG-------------------------- : 773
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : CTTTTCNGGGNTTACACCCTGGATGTTGCC------------------------------ : 764
LpMDHk35 : CTCTTCGGGGNTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCT--------- : 785
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : CTCTTCGGGGTTTNCACCCTGGATGTTGTCAGAGCTAACACATTTGNAGCTCANAANAAG : 786
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : CTCTTCGGGGTTTC---------------------------------------------- : 741
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGGGCTAACACATT---------------- : 770
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : CTCTTCGGGGTTTCCCCCCTGGATGTTGTCAGGGCTAACACATTTGTAGCTCAA------ : 777
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG : 762
LpMDHk61 : CTCTTA------------------------------------------------------ : 701
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG : 467
LpMDHk66 : CTCTTCGGGGTTTCCACCCTGGATGTTGTCAGAGCTAACACATTTGTAGCTCAGAAGAAG : 354
```

FIGURE 37 (cont.)

```
                       *       860         *       880         *       900
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : A----------------------------------------------------------- : 802
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : AACCTCA----------------------------------------------------- : 807
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : AACCTCAGTCTTATCG-------------------------------------------- : 802
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : AACCT------------------------------------------------------- : 767
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT : 527
LpMDHk66 : AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT : 414
```

FIGURE 37 (cont.)

```
                        *        920         *        940         *        960
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : ------------------------------------------------------------ :   -
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : ------------------------------------------------------------ :   -
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : ------------------------------------------------------------ :   -
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : ------------------------------------------------------------ :   -
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAACTGAACAG : 587
LpMDHk66 : CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAAACTGAACAG : 474
```

FIGURE 37 (cont.)

```
                      *       980         *      1000         *      1020
LpMDHk1  : ------------------------------------------------------------ :    -
LpMDHk2  : ------------------------------------------------------------ :    -
LpMDHk3  : ------------------------------------------------------------ :    -
LpMDHk4  : ------------------------------------------------------------ :    -
LpMDHk5  : ------------------------------------------------------------ :    -
LpMDHk6  : ------------------------------------------------------------ :    -
LpMDHk7  : ------------------------------------------------------------ :    -
LpMDHk8  : ------------------------------------------------------------ :    -
LpMDHk9  : ------------------------------------------------------------ :    -
LpMDHk10 : ------------------------------------------------------------ :    -
LpMDHk11 : ------------------------------------------------------------ :    -
LpMDHk12 : ------------------------------------------------------------ :    -
LpMDHk13 : ------------------------------------------------------------ :    -
LpMDHk14 : ------------------------------------------------------------ :    -
LpMDHk15 : ------------------------------------------------------------ :    -
LpMDHk16 : ------------------------------------------------------------ :    -
LpMDHk17 : ------------------------------------------------------------ :    -
LpMDHk18 : ------------------------------------------------------------ :    -
LpMDHk19 : ------------------------------------------------------------ :    -
LpMDHk20 : ------------------------------------------------------------ :    -
LpMDHk21 : ------------------------------------------------------------ :    -
LpMDHk22 : ------------------------------------------------------------ :    -
LpMDHk23 : ------------------------------------------------------------ :    -
LpMDHk24 : ------------------------------------------------------------ :    -
LpMDHk25 : ------------------------------------------------------------ :    -
LpMDHk26 : ------------------------------------------------------------ :    -
LpMDHk27 : ------------------------------------------------------------ :    -
LpMDHk28 : ------------------------------------------------------------ :    -
LpMDHk29 : ------------------------------------------------------------ :    -
LpMDHk30 : ------------------------------------------------------------ :    -
LpMDHk31 : ------------------------------------------------------------ :    -
LpMDHk32 : ------------------------------------------------------------ :    -
LpMDHk33 : ------------------------------------------------------------ :    -
LpMDHk34 : ------------------------------------------------------------ :    -
LpMDHk35 : ------------------------------------------------------------ :    -
LpMDHk36 : ------------------------------------------------------------ :    -
LpMDHk37 : ------------------------------------------------------------ :    -
LpMDHk38 : ------------------------------------------------------------ :    -
LpMDHk39 : ------------------------------------------------------------ :    -
LpMDHk40 : ------------------------------------------------------------ :    -
LpMDHk41 : ------------------------------------------------------------ :    -
LpMDHk42 : ------------------------------------------------------------ :    -
LpMDHk43 : ------------------------------------------------------------ :    -
LpMDHk44 : ------------------------------------------------------------ :    -
LpMDHk45 : ------------------------------------------------------------ :    -
LpMDHk46 : ------------------------------------------------------------ :    -
LpMDHk47 : ------------------------------------------------------------ :    -
LpMDHk48 : ------------------------------------------------------------ :    -
LpMDHk49 : ------------------------------------------------------------ :    -
LpMDHk50 : ------------------------------------------------------------ :    -
LpMDHk51 : ------------------------------------------------------------ :    -
LpMDHk52 : ------------------------------------------------------------ :    -
LpMDHk53 : ------------------------------------------------------------ :    -
LpMDHk54 : ------------------------------------------------------------ :    -
LpMDHk55 : ------------------------------------------------------------ :    -
LpMDHk56 : ------------------------------------------------------------ :    -
LpMDHk57 : ------------------------------------------------------------ :    -
LpMDHk58 : ------------------------------------------------------------ :    -
LpMDHk59 : ------------------------------------------------------------ :    -
LpMDHk60 : ------------------------------------------------------------ :    -
LpMDHk61 : ------------------------------------------------------------ :    -
LpMDHk62 : ------------------------------------------------------------ :    -
LpMDHk63 : ------------------------------------------------------------ :    -
LpMDHk64 : ------------------------------------------------------------ :    -
LpMDHk65 : CTGACAAAGAGGATACAGAACGCTGGGACAGAGGTGGTGGAGGCGAA------------- :  634
LpMDHk66 : CTGACAAAGAGGATACAGAACGCTGGGACAGAGGCGGTGGAGGCGAAGGCTGGTGCTGGC :  534
```

FIGURE 37 (cont.)

```
                        *       1040         *       1060         *       1080
LpMDHk1  : ------------------------------------------------------------ :    -
LpMDHk2  : ------------------------------------------------------------ :    -
LpMDHk3  : ------------------------------------------------------------ :    -
LpMDHk4  : ------------------------------------------------------------ :    -
LpMDHk5  : ------------------------------------------------------------ :    -
LpMDHk6  : ------------------------------------------------------------ :    -
LpMDHk7  : ------------------------------------------------------------ :    -
LpMDHk8  : ------------------------------------------------------------ :    -
LpMDHk9  : ------------------------------------------------------------ :    -
LpMDHk10 : ------------------------------------------------------------ :    -
LpMDHk11 : ------------------------------------------------------------ :    -
LpMDHk12 : ------------------------------------------------------------ :    -
LpMDHk13 : ------------------------------------------------------------ :    -
LpMDHk14 : ------------------------------------------------------------ :    -
LpMDHk15 : ------------------------------------------------------------ :    -
LpMDHk16 : ------------------------------------------------------------ :    -
LpMDHk17 : ------------------------------------------------------------ :    -
LpMDHk18 : ------------------------------------------------------------ :    -
LpMDHk19 : ------------------------------------------------------------ :    -
LpMDHk20 : ------------------------------------------------------------ :    -
LpMDHk21 : ------------------------------------------------------------ :    -
LpMDHk22 : ------------------------------------------------------------ :    -
LpMDHk23 : ------------------------------------------------------------ :    -
LpMDHk24 : ------------------------------------------------------------ :    -
LpMDHk25 : ------------------------------------------------------------ :    -
LpMDHk26 : ------------------------------------------------------------ :    -
LpMDHk27 : ------------------------------------------------------------ :    -
LpMDHk28 : ------------------------------------------------------------ :    -
LpMDHk29 : ------------------------------------------------------------ :    -
LpMDHk30 : ------------------------------------------------------------ :    -
LpMDHk31 : ------------------------------------------------------------ :    -
LpMDHk32 : ------------------------------------------------------------ :    -
LpMDHk33 : ------------------------------------------------------------ :    -
LpMDHk34 : ------------------------------------------------------------ :    -
LpMDHk35 : ------------------------------------------------------------ :    -
LpMDHk36 : ------------------------------------------------------------ :    -
LpMDHk37 : ------------------------------------------------------------ :    -
LpMDHk38 : ------------------------------------------------------------ :    -
LpMDHk39 : ------------------------------------------------------------ :    -
LpMDHk40 : ------------------------------------------------------------ :    -
LpMDHk41 : ------------------------------------------------------------ :    -
LpMDHk42 : ------------------------------------------------------------ :    -
LpMDHk43 : ------------------------------------------------------------ :    -
LpMDHk44 : ------------------------------------------------------------ :    -
LpMDHk45 : ------------------------------------------------------------ :    -
LpMDHk46 : ------------------------------------------------------------ :    -
LpMDHk47 : ------------------------------------------------------------ :    -
LpMDHk48 : ------------------------------------------------------------ :    -
LpMDHk49 : ------------------------------------------------------------ :    -
LpMDHk50 : ------------------------------------------------------------ :    -
LpMDHk51 : ------------------------------------------------------------ :    -
LpMDHk52 : ------------------------------------------------------------ :    -
LpMDHk53 : ------------------------------------------------------------ :    -
LpMDHk54 : ------------------------------------------------------------ :    -
LpMDHk55 : ------------------------------------------------------------ :    -
LpMDHk56 : ------------------------------------------------------------ :    -
LpMDHk57 : ------------------------------------------------------------ :    -
LpMDHk58 : ------------------------------------------------------------ :    -
LpMDHk59 : ------------------------------------------------------------ :    -
LpMDHk60 : ------------------------------------------------------------ :    -
LpMDHk61 : ------------------------------------------------------------ :    -
LpMDHk62 : ------------------------------------------------------------ :    -
LpMDHk63 : ------------------------------------------------------------ :    -
LpMDHk64 : ------------------------------------------------------------ :    -
LpMDHk65 : ------------------------------------------------------------ :    -
LpMDHk66 : TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTTGTTGAGTCATCGCTCCGCGCA :  594
```

FIGURE 37 (cont.)

```
                     *      1100         *      1120         *      1140
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : ------------------------------------------------------------ :   -
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : ------------------------------------------------------------ :   -
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : ------------------------------------------------------------ :   -
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : ------------------------------------------------------------ :   -
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : ATGGCTGGTGATCCAGATGTTTACGAGTGCACGTATGTTCAGTCTGAGTTAACAGAGCTT : 654
```

FIGURE 37 (cont.)

```
                       *       1160         *       1180         *       1200
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : ------------------------------------------------------------ :   -
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : ------------------------------------------------------------ :   -
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : ------------------------------------------------------------ :   -
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : ------------------------------------------------------------ :   -
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : CCATTCTTCGCGTCCAGAGTTAAGCTTGGGAAGGACGGNGTTGAGTCCATCATTTCCTCC : 714
```

FIGURE 37 (cont.)

```
                          *       1220         *       1240         *       1260
LpMDHk1  : ------------------------------------------------------------ :   -
LpMDHk2  : ------------------------------------------------------------ :   -
LpMDHk3  : ------------------------------------------------------------ :   -
LpMDHk4  : ------------------------------------------------------------ :   -
LpMDHk5  : ------------------------------------------------------------ :   -
LpMDHk6  : ------------------------------------------------------------ :   -
LpMDHk7  : ------------------------------------------------------------ :   -
LpMDHk8  : ------------------------------------------------------------ :   -
LpMDHk9  : ------------------------------------------------------------ :   -
LpMDHk10 : ------------------------------------------------------------ :   -
LpMDHk11 : ------------------------------------------------------------ :   -
LpMDHk12 : ------------------------------------------------------------ :   -
LpMDHk13 : ------------------------------------------------------------ :   -
LpMDHk14 : ------------------------------------------------------------ :   -
LpMDHk15 : ------------------------------------------------------------ :   -
LpMDHk16 : ------------------------------------------------------------ :   -
LpMDHk17 : ------------------------------------------------------------ :   -
LpMDHk18 : ------------------------------------------------------------ :   -
LpMDHk19 : ------------------------------------------------------------ :   -
LpMDHk20 : ------------------------------------------------------------ :   -
LpMDHk21 : ------------------------------------------------------------ :   -
LpMDHk22 : ------------------------------------------------------------ :   -
LpMDHk23 : ------------------------------------------------------------ :   -
LpMDHk24 : ------------------------------------------------------------ :   -
LpMDHk25 : ------------------------------------------------------------ :   -
LpMDHk26 : ------------------------------------------------------------ :   -
LpMDHk27 : ------------------------------------------------------------ :   -
LpMDHk28 : ------------------------------------------------------------ :   -
LpMDHk29 : ------------------------------------------------------------ :   -
LpMDHk30 : ------------------------------------------------------------ :   -
LpMDHk31 : ------------------------------------------------------------ :   -
LpMDHk32 : ------------------------------------------------------------ :   -
LpMDHk33 : ------------------------------------------------------------ :   -
LpMDHk34 : ------------------------------------------------------------ :   -
LpMDHk35 : ------------------------------------------------------------ :   -
LpMDHk36 : ------------------------------------------------------------ :   -
LpMDHk37 : ------------------------------------------------------------ :   -
LpMDHk38 : ------------------------------------------------------------ :   -
LpMDHk39 : ------------------------------------------------------------ :   -
LpMDHk40 : ------------------------------------------------------------ :   -
LpMDHk41 : ------------------------------------------------------------ :   -
LpMDHk42 : ------------------------------------------------------------ :   -
LpMDHk43 : ------------------------------------------------------------ :   -
LpMDHk44 : ------------------------------------------------------------ :   -
LpMDHk45 : ------------------------------------------------------------ :   -
LpMDHk46 : ------------------------------------------------------------ :   -
LpMDHk47 : ------------------------------------------------------------ :   -
LpMDHk48 : ------------------------------------------------------------ :   -
LpMDHk49 : ------------------------------------------------------------ :   -
LpMDHk50 : ------------------------------------------------------------ :   -
LpMDHk51 : ------------------------------------------------------------ :   -
LpMDHk52 : ------------------------------------------------------------ :   -
LpMDHk53 : ------------------------------------------------------------ :   -
LpMDHk54 : ------------------------------------------------------------ :   -
LpMDHk55 : ------------------------------------------------------------ :   -
LpMDHk56 : ------------------------------------------------------------ :   -
LpMDHk57 : ------------------------------------------------------------ :   -
LpMDHk58 : ------------------------------------------------------------ :   -
LpMDHk59 : ------------------------------------------------------------ :   -
LpMDHk60 : ------------------------------------------------------------ :   -
LpMDHk61 : ------------------------------------------------------------ :   -
LpMDHk62 : ------------------------------------------------------------ :   -
LpMDHk63 : ------------------------------------------------------------ :   -
LpMDHk64 : ------------------------------------------------------------ :   -
LpMDHk65 : ------------------------------------------------------------ :   -
LpMDHk66 : GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG : 774
```

FIGURE 37 (cont.)

```
LpMDHk1  : --- :   -
LpMDHk2  : --- :   -
LpMDHk3  : --- :   -
LpMDHk4  : --- :   -
LpMDHk5  : --- :   -
LpMDHk6  : --- :   -
LpMDHk7  : --- :   -
LpMDHk8  : --- :   -
LpMDHk9  : --- :   -
LpMDHk10 : --- :   -
LpMDHk11 : --- :   -
LpMDHk12 : --- :   -
LpMDHk13 : --- :   -
LpMDHk14 : --- :   -
LpMDHk15 : --- :   -
LpMDHk16 : --- :   -
LpMDHk17 : --- :   -
LpMDHk18 : --- :   -
LpMDHk19 : --- :   -
LpMDHk20 : --- :   -
LpMDHk21 : --- :   -
LpMDHk22 : --- :   -
LpMDHk23 : --- :   -
LpMDHk24 : --- :   -
LpMDHk25 : --- :   -
LpMDHk26 : --- :   -
LpMDHk27 : --- :   -
LpMDHk28 : --- :   -
LpMDHk29 : --- :   -
LpMDHk30 : --- :   -
LpMDHk31 : --- :   -
LpMDHk32 : --- :   -
LpMDHk33 : --- :   -
LpMDHk34 : --- :   -
LpMDHk35 : --- :   -
LpMDHk36 : --- :   -
LpMDHk37 : --- :   -
LpMDHk38 : --- :   -
LpMDHk39 : --- :   -
LpMDHk40 : --- :   -
LpMDHk41 : --- :   -
LpMDHk42 : --- :   -
LpMDHk43 : --- :   -
LpMDHk44 : --- :   -
LpMDHk45 : --- :   -
LpMDHk46 : --- :   -
LpMDHk47 : --- :   -
LpMDHk48 : --- :   -
LpMDHk49 : --- :   -
LpMDHk50 : --- :   -
LpMDHk51 : --- :   -
LpMDHk52 : --- :   -
LpMDHk53 : --- :   -
LpMDHk54 : --- :   -
LpMDHk55 : --- :   -
LpMDHk56 : --- :   -
LpMDHk57 : --- :   -
LpMDHk58 : --- :   -
LpMDHk59 : --- :   -
LpMDHk60 : --- :   -
LpMDHk61 : --- :   -
LpMDHk62 : --- :   -
LpMDHk63 : --- :   -
LpMDHk64 : --- :   -
LpMDHk65 : --- :   -
LpMDHk66 : AAG : 777
```

FIGURE 37 (cont.)

```
                       *        20         *        40         *        60
LpMDH1 : GNAAACAGNNGCGNCTTTTCCTNCANTGTTGCCGTGCAATCGCTGANAAGTATCCAGAAA :  60

                       *        80         *       100         *       120
LpMDH1 : TCATATACGAGGAAGTAATTATTGATAACTGCTGTATGACGCTCGTGAAGAACCCTGGTA : 120

                       *       140         *       160         *       180
LpMDH1 : CGTTTGATGTATTAGTGATGCCAAATCTATATGGCGACATTATTAGTGATCTATGTGCTG : 180

                       *       200         *       220         *       240
LpMDH1 : GTTTGATCGGAGGCTTGGGCCTAACTCCCAGCTGCAACATTGGTGAAGGTGGCATTTGTC : 240

                       *       260         *       280         *       300
LpMDH1 : TTGCAGAGGCTGTCCATGGCTCTGCACCTGATATATCTGGCAAGAACCTGGCAAACCCAA : 300

                       *       320         *       340         *       360
LpMDH1 : CTGCTCTTATGCTGAGTGCTGTTATGATGTTGCGCCACTTGCAATTNAACGACCAAGCAN : 360

                       *       380         *       400         *
LpMDH1 : AACGGATCCACAATGCTATCCTCCAGACTATCGNCGAGGGGAAGNACANAACTG : 414
```

FIGURE 38

```
                    *        20         *        40         *        60
LpMDHl : KQXXLFXXCCRAIAXKYPEIIYEEVIIDNCCMTLVKNPGTFDVLVMPNLYGDIISDLCAG :  60

                    *        80         *       100         *       120
LpMDHl : LIGGLGLTPSCNIGEGGICLAEAVHGSAPDISGKNLANPTALMLSAVMMLRHLQXNDQAX : 120

                    *
LpMDHl : RIHNAILQTIXEGKXXT : 137
```

FIGURE 39

```
                   *        20         *        40         *        60
LpMDHm : GNCACCNCCAGNNACAACTCTGGTACCTCAATTGCTACTCCACACCTCACTACTTCTACC :  60

                   *        80         *       100         *       120
LpMDHm : AATCCACTACACAGCTTCGAGCTACCCCGCCCCCGCAATCCAAACTACCTCTCCCTAGCA : 120

                   *       140         *       160         *       180
LpMDHm : AATCTACAACATGAAGGCAGTCGTAGCTGGAGCCGCCGGTGGCATTGGACAGCCATTGTC : 180

                   *       200         *       220         *       240
LpMDHm : CCTCCTCCTTAAGACCTGCCCGCTCGTCACTGAGCTCGCCCTATACGATGTCGTCAACGC : 240

                   *       260         *       280         *       300
LpMDHm : CGTCGGTGTCGCGACTGACCTCTCCCACATCTCCTCGCCCGCGAAAGTAACCGGCTACCT : 300

                   *       320         *       340         *       360
LpMDHm : GCCGGCAAATGACGGTATGCAGCAGGCTCTCACTGGCGCCGACATCGTGGTCATCCCCGC : 360

                   *       380         *       400         *       420
LpMDHm : TGGTATTCCCCGCAAGCCCGGCATGACCCGTGACGACCTCTTCAAGATCAACGCCGGCAT : 420

                   *       440         *       460         *       480
LpMDHm : TGTCCAGGGTCTCATCGAGGGTGTCGCCAAGCACTGCCCCAAGGCATACGTTCTCGTCAT : 480

                   *       500         *       520         *       540
LpMDHm : CTCCAACCCCGTCAACTCGACTGTGCCCATCGCCGCCGAGGTGCTGAAGAAGGCCGGTGT : 540

                   *       560         *       580         *       600
LpMDHm : CTTCGACCCCAAGAAGCTCTTCGGTGTCACCACCCTCGATGTCGTCCGCGCCGAGACCTT : 600

                   *       620         *       640         *
LpMDHm : CGTTGCCGAGATCACTGGCGAGAAGGACCCAGCGAAGTTGAACATNCCCGTA : 652
```

FIGURE 40

```
                   *        20         *        40         *        60
LpMDHm : XXPXTTLVPQLLLHTSLLLPIHYTASSYPAPAIQTTSP*QIYNMKAVVAGAAGGIGQPLS :  59

                   *        80         *       100         *       120
LpMDHm : LLLKTCPLVTELALYDVVNAVGVATDLSHISSPAKVTGYLPANDGMQQALTGADIVVIPA : 119

                   *       140         *       160         *       180
LpMDHm : GIPRKPGMTRDDLFKINAGIVQGLIEGVAKHCPKAYVLVISNPVNSTVPIAAEVLKKAGV : 179

                   *       200         *
LpMDHm : FDPKKLFGVTTLDVVRAETFVAEITGEKDPAKLNXPV : 216
```

FIGURE 41

```
                   *       20         *        40         *        60
LpPEPCa : GNGTACACGAAATAGAATCAACGGAAAGCANGAAGTGATGATTGGGTATCAGCATTCTGG :  60

                   *       80         *       100         *       120
LpPEPCa : GAAGGATGCTGGCCGTTTCTCTGCTGGTTGGCACTTGTACAAAGCTCAAGAGGAGCTTAT : 120

                   *      140         *       160         *       180
LpPEPCa : TAAGGTTGCGGAGACGTTTGGGGTTAAGNTGACTATGTTTCATGGACGAGGGGGTACTGT : 180

                   *      200         *       220         *       240
LpPEPCa : TGGAAGAGGTGGCGGCCCTACCCATCTTGCTATACTGTCACAACCTCCAGATACTGTCCA : 240

                   *      260         *       280         *       300
LpPEPCa : TGGATCACTTCGGGTAACTGTTCAAGGTGAAGTCATTGAGCAGTCCTTCGGAGAGGAGCA : 300

                   *      320         *       340         *       360
LpPEPCa : TTTGTGTTTTAGAACGCTTCAACGTTTTACAGCTGCTACTCTTGAACATGGTATGCATCC : 360

                   *      380         *       400         *       420
LpPEPCa : ACCAATCTCACCTAAACCAGAATGGCGTGCTTTGATGGATGAAATGGCTGTTGTTGCCAC : 420

                   *      440         *       460         *       480
LpPEPCa : AGAGGAATACCGTTCCATTGTTTTCCAAGAACCAAGATTTGTTGAGTATTTCCGCCTTGC : 480

                   *      500         *       520         *       540
LpPEPCa : AACACCAGAGCTCGAGTATGGTAGGATGAATATTGGAAGCAGGCCATCAAAACGTAAGCC : 540

                   *      560         *       580         *       600
LpPEPCa : AAGCGGAGGAATCGAATCATTGCGTGCAATTCCTTGGATATTTGCTTGGACACAGACTAG : 600

                   *      620         *       640         *       660
LpPEPCa : ATTCCACCTGCCAGTGTGGCTTGNTTTTGGTGCGGCCTTCAAGCATGTCCTGCAAAAGGA : 660

                   *      680         *       700         *       720
LpPEPCa : CATTCGTANTCTTCAAATCCTTCAGCAGATGTACAACGAGTGGCCGTTTAGGGTTACCAT : 720

                   *      740         *       760
LpPEPCa : AAACCTGGTTGAGATGGTGTTTGCCAAGGGCGATCCAGGTATAGCAGCT : 769
```

FIGURE 42

```
                    *        20         *        40         *        60
LpPEPCa : XTRNRINGKXEVMIGYQHSGKDAGRFSAGWHLYKAQEELIKVAETFGVKXTMFHGRGGTV :  60

                    *        80         *       100         *       120
LpPEPCa : GRGGGPTHLAILSQPPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHP : 120

                    *       140         *       160         *       180
LpPEPCa : PISPKPEWRALMDEMAVVATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSRPSKRKP : 180

                    *       200         *       220         *       240
LpPEPCa : SGGIESLRAIPWIFAWTQTRFHLPVWLXFGAAFKHVLQKDIRXLQILQQMYNEWPFRVTI : 240

                    *
LpPEPCa : NLVEMVFAKGDPGIAA : 256
```

FIGURE 43

```
                    *        20         *        40         *        60
LpPEPCb : GAAGAAGTTGCTGATGTTTTAAGNACATTTNTGTCCTTGCAGAGCTCCCAGCAGATTGTT :  60

                    *        80         *       100         *       120
LpPEPCb : TTGGTGCTTACATCATCTCAATGGCAACTGCCCCATCTGATGTGCTTGCTGTTGAGCTTT : 120

                    *       140         *       160         *       180
LpPEPCb : TGCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTTGAAAAGCTTG : 180

                    *       200         *       220         *       240
LpPEPCb : CAGATCTTGAANCAGCTCCAGCATCTGTTGCACGACTATTTTCAATAGACTGGTACATGA : 240

                    *       260         *       280         *       300
LpPEPCb : ATAGAATCAATGGCAAGCAGGAGGTCATGATTGGATACTCAGACTCTGGGAAGGACGCTG : 300

                    *       320         *       340         *       360
LpPEPCb : GGCGTCTCTCTGCAGCGTGGCAAATGTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA : 360

                    *       380         *       400         *       420
LpPEPCb : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 420

                    *       440         *       460         *       480
LpPEPCb : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC : 480

                    *       500         *       520         *       540
LpPEPCb : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 540

                    *       560         *       580         *       600
LpPEPCb : GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 600

                    *       620         *       640         *       660
LpPEPCb : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 660

                    *       680         *       700         *       720
LpPEPCb : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 720

                    *       740         *       760         *       780
LpPEPCb : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 780

                    *       800         *       820         *       840
LpPEPCb : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 840

                    *       860         *       880         *       900
LpPEPCb : CTGTATGGCTTGGATTTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 900
```

FIGURE 44

```
                        *        920         *        940         *        960
LpPEPCb : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC :  960

                        *        980         *       1000         *       1020
LpPEPCb : TTGAGATGGTTTTTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG : 1020

                        *       1040         *       1060         *       1080
LpPEPCb : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC : 1080

                        *       1100         *       1120         *       1140
LpPEPCb : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC : 1140

                        *       1160         *       1180         *       1200
LpPEPCb : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACATTGAATGTTTGCCAAGCCNACACCC : 1200

                        *       1220         *       1240         *       1260
LpPEPCb : TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG : 1260

                        *       1280         *       1300         *       1320
LpPEPCb : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG : 1320

                        *       1340         *       1360         *       1380
LpPEPCb : CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTTGCTGTGGAATGCAAA : 1380

                        *       1400         *       1420         *       1440
LpPEPCb : ACACAGGCTAGGCCAGTTTGCCTATTTGGAATAACTGTCATCCCGTCAGATGGGGCGTGA : 1440

                        *       1460         *       1480         *       1500
LpPEPCb : ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCATTTTGGCCACTTACATGCCTT : 1500

                        *       1520         *       1540         *       1560
LpPEPCb : TTGGTTATGGATGNACTTTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA : 1560

                        *       1580         *       1600         *       1620
LpPEPCb : ATATGGAACAATGATATTCTGGTNGGATCTAATAATTTGCTTGGCTCTGGCATCGNAATA : 1620

                        *       1640
LpPEPCb : GNGATTTGGAGTNGTTTAAC : 1640
```

FIGURE 44 (cont.)

```
                       *        20         *        40         *        60
LpPEPCb : RSCXCFKXIXVLAELPADCFGAYIISMATAPSDVLAVELLQRECHIKKPLRVVPLFEKLA :  60

                       *        80         *       100         *       120
LpPEPCb : DLEXAPASVARLFSIDWYMNRINGKQEVMIGYSDSGKDAGRLSAAWQMYKAQEDLIKVAK : 120

                       *       140         *       160         *       180
LpPEPCb : QYGVKLTMFHGRGGTVGRGGGPSHLAILSQPPDTIQGSLRVTVQGEVIEHSFGEEHLCFR : 180

                       *       200         *       220         *       240
LpPEPCb : TLQRFTAATLEHGMHPPISPKPEWRAIMDEMAVVATKEYRSIVFQEPRFVEYFRSATPET : 240

                       *       260         *       280         *       300
LpPEPCb : EYGRMNIGSRPSKRKPSGGIESLRAIPWIFAWTQTRFHLPVWLGFGAAFKHIMQKDIRNI : 300

                       *       320         *       340         *       360
LpPEPCb : HTLKEMYNEWPFFRVTLDLLEMVFAKGDPGIAALYDKLLVSEDLQPFGEQLRNNFEETKQ : 360

                       *       380         *       400         *       420
LpPEPCb : LLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAXTLKRIRDPSFEVTPQQAPLSKE : 420

                       *       440         *       460
LpPEPCb : FADEKEPAELVQLNRGSEYAPGLEDTLILTMKGICCGMQNTG : 462
```

FIGURE 45

```
                        *        20         *        40         *        60
LpPEPCb1 : GAAGAAGTTGCTGATGTTTTAAGNACATTTNTGTCCTTGCAGAGCTCCCAGCAGATTGTT :  60
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                        *        80         *       100         *       120
LpPEPCb1 : TTGGTGCTTACATCATCTCAATGGCAACTGCCCCATCTGATGTGCTTGCTGTTGAGCTTT : 120
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                        *       140         *       160         *       180
LpPEPCb1 : TGCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTTGAAAAGCTTG : 180
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                        *       200         *       220         *       240
LpPEPCb1 : CAGATCTTGAANCAGCTCCAGCATCTGTTGCACGACTATTTTCAATAGACTGGTACATGA : 240
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                        *       260         *       280         *       300
LpPEPCb1 : ATAGAATCAATGGCAAGCAGGAGGTCATGATTGGATACTCAGACTCTGGGAAGGACGCTG : 300
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                        *       320         *       340         *       360
LpPEPCb1 : GGCGTCTCTCTGCAGCGTGGCAAATGTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA : 360
LpPEPCb2 : -------------------------GTATAAAGCACAAGAAGATCTCATAAAGGTGGCAA :  35
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                        *       380         *       400         *       420
LpPEPCb1 : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 420
LpPEPCb2 : AGCAATATGGAGTAAAGTTAACAATGTTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG :  95
LpPEPCb3 : ----------------------AATGTTT-NTGGAAGAGGTGGAACGGTTGGCAGAGGAG :  37
LpPEPCb4 : ---------------------------------------------------GCANAGGAG :   9
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -
```

FIGURE 46

```
                       *       440         *       460         *       480
LpPEPCb1 : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC : 480
LpPEPCb2 : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC : 155
LpPEPCb3 : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACTAGACACGATACAAGGATCACTTC :  97
LpPEPCb4 : GTGGTCCCAGTCATCTTGCTATATTATCTCAACCACCAGACACGATACAAGGATCACTTC :  69
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       500         *       520         *       540
LpPEPCb1 : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 540
LpPEPCb2 : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGGGGAACACTTGTGCTTCA : 215
LpPEPCb3 : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 157
LpPEPCb4 : GTGTAACAGTTCAAGGCGAGGTCATAGAGCACTCATTTGGAGAGGAACACTTGTGCTTCA : 129
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       560         *       580         *       600
LpPEPCb1 : NAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCGC : 600
LpPEPCb2 : GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 275
LpPEPCb3 : GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 217
LpPEPCb4 : GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 189
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       620         *       640         *       660
LpPEPCb1 : CCAAACCAGAATGGCNTGCTATAATGGATGANATGGCTGTAGNGGCAGCAAAAGAAAATC : 660
LpPEPCb2 : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 335
LpPEPCb3 : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 277
LpPEPCb4 : CCAAGCCAGAATGGCGTGCTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAATATC : 249
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       680         *       700         *       720
LpPEPCb1 : GATCAATTGNCTTCCAAGAACCGCNTTTTGNCNAATA----------------------- : 697
LpPEPCb2 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 395
LpPEPCb3 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 337
LpPEPCb4 : GATCAATTGTCTTCCAAGAACCACGTTTTGTCGAATACTTCCGCTCGGCAACACCTGAGA : 309
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       740         *       760         *       780
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 455
LpPEPCb3 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 397
LpPEPCb4 : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 369
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                       *       800         *       820         *       840
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 515
LpPEPCb3 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACGAGGTTTCATCTTC : 457
LpPEPCb4 : TAGAATCGCTCCGTGCAATTCCATGGATCTTTGCTTGGACACAGACAAGGTTTCATCTTC : 429
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -
```

FIGURE 46 (cont.)

108/241

```
                    *        860         *        880         *        900
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : CTGTATGGCTTGGATTTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 575
LpPEPCb3 : CTGTATGGCTTGGATTTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 517
LpPEPCb4 : CTGTATGGCTTGGATTTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 489
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *        920         *        940         *        960
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC : 635
LpPEPCb3 : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC : 577
LpPEPCb4 : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTTAGGGTCACCCTTGACTTGC : 549
LpPEPCb5 : ------------------------------------------------------------ :   -
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *        980         *       1000         *       1020
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : TTGAGATGGTTTTTGCCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG : 695
LpPEPCb3 : TTGAGATGGTTTTTGCCAAGGGAGATCCAGGGATTGCTGCTTTATATGACAAATTGCTTG : 637
LpPEPCb4 : TTGAGATGGTTTTTGCCGAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG : 609
LpPEPCb5 : -------GGTTTTTG-CNAGGGAGATCC-GG-ATTGCTGCTTTATATGACAAATTGCTTG :  50
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *       1040         *       1060         *       1080
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGANAAACAACTTTGAAGAGACGAAAC : 755
LpPEPCb3 : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC : 697
LpPEPCb4 : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCAGCTGAGAAACAACTTTGAAGAGACGAAAC : 669
LpPEPCb5 : TGTCTGAAGATCTGCAGCCCTTTGGGGAGCNGCTGAGAAACAACTTTGAAGAGACGAAAC : 110
LpPEPCb6 : ------------------------------------------------------------ :   -

                    *       1100         *       1120         *       1140
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : AGNTACTCCTTAAGGTTGTTGNCCACAAGG------------------------------ : 785
LpPEPCb3 : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC : 757
LpPEPCb4 : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAGGGGGATCCTTACCTGAAGC : 729
LpPEPCb5 : AGTTACTCCTTCAGGTTGCTGGCCACAAGGACGTTCTTGAAGGGGATCCTTACCTGAAGC : 170
LpPEPCb6 : ----------------------------GGACGTTCTTGAAGGGGATCCTTACCTGAAGC :  32

                    *       1160         *       1180         *       1200
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : AGCGTCTGCGGGTGCGTGAGTCATAC---------------------------------- : 783
LpPEPCb4 : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACA------------------------- : 764
LpPEPCb5 : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACATTGAATGTTTGCCAAGCCTACACCC : 230
LpPEPCb6 : AGCGTCTGCGGTTGCGTGAGTCATACATCACAACATTGAATGTTTGCCAAGCGNNCACCC :  92

                    *       1220         *       1240         *       1260
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG : 290
LpPEPCb6 : TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG : 152
```

FIGURE 46 (cont.)

```
                      *      1280         *      1300         *      1320
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG : 350
LpPEPCb6 : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG : 212

                      *      1340         *      1360         *      1380
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTA-TTGCTGTGGAATGCAAA : 409
LpPEPCb6 : CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTTGCTGTGGAATGCAAA : 272

                      *      1400         *      1420         *      1440
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ACACAGGCTAGGCCAGTTTGCCTA-TTGGAATAACTGTCATTCCGTCAGATGGGGCGTGA : 468
LpPEPCb6 : ACACAGGCTAGGCCAGTTTGCCTATTTGGAATAACTGTCATCCCGTCAGAT-GGGCGTGA : 331

                      *      1460         *      1480         *      1500
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCATTTTGGCCACTTACATGCCTT : 528
LpPEPCb6 : ATATGTGTGTTCCCCAAATGCTAGTGAACCCTGGAGGCA-TTTGGCCACTTACATGCCTT : 390

                      *      1520         *      1540         *      1560
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : TTGGTTATGNATGNAC-TTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA : 587
LpPEPCb6 : TTGGTTATGGATGNACTTTGATCTTAATGTCAANGGTTGTTGAAGCCTGATCTAAATNAA : 450

                      *      1580         *      1600         *      1620
LpPEPCb1 : ------------------------------------------------------------ :   -
LpPEPCb2 : ------------------------------------------------------------ :   -
LpPEPCb3 : ------------------------------------------------------------ :   -
LpPEPCb4 : ------------------------------------------------------------ :   -
LpPEPCb5 : ATATGGAACAATGATATTCTGG-NGGATCTAATAATTTGCTTGGCTCTGGCATCGNAATA : 646
LpPEPCb6 : ATATGGAACAATGATATTCTGGTTGTTTCTTA---------------------------- : 482

                      *      1640
LpPEPCb1 : -------------------- :   -
LpPEPCb2 : -------------------- :   -
LpPEPCb3 : -------------------- :   -
LpPEPCb4 : -------------------- :   -
LpPEPCb5 : GNGATTTGGAGTNGTTTAAC : 666
LpPEPCb6 : -------------------- :   -
```

FIGURE 46 (cont.)

```
                    *        20         *        40         *        60
LpPEPCc : AGCANTCTGTNCTTNCCANCAACCACGTTTTGTNCGAATACTTNCCGCTCGGCAACACCT :  60

                    *        80         *       100         *       120
LpPEPCc : GCACACTGAATATGGTCGGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTG : 120

                    *       140         *       160         *       180
LpPEPCc : GAGGCATAGAATCGCTCCGTGCAATTCCATGCATCTTTGNTTGGACACAGACAAGGNTTN : 180

                    *       200         *       220
LpPEPCc : ATNTTCCTGTATGNCTTGNATTCGNCTCCACCNCCACCCCCNTA : 224
```

FIGURE 47

```
                      *        20         *        40         *        60
LpPEPCc : XSXLXXNHVLXEYXPLGNTCTLNMVGMNIGSRPSKRKPSGGIESLRAIPCIFXWTQTRXX : 60

                      *
LpPEPCc : XPVXLXFXSTXTP : 73
```

FIGURE 48

```
                       *        20         *         40         *         60
LpPEPCd : GTTNCTGGAACNAAGGATCTTCTTGAAGGTGATCCCTACCTGAAGCAGCGGCTCCGCCTC :  60

                       *        80         *        100         *        120
LpPEPCd : CGTGACGCGTACATCACCACCATGAACGTATGCCAGGCCTACACATTGAAGCGGATCCGT : 120

                       *       140         *        160         *        180
LpPEPCd : GACCCAGACTACCACGTCGCACTGCGGCCCCATCTTTCCAAGGAGGTTATGGACACAAGC : 180

                       *       200         *        220         *        240
LpPEPCd : AAGCCGGCTTCCGAGCTTGTGACGCTGAACCCGGCCAGCGAGTACGCCCCGGGGCTGGAG : 240

                       *       260         *        280         *        300
LpPEPCd : GACACCCTCATCTTGACCATGAAGGGCGTTGCTGCCGGTCTGCAAAACACCGGTTAGGGC : 300

                       *       320         *        340         *        360
LpPEPCd : CAGGAGAGATGCCTGATCACCATCTTTTTGTATCTTCATGATGATGCGATGTTTTTCTTT : 360

                       *       380         *        400         *        420
LpPEPCd : AGTCGTTTGCGGTGGGCCTTATATCTCTCGGACGTAGCTGCATCTGTCTCCCTGCTCAGT : 420

                       *       440         *        460         *        480
LpPEPCd : GAGGAATAATGGCGTTTCGCCCAAGTATATTGATAAATAAAGGGAACCGATGTTAATTTC : 480

                       *       500         *        520
LpPEPCd : AGATTTGTTTGTTAGTAATTGTTCTATTTATTTTGCGAAAAAAAAAA : 527
```

FIGURE 49

```
                        *       20        *        40        *       60
LpPEPCd : VXGXKDLLEGDPYLKQRLRLRDAYITTMNVCQAYTLKRIRDPDYHVALRPHLSKEVMDTS : 60

                        *       80        *
LpPEPCd : KPASELVTLNPASEYAPGLEDTLILTMKGVAAGLQNTG : 98
```

FIGURE 50

```
                  *        20         *        40         *        60
LpPEPCe : GTTACACGCGCAGTTTGCTTGTTAGCAAGGNAGATGGCTGCTAACTTGTACTTCTCTCAG :  60

                  *        80         *       100         *       120
LpPEPCe : ATAGAAGATCTGATGTTTGAGCTCTCTATGTGGCGCTGCAGTGATGAACTTAGGGTCCGT : 120

                  *       140         *       160         *       180
LpPEPCe : GCAGATGAAGTACATCTGTCCTCAAAAAAAAAATCTGCAAAGCATTACATAGAGTTCTGG : 180

                  *       200         *       220         *       240
LpPEPCe : AAGCAAGTTCCTCCAAATGAACCTTATCGTGTCATACTTGGCGATGTCAGGGATAAACTG : 240

                  *       260         *       280         *       300
LpPEPCe : TACTATACGCGCGAACGTTCTCGCCACATATTGACAACTGGAATTTCAGACATTCCAGAA : 300

                  *       320         *       340         *       360
LpPEPCe : GNGTCAACTTTTACTAATGTTGAACTGTTTCTGGAACCTCTTGAGCTGTGCTACAGATCC : 360

                  *       380         *       400         *       420
LpPEPCe : TTATCTTNCTGTGGNGACAAANCTATTGCTGANGGAAGCCTTCTTGATTTCTNGCGNNCN : 420

                  *       440         *
LpPEPCe : GNATCNACTTTGTGGGCTTACTCTNGCGAA : 450
```

FIGURE 51

```
                    *        20         *        40         *        60
LpPEPCe : VTRAVCLLARXMAANLYFSQIEDLMFELSMWRCSDELRVRADEVHLSSKKKSAKHYIEFW :  60

                    *        80         *       100         *       120
LpPEPCe : KQVPPNEPYRVILGDVRDKLYYTRERSRHILTTGISDIPEXSTFTNVELFLEPLELCYRS : 120

                    *       140         *
LpPEPCe : LSXCXDKXIAXGSLLDFXXXXXTLWAYSXE : 150
```

FIGURE 52

```
                    *        20         *        40         *        60
LpPEPCf : GGGGTGGTGGCCCTNCTCACCTTGCCTNCCTGTCTCANCCACCAGNCACAATCAACGGAT :  60

                    *        80         *       100         *       120
LpPEPCf : CACTCCGGGTGACTGTTCAAGGTGAAGTTATTGAGCAGAGCTTTGGGGAGGAACACTTGT : 120

                    *       140         *       160         *       180
LpPEPCf : GCTTCAGGACGCTGCAGCGTTTCACAGCTGCTACTCTTGAGCATGGGATGCGTCCACCCA : 180

                    *       200         *       220         *       240
LpPEPCf : TTTCACCAAAGCCAGAGTGGCGAGCTCTTCTTGATGAGATGGCTGTGGTTGCAACTGAGG : 240

                    *       260         *       280         *       300
LpPEPCf : AATACCGGTCAATCGTCTTCCAAGAACCACGCTTCGTCGAGTATTTCCGCCTTGCAACAC : 300

                    *       320         *       340         *       360
LpPEPCf : CAGAGACAGAGTATGGCAGGATGAATATAGGAAGCAGGCCATCAAAGAGAAAACCAAGTG : 360

                    *       380         *       400         *       420
LpPEPCf : GTGGCATTGAATCACTCCGTGCAATTCCATGGATCTTCGCATGGACGCAGACACGGTTCC : 420

                    *       440         *       460         *       480
LpPEPCf : ACCTTCCAGTCTGGTTGGGCTTTGGTGGTGCATTCAAGCATATCCTCAAGAAGGACATCA : 480

                    *       500         *       520         *       540
LpPEPCf : GAAATTTCCATATGCTCCAGGAGATGTACAACGAGTGGCCATTTTTCAGGGTCACGATCG : 540

                    *       560         *       580         *       600
LpPEPCf : ATCTTGTTGAGATGGTGTTCGCCAAGGGTAACCCTGGCATTGCTGCCTTGTATGACAGGC : 600

                    *       620         *       640
LpPEPCf : TCCTGGTTTCAGAGGAGCTACAGCCACTGGGTGACAAGCTGAGG : 644
```

FIGURE 53

```
                  *        20         *        40         *        60
LpPEPCf : GGGPXHLAXLSXPPXTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPI :  60

                  *        80         *       100         *       120
LpPEPCf : SPKPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSRPSKRKPSG : 120

                  *       140         *       160         *       180
LpPEPCf : GIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHILKKDIRNFHMLQEMYNEWPFFRVTID : 180

                  *       200         *
LpPEPCf : LVEMVFAKGNPGIAALYDRLLVSEELQPLGDKLR : 214
```

FIGURE 54

```
                       *        20          *         40          *         60
TrMDHa : GGCTTCTTAAAAACNCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA :  60

                       *        80          *        100          *        120
TrMDHa : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 120

                       *       140          *        160          *        180
TrMDHa : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 180

                       *       200          *        220          *        240
TrMDHa : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 240

                       *       260          *        280          *        300
TrMDHa : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 300

                       *       320          *        340          *        360
TrMDHa : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 360

                       *       380          *        400          *        420
TrMDHa : GATGTGATGACAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 420

                       *       440          *        460          *        480
TrMDHa : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 480

                       *       500          *        520          *        540
TrMDHa : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 540

                       *       560          *        580          *        600
TrMDHa : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 600

                       *       620          *        640          *        660
TrMDHa : AATGTTATAATATGGGGGAAATNATTCATCAACTCAATACCCTGNTGTNAACCACNCAAC : 660

                       *
TrMDHa : CGTTAAAATCTCCT : 674
```

FIGURE 55

```
                 *        20         *        40         *        60
TrMDHa : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAAESLNGVKMELVD :  60

                 *        80         *       100         *       120
TrMDHa : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMERKDVMTKNVSIYKSQASALEKH : 120

                 *       140         *       160         *       180
TrMDHa : AAANCKVLVVANPANTNALILKEYAPSIPEKNISALTRLDHNRALGQISERLNVEVSDVK : 180

                 *       200
TrMDHa : NVIIWGKXFINSIPXCXPXNR : 201
```

FIGURE 56

120/241

```
                      *        20         *        40         *        60
TrMDHa1   : GTNTTCTTGNAAACNCNCTAATNTCTTTTCTATTGTNCTNNTTTCTTCGATCTATTTCCA :  60
TrMDHa2   : -GCNACNTATAAGCTCTTTNNNCTNAGCTCTATTGTTCTTATTTCTTCGATCTATATCCA :  59
TrMDHa3   : -GCNTCTT-AAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA :  57
TrMDHa4   : -GCATCTT-AAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA :  57
TrMDHa5   : --CTTCTT-NAAAC-CACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCC- :  55
TrMDHa6   : -----CNTTAAAACNCACTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTT-CN :  54
TrMDHa7   : --------------GCANTAAACTCTTTTNTATTGTTCTTNTTTCTTCGATCTATTTCC- :  45
TrMDHa8   : --------------GCANTAAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCC- :  45
TrMDHa9   : ---------------CACT-AACTCTTTTCT-TTGTTCTTNTTTCTTCGATC-ATTTCC- :  41
TrMDHa10  : ------------------TAAACTCTTNTCTATTGTTCTTNTTTCTTCGATCTATTTCC- :  41
TrMDHa11  : -------------------AAACTCTTTTCTATTGTTCTTATTTCTTCGATCTATTTCCA :  41

                      *        80         *       100         *       120
TrMDHa1   : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCNCTGGTGCTGCAGGACAACTTGGGTATGCT : 120
TrMDHa2   : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 119
TrMDHa3   : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 117
TrMDHa4   : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 117
TrMDHa5   : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT : 115
TrMDHa6   : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAACTTGGGTATGCT : 114
TrMDHa7   : ATGGCC-AAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 104
TrMDHa8   : ATGGCC-AAGACCCAGTTCGTGTTCTTGT-CCTGGTGCTGCAGGACAAATTGGGTATGCT : 103
TrMDHa9   : ATGGCC-AAGACCCAGTTCGTGTTCTTGT-ACTGGTGCTGCAGGACAACTTGGGTATGCT :  99
TrMDHa10  : ATGGCC-AAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 100
TrMDHa11  : ATGGCCAAAGACCCAGTTCGTGTTCTTGTCACTGGTGCTGCAGGACAAATTGGGTATGCT : 101

                      *       140         *       160         *       180
TrMDHa1   : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGNCCTGACCANNCTGTGATCCTNCAC : 180
TrMDHa2   : CTCGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 179
TrMDHa3   : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 177
TrMDHa4   : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 177
TrMDHa5   : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 175
TrMDHa6   : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 174
TrMDHa7   : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 164
TrMDHa8   : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 163
TrMDHa9   : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 159
TrMDHa10  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 160
TrMDHa11  : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 161

                      *       200         *       220         *       240
TrMDHa1   : ATGCTTGACATTNCACCTGCAG-------------------------------------- : 202
TrMDHa2   : ATGCTTGACATCCCACCTGCAGCCGAATCACTGAACGGTGTAAAAATGGAGTTGGTGGAT : 239
TrMDHa3   : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 237
TrMDHa4   : ATGCTTGACATTCCACCTGCAGCCGAATCACTGAACGGTGTTAAAATGGAGTTGGTGGAT : 237
TrMDHa5   : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 235
TrMDHa6   : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 234
TrMDHa7   : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 224
TrMDHa8   : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 223
TrMDHa9   : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 219
TrMDHa10  : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 220
TrMDHa11  : ATGCTTGACATTCCACCTGCAGCCGAATCACTCAACGGTGTTAAAATGGAGTTGGTGGAT : 221
```

FIGURE 57

121/241

```
                   *         260         *         280         *         300
TrMDHa1   : ------------------------------------------------------------ :   -
TrMDHa2   : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACCACTGATGTGGTTGAGGCATGCACT : 299
TrMDHa3   : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 297
TrMDHa4   : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 297
TrMDHa5   : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 295
TrMDHa6   : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 294
TrMDHa7   : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 284
TrMDHa8   : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 283
TrMDHa9   : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 279
TrMDHa10  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 280
TrMDHa11  : GCTGCATTCCCTCTTCTTAAAGGAGTTGTTGCTACAACTGATGTGGTTGAGGCATGCACT : 281

                   *         320         *         340         *         360
TrMDHa1   : ------------------------------------------------------------ :   -
TrMDHa2   : GGGGTCAATATTGCCGTTATGGTTGGCGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 359
TrMDHa3   : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 357
TrMDHa4   : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 357
TrMDHa5   : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 355
TrMDHa6   : GGTGTNAATATTGACGNTATGGNTGGNGGGTTNCNTACNANACAACGTNT---------- : 344
TrMDHa7   : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 344
TrMDHa8   : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 343
TrMDHa9   : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 339
TrMDHa10  : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 340
TrMDHa11  : GGTGTCAATATTGCCGTTATGGTTGGTGGGTTCCCTANAAAAGAANGTATGGAGAGGAAA : 341

                   *         380         *         400         *         420
TrMDHa1   : ------------------------------------------------------------ :   -
TrMDHa2   : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 419
TrMDHa3   : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 417
TrMDHa4   : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 417
TrMDHa5   : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 415
TrMDHa6   : ------------------------------------------------------------ :   -
TrMDHa7   : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 404
TrMDHa8   : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 403
TrMDHa9   : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 399
TrMDHa10  : GATGTGATGACAAAAAAATGTCTCTATTTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 400
TrMDHa11  : GATGTGATGAC-AAAAAATGTCTCTATTTACAAGTCTTAAGCTTTTGNCCTTGAAAAACAT : 400

                   *         440         *         460         *         480
TrMDHa1   : ------------------------------------------------------------ :   -
TrMDHa2   : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 479
TrMDHa3   : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 477
TrMDHa4   : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 477
TrMDHa5   : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 475
TrMDHa6   : ------------------------------------------------------------ :   -
TrMDHa7   : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 464
TrMDHa8   : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 463
TrMDHa9   : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 459
TrMDHa10  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 460
TrMDHa11  : GCTGCTGCAAACTGCAAGGTTCTTGTTGTTGNCAACCCACCAAACACCAATGCATTGATC : 460
```

FIGURE 57 (cont.)

122/241

```
                         *        500         *        520         *        540
TrMDHa1   : ------------------------------------------------------------ :   -
TrMDHa2   : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 539
TrMDHa3   : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 537
TrMDHa4   : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 537
TrMDHa5   : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 535
TrMDHa6   : ------------------------------------------------------------ :   -
TrMDHa7   : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 524
TrMDHa8   : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 523
TrMDHa9   : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 519
TrMDHa10  : TTGAAGGAATATGCTCCATCCATTCCTGAGAAAAACATTTCTGCTTTGACTAGATTGGAC : 520
TrMDHa11  : TTGAAGGAATATGCTCCATNCATTCCTGANAAAAACATTTNTGCTTTGACTAGATTGGAC : 520

                         *        560         *        580         *        600
TrMDHa1   : ------------------------------------------------------------ :   -
TrMDHa2   : CATAACAGGGCACTNGGTCA---------------------------------------- : 559
TrMDHa3   : CATAACAGGGCACTAGGTCAAATTTCTGAA------------------------------ : 567
TrMDHa4   : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAA---------------------- : 575
TrMDHa5   : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 595
TrMDHa6   : ------------------------------------------------------------ :   -
TrMDHa7   : CATAACAGGGCACTAGGTCAAATTTCTGAAAGAC-------------------------- : 558
TrMDHa8   : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 583
TrMDHa9   : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGG-- : 577
TrMDHa10  : CATAACAGGGCACTAGGTCAAATTTCTGAAAGACTAAACGTTGAAGTTTCTGATGTGAAA : 580
TrMDHa11  : CATAACAGGGCACTAGGGCAAATTTNTGAAANACTAAACGTTGAAGTTTNTGATGTGAAA : 580

                         *        620         *        640         *        660
TrMDHa1   : ------------------------------------------------------------ :   -
TrMDHa2   : ------------------------------------------------------------ :   -
TrMDHa3   : ------------------------------------------------------------ :   -
TrMDHa4   : ------------------------------------------------------------ :   -
TrMDHa5   : AATGTTAT-A-AT----------------------------------------------- : 606
TrMDHa6   : ------------------------------------------------------------ :   -
TrMDHa7   : ------------------------------------------------------------ :   -
TrMDHa8   : AATGTTATAATCTGGG-------------------------------------------- : 599
TrMDHa9   : ------------------------------------------------------------ :   -
TrMDHa10  : AATGTTATAATCTG---------------------------------------------- : 594
TrMDHa11  : AATGTTAT-ATATGGGGGAAATNATTCATCAACTCAATACCCTGNTGTNAACCACNCAAC : 639

                         *
TrMDHa1   : -------------- :   -
TrMDHa2   : -------------- :   -
TrMDHa3   : -------------- :   -
TrMDHa4   : -------------- :   -
TrMDHa5   : -------------- :   -
TrMDHa6   : -------------- :   -
TrMDHa7   : -------------- :   -
TrMDHa8   : -------------- :   -
TrMDHa9   : -------------- :   -
TrMDHa10  : -------------- :   -
TrMDHa11  : CGTTAAAATCTCCT : 653
```

FIGURE 57 (cont.)

```
                 *        20         *        40         *        60
TrMDHb : TTCTCCCANAATCNNGAAANCGCCCANACATCACACAACATAACACCTTACTCTNCTTTC :   60

                 *        80         *       100         *       120
TrMDHb : TCTCTNAACAAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTCGATTCCTTCCATTTCT :  120

                 *       140         *       160         *       180
TrMDHb : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT :  180

                 *       200         *       220         *       240
TrMDHb : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC :  240

                 *       260         *       280         *       300
TrMDHb : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG :  300

                 *       320         *       340         *       360
TrMDHb : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA :  360

                 *       380         *       400         *       420
TrMDHb : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG :  420

                 *       440         *       460         *       480
TrMDHb : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA :  480

                 *       500         *       520         *       540
TrMDHb : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA :  540

                 *       560         *       580         *       600
TrMDHb : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA :  600

                 *       620         *       640         *       660
TrMDHb : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT :  660

                 *       680         *       700         *       720
TrMDHb : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT :  720

                 *       740         *       760         *       780
TrMDHb : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC :  780

                 *       800         *       820         *       840
TrMDHb : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT :  840

                 *       860         *       880         *       900
TrMDHb : AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCACATTCGCGATTGG :  900

                 *       920         *       940         *       960
TrMDHb : GTTCTTGGAACTCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC :  960
```

FIGURE 58

```
                 *      980         *      1000         *      1020
TrMDHb : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAAA : 1020

                 *      1040        *      1060         *      1080
TrMDHb : ATTGTTCAAGGACTTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA : 1080

                 *      1100        *
TrMDHb : GAGTTATCCGAGGAAAAGAGTTTGGCATACT : 1111
```

FIGURE 58 (cont.)

```
                *       20         *       40         *       60
TrMDHb : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAAESLNGVKMELVD :  60

                *       80         *      100         *      120
TrMDHb : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMERKDVMSKNVSIYKSQASALEKH : 120

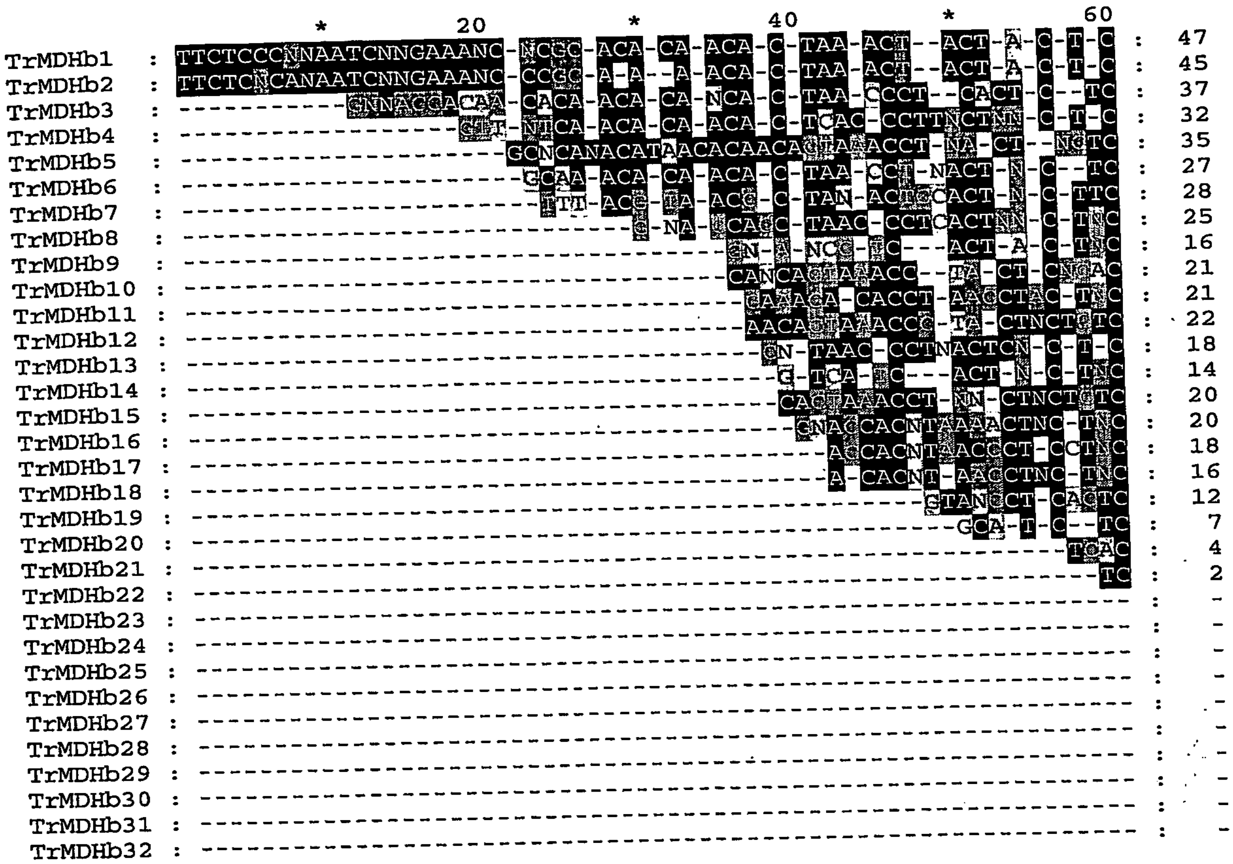
                *      140         *      160         *      180
TrMDHb : AAANCKVLVVANPANTNALILKEFAPSIPEKNISCLTRLDHNRALGQISERLNVQVSDVK : 180

                *      200         *      220         *      240
TrMDHb : NVIIWGNHSSTQYPDVNHATVNTPAGEKPVRELVSDDAWLNGEFISTVQQRGAAIIKARK : 240

                *      260         *      280         *      300
TrMDHb : LSSALSAASAACDHIRDWVLGTPQGTFVSMGVYSDGSYNVPAGLIYSFPVTTANGEWKIV : 300

                *      320
TrMDHb : QGLSIDEFSRKKLDLTAEELSEEKSLAY : 328
```

FIGURE 59



20
40
60
TrMDHb1 : 47
TrMDHb2 : 45
TrMDHb3 : 37
TrMDHb4 : 32
TrMDHb5 : 35
TrMDHb6 : 27
TrMDHb7 : 28
TrMDHb8 : 25
TrMDHb9 : 16
TrMDHb10 : 21
TrMDHb11 : 21
TrMDHb12 : 22
TrMDHb13 : 18
TrMDHb14 : 14
TrMDHb15 : 20
TrMDHb16 : 20
TrMDHb17 : 18
TrMDHb18 : 16
TrMDHb19 : 12
TrMDHb20 : 7
TrMDHb21 : 4
TrMDHb22 : 2
TrMDHb23 : -
TrMDHb24 : -
TrMDHb25 : -
TrMDHb26 : -
TrMDHb27 : -
TrMDHb28 : -
TrMDHb29 : -
TrMDHb30 : -
TrMDHb31 : -
TrMDHb32 : -

FIGURE 60

```
                    *        80         *        100         *        120
TrMDHb1  : TCT---AAACAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCCAGTTCT : 104
TrMDHb2  : TCT---AAACAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCCAGTTCT : 102
TrMDHb3  : TNA---AACAAAAACTGTTCTTCCACTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  94
TrMDHb4  : TCT:NAAACAAANGCTATTCTTCATCTCTTAATCTTCGCGGTTCGATTCCTTCCGTTTCT :  91
TrMDHb5  : TCT-N-AA-NAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCC-GTTCT :  91
TrMDHb6  : TCT---NAACAAAACTATTCTTCATCTCTTAATCTTCGCGGTTCGATTCCTTCCGGGTCT :  84
TrMDHb7  : TNN---AACAAAAACTATTCTTNATCTCTTAATCTTCGCGGTTCGATTCCTTCCGTTTCT :  85
TrMDHb8  : TCT-NNAACAAAAACTATTCTTCATCTCTTAATCTTCGCGGTTCGATTCCTTCCGTTTCT :  84
TrMDHb9  : TCN---AACAAAAACTGTTCTTCC-CTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  72
TrMDHb10 : TCTCA-AAC-AAAACTGNTCTTCCTCTCTTAA-CTTCCCTGTTCGATTCCTTCCACTTCT :  78
TrMDHb11 : TCTCTNAAC-AAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCCAGTTCT :  80
TrMDHb12 : TCTCT-NAACAAAACTGTTCTTCCTCTCTTNATCTTCCCTGTTCGATTCCTTCCACTTCT :  81
TrMDHb13 : TCT-N-AAANAAAACTATTCTT-ATCTCTTAATCTTCGCGGTTCGATTCCTTCCGTTTCT :  75
TrMDHb14 : TNC---AANAAAAACTGTTCTTCCACTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  71
TrMDHb15 : TCTCT-AAACAAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTCGATTCCTTCCACTTCT :  79
TrMDHb16 : TCTCTNAAC-AAAACTGTTCTTCCTCTCTTNATCTTCCCTGTTTGATTCCTTCC-GTTCT :  78
TrMDHb17 : TCT-CAAACAAAAACTGTTCTTC-GCTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  76
TrMDHb18 : TCTCTCAAC-AAAACTGTTCTTCCTCTCTTAATCTTCCCTGTTTGATTCCTTCC-GTTCT :  74
TrMDHb19 : TCT-NNAACAAAAACTGTTCTTC-GCTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  70
TrMDHb20 : TNA---AACAAAAACTGTTCTT-CNCTCTTAATCTTCCCTGTTCGATTCCTTCTATTTCT :  63
TrMDHb21 : GCTCTNAACAAAAACTGTTCTTCCTCGCTTNATCTTCCCTGTTTGATTCCTTCC-GTTCT :  63
TrMDHb22 : TCT--NAACAAAAACTGTTCTTC-GCTCTTNATCTTCCCTGTTCGATTCCTTCTATTTCT :  59
TrMDHb23 : --------CAAAAACTGCTCTTCCTCTCTTNATCTTCCCTGTTCGATTCCTTCC-CTTCT :  51
TrMDHb24 : ----------AAAACTGTTCTTCCTCTCTTNATCTTCCCTGTTCGATTCCTTCC-CTTCT :  49
TrMDHb25 : --------------GNNTTCTTCCTCTCTTCAACTTCCCTGTTTGATTCCTTCCAGTTCT :  46
TrMDHb26 : ---------------GGTTCTTC-GCTCTTATNCTTCCCTGTTCGATTCCTTCTATTTCT :  44
TrMDHb27 : --------------------TTCCTCTCTTNATCTTCCCTGTTTGATTCCTTCC-GTTCT :  39
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ------------------------------------------------------------ :   -
```

FIGURE 60 (cont.)

```
                        *       140         *       160         *       180
TrMDHb1   : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 164
TrMDHb2   : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 162
TrMDHb3   : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 154
TrMDHb4   : TCAGCAATGGCCAAAGACCCAGTTCGTGTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 151
TrMDHb5   : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 151
TrMDHb6   : TCAGCAATGGCCAAAGACCCAGTTCGTGTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 144
TrMDHb7   : TCAGCAATGGCCAAAGACCCAGTTCGTGTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 145
TrMDHb8   : TCAGCAATGGCCAAAGACCCAGTTCGTGTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 144
TrMDHb9   : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 132
TrMDHb10  : TCAAAAATGGCCNAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCNGGGCAAATTGGT : 138
TrMDHb11  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 140
TrMDHb12  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 141
TrMDHb13  : TCAGCAATGGCCAAAGACCCAGTTCGTCTCCTCGTTACTGGTGCTGCAGGCCAAATTGGT : 135
TrMDHb14  : TCAAAAATGGCCAAANACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 131
TrMDHb15  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 139
TrMDHb16  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 138
TrMDHb17  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 136
TrMDHb18  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 134
TrMDHb19  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 130
TrMDHb20  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 123
TrMDHb21  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 123
TrMDHb22  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 119
TrMDHb23  : T-NAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 110
TrMDHb24  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 109
TrMDHb25  : TCAAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 106
TrMDHb26  : T-NAAAATGGCCAAAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGCCAAATTGGT : 103
TrMDHb27  : TC-AAAATGGCC-AAGACCCAGTTCGTGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT :  97
TrMDHb28  : ------------------------------------------------------------ :   -
TrMDHb29  : ------------------------------------------------------------ :   -
TrMDHb30  : ------------------------------------------------------------ :   -
TrMDHb31  : ------------------------------------------------------------ :   -
TrMDHb32  : ------------------------------------------------------------ :   -
```

FIGURE 60 (cont.)

```
                     *       200         *       220         *       240
TrMDHb1  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 224
TrMDHb2  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 222
TrMDHb3  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 214
TrMDHb4  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211
TrMDHb5  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 211
TrMDHb6  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204
TrMDHb7  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 205
TrMDHb8  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 204
TrMDHb9  : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 192
TrMDHb10 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198
TrMDHb11 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 200
TrMDHb12 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 201
TrMDHb13 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 195
TrMDHb14 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 191
TrMDHb15 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 199
TrMDHb16 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 198
TrMDHb17 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 196
TrMDHb18 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 194
TrMDHb19 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 190
TrMDHb20 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183
TrMDHb21 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 183
TrMDHb22 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 179
TrMDHb23 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 170
TrMDHb24 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 169
TrMDHb25 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 166
TrMDHb26 : TATACACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 163
TrMDHb27 : TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC : 157
TrMDHb28 : -------------------------GGGGAGTGATGCTTGGTCCTGAT-NACCTGTGATC :  34
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ------------------------------------------------------------ :   -
```

FIGURE 60 (cont.)

```
                    *         260         *         280         *         300
TrMDHb1  : CTACACATGCTTGATATTCCACCGGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGATG : 284
TrMDHb2  : CTACACATGCTTGATATTCCACCGGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 282
TrMDHb3  : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 274
TrMDHb4  : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 271
TrMDHb5  : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 271
TrMDHb6  : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGNCATTGAATGGAGTTAAAATGGAGTTG : 264
TrMDHb7  : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 265
TrMDHb8  : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 264
TrMDHb9  : CTTGACATGCTTGATATTGCTGCAGNAGNAGAGTNATTGAATGGAGGTAAAATGGAGCTG : 252
TrMDHb10 : CTACACATGCTTGATATTCCACCGGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 258
TrMDHb11 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 260
TrMDHb12 : CTACACATGCTTGATATTCCACCGGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 261
TrMDHb13 : CTTCACATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 255
TrMDHb14 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 251
TrMDHb15 : CTACACATGCTTGATATTCCACCGGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 259
TrMDHb16 : CTACACATGCTTGATATTCCACCGGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 258
TrMDHb17 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 256
TrMDHb18 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 254
TrMDHb19 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 250
TrMDHb20 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 243
TrMDHb21 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 243
TrMDHb22 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 239
TrMDHb23 : CTACACATGCTTGATATTCCACCGGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 230
TrMDHb24 : CTACACATGCTTGATATTCCACCGGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 229
TrMDHb25 : CTTCACATGCTTGATATTCCTACAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 226
TrMDHb26 : CTTCACATGCTTGATATTCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG : 223
TrMDHb27 : CTTCACATGCTTGATATTCTTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG : 217
TrMDHb28 : CTT-NCATGCTTGATATCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAAATGGAGTTG :  93
TrMDHb29 : -------------NTATTCCTNCNGCAGCNGAGT-NTTGAATGGAG-TAAGATGGAGTTG :  45
TrMDHb30 : --------------TATTCCT-CGGCAGCAGAGT-NTTGAATGGAG-TAAGATGGAGTTG :  43
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ------------------------------------------------------------ :   -
```

FIGURE 60 (cont.)

```
                 *        320         *        340         *        360
TrMDHb1  : GNCGATGCTGNATTNNCACTTGTTAAAGGNGANGGTGCT--------------------- : 323
TrMDHb2  : GTCGATGCTGCATTTCCACTTGTTAAAGGTGNTGATGNTACAACTGATGATGGNGACGNA : 342
TrMDHb3  : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 334
TrMDHb4  : GTGGATGCTGCATTTCCACTTCTTAAAGGGGTTGTTGCTACAACTGATGTTGTTGAAGCA : 331
TrMDHb5  : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 331
TrMDHb6  : GTGGATGCTGCATTTCCACTTCTTAAAGGGGTTGTTGCTACAACTGATGTTGTTGAAGCA : 324
TrMDHb7  : GGGGATGCTGCATTTCCACTTCTTAAAGGGGTTGTTGCTACAACTGATGTTGTTGAAGCA : 325
TrMDHb8  : GTGGATGCTGCATTTCCACTTCTTAAAGGGGTTGTTGCTACAACTGATGTTGTTGAAGCA : 324
TrMDHb9  : CGGGATGCTGNATTNNAACTTCTTAGAGGGGCCGGGGCTACGACTGATGCTGGCCAAGCA : 312
TrMDHb10 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 318
TrMDHb11 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 320
TrMDHb12 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 321
TrMDHb13 : GTGGATGCTGCATTTCCACTTCTTAAAGGGGTTGTTGCTACAACTGATGTTGTTGAAGCA : 315
TrMDHb14 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 311
TrMDHb15 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 319
TrMDHb16 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 318
TrMDHb17 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 316
TrMDHb18 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 314
TrMDHb19 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 310
TrMDHb20 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 303
TrMDHb21 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 303
TrMDHb22 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 299
TrMDHb23 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 290
TrMDHb24 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 289
TrMDHb25 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 286
TrMDHb26 : GTGGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAAGCA : 283
TrMDHb27 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 277
TrMDHb28 : GTGGATGCTGCATTTCCACTTCTTAAAGGCATTGTTGCTACAACTGATGTTGTTGAAGCA : 153
TrMDHb29 : GTCGATGCTGCATTTCCACTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 105
TrMDHb30 : GTCGATGCTGCATTTCC-CTTCTTAAAGGTGTTGTTGCTACAACTGATGTTGTTGAGGCA : 102
TrMDHb31 : ------------------------------------------------------------ :   -
TrMDHb32 : ------------------------------------------------------------ :   -
```

FIGURE 60 (cont.)

```
                          *       380         *       400         *       420
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : TNNNCTGG---------------------------------------------------- : 350
TrMDHb3  : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 394
TrMDHb4  : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 391
TrMDHb5  : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 391
TrMDHb6  : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 384
TrMDHb7  : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 385
TrMDHb8  : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 384
TrMDHb9  : TGCGCTGCA-CCCATATNGCNN-------------------------------------- : 333
TrMDHb10 : TGCACTGGAGTCAATATGGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAN : 378
TrMDHb11 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 380
TrMDHb12 : TGCACTGGAGTCAATATGGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 381
TrMDHb13 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 375
TrMDHb14 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 371
TrMDHb15 : TGCACTGGAGTCAATATGGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 379
TrMDHb16 : TGCACTGGAGTCAATATGGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 378
TrMDHb17 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 376
TrMDHb18 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 374
TrMDHb19 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 370
TrMDHb20 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTNTGGAG : 363
TrMDHb21 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 363
TrMDHb22 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 359
TrMDHb23 : TGCACTGGAGTCAATATGGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 350
TrMDHb24 : TGCACTGGAGTCAATATGGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 349
TrMDHb25 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 346
TrMDHb26 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 343
TrMDHb27 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 337
TrMDHb28 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 213
TrMDHb29 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 165
TrMDHb30 : TGCACTGGAGTCAATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 162
TrMDHb31 : --------------------------------------------------------GGAG :   4
TrMDHb32 : --------------------------------------------------------NNNN :   4
```

FIGURE 60 (cont.)

```
                     *       440         *       460         *       480
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 454
TrMDHb4  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 451
TrMDHb5  : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 451
TrMDHb6  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 444
TrMDHb7  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCAGCCCTTGAA : 445
TrMDHb8  : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 444
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 438
TrMDHb11 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 440
TrMDHb12 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 441
TrMDHb13 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 435
TrMDHb14 : AGGAAGGATGTGATGACTAANAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 431
TrMDHb15 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 439
TrMDHb16 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 438
TrMDHb17 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 436
TrMDHb18 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 434
TrMDHb19 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 430
TrMDHb20 : AGGAAGGATGTGATGACTAAGANTGTCTCTATTTACAANANNNAGNCTTNTGNCCTTGAA : 423
TrMDHb21 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 423
TrMDHb22 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 419
TrMDHb23 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 410
TrMDHb24 : AGGAAGGATGTTATGTCTAAGAACGTCTCTATTTACAAGTCCCAAGCTTCTGCCCTTGAA : 409
TrMDHb25 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 406
TrMDHb26 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 403
TrMDHb27 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 397
TrMDHb28 : AGGAAGGATGTGATGACTAAGAATGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 273
TrMDHb29 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 225
TrMDHb30 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA : 222
TrMDHb31 : AGGAAGGATGTGATGTCTAAGAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA :  64
TrMDHb32 : NNGNANGNNGTGATGTCTAANAACGTCTCTATTTACAAGTCCCAGGCTTCTGCCCTTGAA :  64
```

FIGURE 60 (cont.)

```
                  *       500         *       520         *       540
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 514
TrMDHb4  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 511
TrMDHb5  : AAGCATGCTGCTGCCAACTGCAAGGNTTTGGTTGNTGCTAACCCANC-AACACCAATGCA : 510
TrMDHb6  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 504
TrMDHb7  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 505
TrMDHb8  : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 504
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 498
TrMDHb11 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGC-AACACCAATGCA : 499
TrMDHb12 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 501
TrMDHb13 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 495
TrMDHb14 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGG----------------------------- : 462
TrMDHb15 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 499
TrMDHb16 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 498
TrMDHb17 : AAGCATGCTGCTGCCAACTGCAAGGNTTTGGGTATTGCTAACCCANCAAATACCAATGCA : 496
TrMDHb18 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGC-AACACCAATGCA : 493
TrMDHb19 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 490
TrMDHb20 : AAGGATNCTG-------------------------------------------------- : 433
TrMDHb21 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 483
TrMDHb22 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 479
TrMDHb23 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 470
TrMDHb24 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 469
TrMDHb25 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 466
TrMDHb26 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 463
TrMDHb27 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 457
TrMDHb28 : AAGCAAGCTGCTGCCAACTGCAAGGTTTTGGTTATTGCTAACCCAGCAAATACCAATGCA : 333
TrMDHb29 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 285
TrMDHb30 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 282
TrMDHb31 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 124
TrMDHb32 : AAGCATGCTGCTGCCAACTGCAAGGTTTTGGTTGTTGCTAACCCAGCAAACACCAATGCA : 124
```

FIGURE 60 (cont.)

```
                       *       560         *       580         *       600
TrMDHb1   : ------------------------------------------------------------ :   -
TrMDHb2   : ------------------------------------------------------------ :   -
TrMDHb3   : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 574
TrMDHb4   : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 571
TrMDHb5   : TTGATCTTGNAGGAATGNGCT--------------------------------------- : 531
TrMDHb6   : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 564
TrMDHb7   : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 565
TrMDHb8   : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 564
TrMDHb9   : ------------------------------------------------------------ :   -
TrMDHb10  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTNGACTAGA : 558
TrMDHb11  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 559
TrMDHb12  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 561
TrMDHb13  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 555
TrMDHb14  : ------------------------------------------------------------ :   -
TrMDHb15  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 559
TrMDHb16  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 558
TrMDHb17  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGANAAAAACATTTCANGTTTG------ : 550
TrMDHb18  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 553
TrMDHb19  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 550
TrMDHb20  : ------------------------------------------------------------ :   -
TrMDHb21  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 543
TrMDHb22  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 539
TrMDHb23  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 530
TrMDHb24  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 529
TrMDHb25  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 526
TrMDHb26  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 523
TrMDHb27  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 517
TrMDHb28  : TTGATCTTGAAGGAGTTTGCTCCATCTATTCCAGAGAAAAACATTTCAGGTTTGACTAGA : 393
TrMDHb29  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 345
TrMDHb30  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 342
TrMDHb31  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 184
TrMDHb32  : TTGATCTTGAAGGAATTTGCTCCATCTATTCCAGAGAAAAACATTTCTTGTTTGACTAGA : 184
```

FIGURE 60 (cont.)

```
                         *       620         *       640         *       660
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : CTTGATCACAA------------------------------------------------- : 585
TrMDHb4  : CTTGATCACAACAGGGCATTGG-------------------------------------- : 593
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : CTTGATCAC--------------------------------------------------- : 573
TrMDHb7  : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAG---------------------- : 603
TrMDHb8  : CTTGATCACAACAGGGCATTGGGCCAAATTTCT--------------------------- : 597
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : CTTGATCAC--------------------------------------------------- : 567
TrMDHb11 : CTTGATCACC-------------------------------------------------- : 569
TrMDHb12 : CTTGATCACAACAGGGCATTGGGCCAAATTT----------------------------- : 592
TrMDHb13 : CTTGATCACAACAGGGCATTGGGCCAAATT------------------------------ : 585
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : CTTGATCACAACAG---------------------------------------------- : 573
TrMDHb16 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAAT--------------- : 603
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAG---------------------- : 591
TrMDHb19 : CTTGATCACAACAGGGCATTG--------------------------------------- : 571
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTG------------------ : 585
TrMDHb22 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAAGTTTCTGAT : 599
TrMDHb23 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAG---------------------- : 568
TrMDHb24 : CTTGATCACAACAGGGCATTGGGCCAAAT------------------------------- : 558
TrMDHb25 : CGTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT : 586
TrMDHb26 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAAGTTTCTGAT : 583
TrMDHb27 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTC---- : 573
TrMDHb28 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAAGTTTCTGAT : 453
TrMDHb29 : CTTGATCACAACAGGGCATTGNGCCAAATTTCTGAAAGATTGAATGTCCAAGTTTCTGAT : 405
TrMDHb30 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTCCAAGTTTCTGAT : 402
TrMDHb31 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT : 244
TrMDHb32 : CTTGATCACAACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAAGTTTCTGAT : 244
```

FIGURE 60 (cont.)

```
                        *       680         *       700         *       720
TrMDHb1   : ------------------------------------------------------------ :   -
TrMDHb2   : ------------------------------------------------------------ :   -
TrMDHb3   : ------------------------------------------------------------ :   -
TrMDHb4   : ------------------------------------------------------------ :   -
TrMDHb5   : ------------------------------------------------------------ :   -
TrMDHb6   : ------------------------------------------------------------ :   -
TrMDHb7   : ------------------------------------------------------------ :   -
TrMDHb8   : ------------------------------------------------------------ :   -
TrMDHb9   : ------------------------------------------------------------ :   -
TrMDHb10  : ------------------------------------------------------------ :   -
TrMDHb11  : ------------------------------------------------------------ :   -
TrMDHb12  : ------------------------------------------------------------ :   -
TrMDHb13  : ------------------------------------------------------------ :   -
TrMDHb14  : ------------------------------------------------------------ :   -
TrMDHb15  : ------------------------------------------------------------ :   -
TrMDHb16  : ------------------------------------------------------------ :   -
TrMDHb17  : ------------------------------------------------------------ :   -
TrMDHb18  : ------------------------------------------------------------ :   -
TrMDHb19  : ------------------------------------------------------------ :   -
TrMDHb20  : ------------------------------------------------------------ :   -
TrMDHb21  : ------------------------------------------------------------ :   -
TrMDHb22  : GTAAAGAATGT------------------------------------------------- : 610
TrMDHb23  : ------------------------------------------------------------ :   -
TrMDHb24  : ------------------------------------------------------------ :   -
TrMDHb25  : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 646
TrMDHb26  : ------------------------------------------------------------ :   -
TrMDHb27  : ------------------------------------------------------------ :   -
TrMDHb28  : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 513
TrMDHb29  : GTAAAGAATGTCATTATCTGGNGTAATCATTCATCAACTCAGCATCCTGATGTCAACCAT : 465
TrMDHb30  : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 462
TrMDHb31  : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 304
TrMDHb32  : GTAAAGAATGTCATTATCTGGGGTAATCATTCATCAACTCAGTATCCTGATGTCAACCAT : 304
```

FIGURE 60 (cont.)

138/241

```
                    *       740         *        760         *        780
TrMDHb1   : ------------------------------------------------------------ :   -
TrMDHb2   : ------------------------------------------------------------ :   -
TrMDHb3   : ------------------------------------------------------------ :   -
TrMDHb4   : ------------------------------------------------------------ :   -
TrMDHb5   : ------------------------------------------------------------ :   -
TrMDHb6   : ------------------------------------------------------------ :   -
TrMDHb7   : ------------------------------------------------------------ :   -
TrMDHb8   : ------------------------------------------------------------ :   -
TrMDHb9   : ------------------------------------------------------------ :   -
TrMDHb10  : ------------------------------------------------------------ :   -
TrMDHb11  : ------------------------------------------------------------ :   -
TrMDHb12  : ------------------------------------------------------------ :   -
TrMDHb13  : ------------------------------------------------------------ :   -
TrMDHb14  : ------------------------------------------------------------ :   -
TrMDHb15  : ------------------------------------------------------------ :   -
TrMDHb16  : ------------------------------------------------------------ :   -
TrMDHb17  : ------------------------------------------------------------ :   -
TrMDHb18  : ------------------------------------------------------------ :   -
TrMDHb19  : ------------------------------------------------------------ :   -
TrMDHb20  : ------------------------------------------------------------ :   -
TrMDHb21  : ------------------------------------------------------------ :   -
TrMDHb22  : ------------------------------------------------------------ :   -
TrMDHb23  : ------------------------------------------------------------ :   -
TrMDHb24  : ------------------------------------------------------------ :   -
TrMDHb25  : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC : 706
TrMDHb26  : ------------------------------------------------------------ :   -
TrMDHb27  : ------------------------------------------------------------ :   -
TrMDHb28  : GCAACTGTTAACACCCCCGCCGGGGAGAAGCCTGTCCGTGAACTTGTTT----------- : 562
TrMDHb29  : GCAACTGTTAACACCCNCGCTGNNGAGAAGCCTGNCCGTGAGCTNGTTTC---------- : 515
TrMDHb30  : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC : 522
TrMDHb31  : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC : 364
TrMDHb32  : GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGTTTCTGATGACGCC : 364
```

FIGURE 60 (cont.)

```
                     *        800         *        820         *        840
TrMDHb1   : ------------------------------------------------------------ :   -
TrMDHb2   : ------------------------------------------------------------ :   -
TrMDHb3   : ------------------------------------------------------------ :   -
TrMDHb4   : ------------------------------------------------------------ :   -
TrMDHb5   : ------------------------------------------------------------ :   -
TrMDHb6   : ------------------------------------------------------------ :   -
TrMDHb7   : ------------------------------------------------------------ :   -
TrMDHb8   : ------------------------------------------------------------ :   -
TrMDHb9   : ------------------------------------------------------------ :   -
TrMDHb10  : ------------------------------------------------------------ :   -
TrMDHb11  : ------------------------------------------------------------ :   -
TrMDHb12  : ------------------------------------------------------------ :   -
TrMDHb13  : ------------------------------------------------------------ :   -
TrMDHb14  : ------------------------------------------------------------ :   -
TrMDHb15  : ------------------------------------------------------------ :   -
TrMDHb16  : ------------------------------------------------------------ :   -
TrMDHb17  : ------------------------------------------------------------ :   -
TrMDHb18  : ------------------------------------------------------------ :   -
TrMDHb19  : ------------------------------------------------------------ :   -
TrMDHb20  : ------------------------------------------------------------ :   -
TrMDHb21  : ------------------------------------------------------------ :   -
TrMDHb22  : ------------------------------------------------------------ :   -
TrMDHb23  : ------------------------------------------------------------ :   -
TrMDHb24  : ------------------------------------------------------------ :   -
TrMDHb25  : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTG-------------- : 752
TrMDHb26  : ------------------------------------------------------------ :   -
TrMDHb27  : ------------------------------------------------------------ :   -
TrMDHb28  : ------------------------------------------------------------ :   -
TrMDHb29  : ------------------------------------------------------------ :   -
TrMDHb30  : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT : 582
TrMDHb31  : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT : 424
TrMDHb32  : TGGTTGAATGGAGAATTCATATCTACCGTTCAACAACGTGGTGCTGCAATTATTAAGGCT : 424
```

FIGURE 60 (cont.)

```
                         *       860         *       880         *       900
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : ------------------------------------------------------------ :   -
TrMDHb4  : ------------------------------------------------------------ :   -
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : ------------------------------------------------------------ :   -
TrMDHb7  : ------------------------------------------------------------ :   -
TrMDHb8  : ------------------------------------------------------------ :   -
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : ------------------------------------------------------------ :   -
TrMDHb11 : ------------------------------------------------------------ :   -
TrMDHb12 : ------------------------------------------------------------ :   -
TrMDHb13 : ------------------------------------------------------------ :   -
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : ------------------------------------------------------------ :   -
TrMDHb16 : ------------------------------------------------------------ :   -
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : ------------------------------------------------------------ :   -
TrMDHb19 : ------------------------------------------------------------ :   -
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : ------------------------------------------------------------ :   -
TrMDHb22 : ------------------------------------------------------------ :   -
TrMDHb23 : ------------------------------------------------------------ :   -
TrMDHb24 : ------------------------------------------------------------ :   -
TrMDHb25 : ------------------------------------------------------------ :   -
TrMDHb26 : ------------------------------------------------------------ :   -
TrMDHb27 : ------------------------------------------------------------ :   -
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : AGAAAGCTTTCAAGTG-------------------------------------------- : 598
TrMDHb31 : AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCACATTCGCGATTGG : 484
TrMDHb32 : AGAAAGCTTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTGCGACCACATTCGCGATTGG : 484
```

FIGURE 60 (cont.)

```
                    *       920         *       940         *       960
TrMDHb1  : ------------------------------------------------------------ :   -
TrMDHb2  : ------------------------------------------------------------ :   -
TrMDHb3  : ------------------------------------------------------------ :   -
TrMDHb4  : ------------------------------------------------------------ :   -
TrMDHb5  : ------------------------------------------------------------ :   -
TrMDHb6  : ------------------------------------------------------------ :   -
TrMDHb7  : ------------------------------------------------------------ :   -
TrMDHb8  : ------------------------------------------------------------ :   -
TrMDHb9  : ------------------------------------------------------------ :   -
TrMDHb10 : ------------------------------------------------------------ :   -
TrMDHb11 : ------------------------------------------------------------ :   -
TrMDHb12 : ------------------------------------------------------------ :   -
TrMDHb13 : ------------------------------------------------------------ :   -
TrMDHb14 : ------------------------------------------------------------ :   -
TrMDHb15 : ------------------------------------------------------------ :   -
TrMDHb16 : ------------------------------------------------------------ :   -
TrMDHb17 : ------------------------------------------------------------ :   -
TrMDHb18 : ------------------------------------------------------------ :   -
TrMDHb19 : ------------------------------------------------------------ :   -
TrMDHb20 : ------------------------------------------------------------ :   -
TrMDHb21 : ------------------------------------------------------------ :   -
TrMDHb22 : ------------------------------------------------------------ :   -
TrMDHb23 : ------------------------------------------------------------ :   -
TrMDHb24 : ------------------------------------------------------------ :   -
TrMDHb25 : ------------------------------------------------------------ :   -
TrMDHb26 : ------------------------------------------------------------ :   -
TrMDHb27 : ------------------------------------------------------------ :   -
TrMDHb28 : ------------------------------------------------------------ :   -
TrMDHb29 : ------------------------------------------------------------ :   -
TrMDHb30 : ------------------------------------------------------------ :   -
TrMDHb31 : GTTCTTGGAACTCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC : 544
TrMDHb32 : GTTCTTGGAACTCCCCAGGGCACCTTCGTTTCAATGGGAGTGTATTCTGATGGTTCTTAC : 544
```

FIGURE 60 (cont.)

```
                        *       980         *      1000         *      1020
TrMDHb1   : ------------------------------------------------------------ :   -
TrMDHb2   : ------------------------------------------------------------ :   -
TrMDHb3   : ------------------------------------------------------------ :   -
TrMDHb4   : ------------------------------------------------------------ :   -
TrMDHb5   : ------------------------------------------------------------ :   -
TrMDHb6   : ------------------------------------------------------------ :   -
TrMDHb7   : ------------------------------------------------------------ :   -
TrMDHb8   : ------------------------------------------------------------ :   -
TrMDHb9   : ------------------------------------------------------------ :   -
TrMDHb10  : ------------------------------------------------------------ :   -
TrMDHb11  : ------------------------------------------------------------ :   -
TrMDHb12  : ------------------------------------------------------------ :   -
TrMDHb13  : ------------------------------------------------------------ :   -
TrMDHb14  : ------------------------------------------------------------ :   -
TrMDHb15  : ------------------------------------------------------------ :   -
TrMDHb16  : ------------------------------------------------------------ :   -
TrMDHb17  : ------------------------------------------------------------ :   -
TrMDHb18  : ------------------------------------------------------------ :   -
TrMDHb19  : ------------------------------------------------------------ :   -
TrMDHb20  : ------------------------------------------------------------ :   -
TrMDHb21  : ------------------------------------------------------------ :   -
TrMDHb22  : ------------------------------------------------------------ :   -
TrMDHb23  : ------------------------------------------------------------ :   -
TrMDHb24  : ------------------------------------------------------------ :   -
TrMDHb25  : ------------------------------------------------------------ :   -
TrMDHb26  : ------------------------------------------------------------ :   -
TrMDHb27  : ------------------------------------------------------------ :   -
TrMDHb28  : ------------------------------------------------------------ :   -
TrMDHb29  : ------------------------------------------------------------ :   -
TrMDHb30  : ------------------------------------------------------------ :   -
TrMDHb31  : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAA- : 603
TrMDHb32  : AACGTACCAGCTGGACTCATCTATTCATTCCCTGTCACCACTGCTAATGGGGAATGGAAA : 604
```

FIGURE 60 (cont.)

```
                     *       1040         *        1060         *        1080
TrMDHb1   : ------------------------------------------------------------ :   -
TrMDHb2   : ------------------------------------------------------------ :   -
TrMDHb3   : ------------------------------------------------------------ :   -
TrMDHb4   : ------------------------------------------------------------ :   -
TrMDHb5   : ------------------------------------------------------------ :   -
TrMDHb6   : ------------------------------------------------------------ :   -
TrMDHb7   : ------------------------------------------------------------ :   -
TrMDHb8   : ------------------------------------------------------------ :   -
TrMDHb9   : ------------------------------------------------------------ :   -
TrMDHb10  : ------------------------------------------------------------ :   -
TrMDHb11  : ------------------------------------------------------------ :   -
TrMDHb12  : ------------------------------------------------------------ :   -
TrMDHb13  : ------------------------------------------------------------ :   -
TrMDHb14  : ------------------------------------------------------------ :   -
TrMDHb15  : ------------------------------------------------------------ :   -
TrMDHb16  : ------------------------------------------------------------ :   -
TrMDHb17  : ------------------------------------------------------------ :   -
TrMDHb18  : ------------------------------------------------------------ :   -
TrMDHb19  : ------------------------------------------------------------ :   -
TrMDHb20  : ------------------------------------------------------------ :   -
TrMDHb21  : ------------------------------------------------------------ :   -
TrMDHb22  : ------------------------------------------------------------ :   -
TrMDHb23  : ------------------------------------------------------------ :   -
TrMDHb24  : ------------------------------------------------------------ :   -
TrMDHb25  : ------------------------------------------------------------ :   -
TrMDHb26  : ------------------------------------------------------------ :   -
TrMDHb27  : ------------------------------------------------------------ :   -
TrMDHb28  : ------------------------------------------------------------ :   -
TrMDHb29  : ------------------------------------------------------------ :   -
TrMDHb30  : ------------------------------------------------------------ :   -
TrMDHb31  : ------------------------------------------------------------ :   -
TrMDHb32  : ATTGTTCAAGGACTTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA : 664
```

FIGURE 60 (cont.)

```
                    *        1100           *
TrMDHb1  : ------------------------------- :   -
TrMDHb2  : ------------------------------- :   -
TrMDHb3  : ------------------------------- :   -
TrMDHb4  : ------------------------------- :   -
TrMDHb5  : ------------------------------- :   -
TrMDHb6  : ------------------------------- :   -
TrMDHb7  : ------------------------------- :   -
TrMDHb8  : ------------------------------- :   -
TrMDHb9  : ------------------------------- :   -
TrMDHb10 : ------------------------------- :   -
TrMDHb11 : ------------------------------- :   -
TrMDHb12 : ------------------------------- :   -
TrMDHb13 : ------------------------------- :   -
TrMDHb14 : ------------------------------- :   -
TrMDHb15 : ------------------------------- :   -
TrMDHb16 : ------------------------------- :   -
TrMDHb17 : ------------------------------- :   -
TrMDHb18 : ------------------------------- :   -
TrMDHb19 : ------------------------------- :   -
TrMDHb20 : ------------------------------- :   -
TrMDHb21 : ------------------------------- :   -
TrMDHb22 : ------------------------------- :   -
TrMDHb23 : ------------------------------- :   -
TrMDHb24 : ------------------------------- :   -
TrMDHb25 : ------------------------------- :   -
TrMDHb26 : ------------------------------- :   -
TrMDHb27 : ------------------------------- :   -
TrMDHb28 : ------------------------------- :   -
TrMDHb29 : ------------------------------- :   -
TrMDHb30 : ------------------------------- :   -
TrMDHb31 : ------------------------------- :   -
TrMDHb32 : GAGTTATCCGAGGAAAAGAGTTTGGCATACT : 695
```

FIGURE 60 (cont.)

```
                    *        20         *        40         *        60
TrMDHc : AAAGNGAATTGGAATATACGACACTCCATTCCATACTTCCATTCCNTACTTTGCTTTCTC :  60

                    *        80         *       100         *       120
TrMDHc : GCTCTCTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGG : 120

                    *       140         *       160         *       180
TrMDHc : CCGTCGATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGC : 180

                    *       200         *       220         *       240
TrMDHc : CGTGGCTATGCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGC : 240

                    *       260         *       280         *       300
TrMDHc : GGGATCGGCCAGCCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCT : 300

                    *       320         *       340         *       360
TrMDHc : CTTTATGATATTGCTGGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGA : 360

                    *       380         *       400         *       420
TrMDHc : TCTGAGGTAACTGGGTATGCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGAT : 420

                    *       440         *       460         *       480
TrMDHc : GTTGTTATAATTCCTGCTGGTGTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTC : 480

                    *       500         *       520         *       540
TrMDHc : AATATTAACGCTGGCATTGTCAAGTCACTTGCCACTGCTATTTCTAAGTACTGCCCCCAT : 540

                    *       560         *       580         *       600
TrMDHc : GCCCTTGTTAACATGATAAGCAACCCTGTGAACTCCACCGTTCCCATTGCTGCAGAGGTT : 600

                    *       620         *       640         *       660
TrMDHc : TTCAAGAAGGCAGGGACATATGACGAGAAGAGATTGTTTGGGGTTACAACCCTTGATGTA : 660

                    *       680         *       700         *       720
TrMDHc : GTCAGGGCAAAAACTTTCTATGCCGGGAAAGCTAAAGTTCCAGTTGCCGAGGTCAATGTA : 720

                    *       740         *       760         *       780
TrMDHc : CCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTTCCATTATTTTNTCAGGCAACACCT : 780

                    *       800         *       820         *       840
TrMDHc : CAAGCCAATCTGGGTGATGATACCCTTAAGGNTTTAACGGNANGGACACAAGATGGAGGA : 840

                    *       860         *       880         *       900
TrMDHc : ACAGAAGTTGNGACCGCCAAGGCTGGAAAGGGTTCTGCAACTTTGTCAATGGCTTATGCT : 900

                    *       920         *       940         *       960
TrMDHc : GGAGCCATATTTGCTGATGCTNGCCTCAAAGGNCTGAATGGAGTTCCAGATGTTATTGAG : 960
```

FIGURE 61

```
                  *        980          *        1000          *       1020
TrMDHc : TGCTCATATGTGCAATCCAATATCATCTCTGACCTTCCTTTCTTTGCTTCCAAGGTGAGG : 1020

                  *       1040          *        1060          *       1080
TrMDHc : ATTGGGAAGAATGGTGTGGAAGAAATTCTGGGCTTAGGTTCTCTCACAGATTTCGAGCAA : 1080

                  *       1100          *        1120          *       1140
TrMDHc : CAAGGCCTTGAAAACCTCAAGGCTGAACTCAAATCATCTATTGAAAAGGGAATCAAATTT : 1140

                  *       1160          *        1180          *       1200
TrMDHc : GCCTCCCAGTAATCGAACATGTCATACATTACTGGATTTTTCCATTTAGAACCAGATCAA : 1200

                  *       1220          *        1240          *       1260
TrMDHc : ATTTTGCAAATTCAGAACAATTGTTTGTAATGTTGCCGGTAGGTATACCCCTAGATTTAA : 1260

                  *       1280          *        1300          *       1320
TrMDHc : TAAGTAAATCTGCGAGAGCAGTTTATTGCTGCAGGGACTGAAATTAAAACCAGTTTTAGG : 1320

                  *       1340          *        1360          *       1380
TrMDHc : TTGGCCTTTCCATTCGTAATGGCCCTTCATTGTTGCATGNTTTCATATAATGCAATTGAA : 1380

                  *       1400
TrMDHc : GGGTGNTGGNCANCGATACACANCCCCC : 1408
```

FIGURE 61 (cont.)

```
                   *        20         *        40         *        60
TrMDHc : MRPSMLRSVQSAVSRASSHLTRRGYATEPVPERKVAILGAAGGIGQPLSLLMKLNPLVST :  60

                   *        80         *       100         *       120
TrMDHc : LSLYDIAGTPGVAADVSHINSRSEVTGYAGEEELGKALEGADVVIIPAGVPRKPGMTRDD : 120

                   *       140         *       160         *       180
TrMDHc : LFNINAGIVKSLATAISKYCPHALVNMISNPVNSTVPIAAEVFKKAGTYDEKRLFGVTTL : 180

                   *       200         *       220         *       240
TrMDHc : DVVRAKTFYAGKAKVPVAEVNVPVIGGHAGVTILPLFXQATPQANLGDDTLKXLTXXTQD : 240

                   *       260         *       280         *       300
TrMDHc : GGTEVXTAKAGKGSATLSMAYAGAIFADAXLKXLNGVPDVIECSYVQSNIISDLPFFASK : 300

                   *       320         *       340
TrMDHc : VRIGKNGVEEILGLGSLTDFEQQGLENLKAELKSSIEKGIKFASQ : 345
```

FIGURE 62

```
                 *        20         *        40         *        60
TrMDHc1  : AAAGNGAATTGGAATNT-CGAC-CTCCATTCCNTACT-TTATTTCATTCATCGCTCTCTCTCT :  60
TrMDHc2  : ---GTTNATTGGAATATACNCCACTCCATTCCATACT-TTATTTCATTCATCGCTCTCTCTCT :  59
TrMDHc3  : -------------------GNNCATCCA-CACTCCCTTCCCTACTTCCTTT-NTTTATCGCT :  42
TrMDHc4  : -------------------------------GNACT-CCATTCCNTACTTTNTTTNTTNTCC :  30
TrMDHc5  : ---------------------------------GCATCC-TTCCNTACTTT-NTTTTTCGCT :  27
TrMDHc6  : ---------------------------------CNTCCATCCCNTACTTT-NTTCNTCGCT :  27
TrMDHc7  : ---------------------------------GNTTCCTTCCCTACTTT-CTTTCCATCC :  27
TrMDHc8  : ----------------------------------TGCCATTCCNTACTTTNTTTATTNTCC :  27
TrMDHc9  : -----------------------------------TCCATTCCNTACTGT-ATTTNTCGCT :  25
TrMDHc10 : -----------------------------------TCC-TTCCATACTTTCATTCATCGCT :  25
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : --------------------------------------------------------------- :   -
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

              *        80         *       100         *       120
TrMDHc1  : CTCTCTCTCTTTATTCTCGAAAAGCTTGTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG : 122
TrMDHc2  : CTCTCTCT-T-TATTCTCGAAAAGCTTTTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG : 119
TrMDHc3  : CTCTCTCTTTTTATTCTCGAAAAGCTTTTTCAGCCATCAACGGAGAGAATTATGAGTCCGTCG : 105
TrMDHc4  : CTCTCTCTCTCTATTCTCGAAAAGCTTTTTCAGCC-ACAACG-AGAGAATAATGAGGCCGTCG :  91
TrMDHc5  : CTCTCTC--TTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG :  88
TrMDHc6  : CTCTCTC--TTTATTCTCGAAAAGCTTTTT-AGCCAACAACGGAGAGAATTATGAGGCCGTCG :  87
TrMDHc7  : CTCTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG :  90
TrMDHc8  : CTCTCTCTCTTTATTCTCGAAAAGCTTTTTCAGCCAACAACG-AGAGAATAATGAGGCCGTCG :  89
TrMDHc9  : CTCTCTCTTTATATTCTCGAAAAGCTTTTT-NGCCATCAACGGAGAGAATTATGAGGCCGTCG :  87
TrMDHc10 : CTCTCTC--TTTATTCTCGAAAAGCTTTTTCAGCCAACAACGGAGAGAATTATGAGGCCGTCG :  86
TrMDHc11 : -----------GNNTCTCG-AAAGCTTTTT-NGCC--TAACGGAGAGAATTATGAGGCCGTCG :  48
TrMDHc12 : -------------TTCTCAAAAAGCTTTTT-AGCC-ACAACG-AGAGAA-AATGAGGCCGTCG :  46
TrMDHc13 : -------------TTCTCG-AAAGCTTTTTCAGCC-ACAACGNANAGAATAATGAGGCCGTCG :  48
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

            *       140         *       160         *       180
TrMDHc1  : ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT : 185
TrMDHc2  : ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCCTCTCACCTAACCCGCCGTGGCTAT : 182
TrMDHc3  : ATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 168
TrMDHc4  : ATGCTCAGATCTGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT : 154
TrMDHc5  : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 151
TrMDHc6  : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 150
TrMDHc7  : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 153
TrMDHc8  : ATGCTCAGATCCGTCCAATCAGCCGTATCCCGCGCCTCGTCTCACCTAACCCGCCGTGGCTAT : 152
TrMDHc9  : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 150
TrMDHc10 : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 149
TrMDHc11 : ATGTTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTTCTCACCTAACCCGCCGTGGCTAT : 111
TrMDHc12 : ATGCTCAGATCTGTCC-ATCAGCCGTATCCCGCGCCTCCTCTCACCTAACCCGCCGTGGGTAT : 108
TrMDHc13 : ATGCTCAGATCTGTCCAATCAGCCGTATCCCGGGCCTCCTCTCACCTAACCCGCCGTGGGTAT : 111
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -
```

FIGURE 63

149/241

```
                  *        200         *        220         *        240         *
TrMDHc1  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG : 248
TrMDHc2  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG : 245
TrMDHc3  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 231
TrMDHc4  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG : 217
TrMDHc5  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 214
TrMDHc6  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 213
TrMDHc7  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 216
TrMDHc8  : GCTACCGAACCAGTTCCAGAACGCAGGGTGGCCATTCTCGGTGCTGCTGGCGGGATCGGACAG : 215
TrMDHc9  : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 213
TrMDHc10 : GCTACCGAACCAGTTCCAGAACGCAAGGNGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 212
TrMDHc11 : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCCGGCGGGATCGGCCAG : 174
TrMDHc12 : GCTACCGAACCAGTTCCAGAACGCAAGGTGGCCATTCTCGGCGCTGCTGGCGGGATCGGCCAG : 171
TrMDHc13 : GCTACCGAACCAGTTCCAGAACGCAAGGNGGCCATTCTCGGTGCTGCCGGCGGGATCGGACAG : 174
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

                 260         *        280         *        300         *
TrMDHc1  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 311
TrMDHc2  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 308
TrMDHc3  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 294
TrMDHc4  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 280
TrMDHc5  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 277
TrMDHc6  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 276
TrMDHc7  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 279
TrMDHc8  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 278
TrMDHc9  : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 276
TrMDHc10 : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 275
TrMDHc11 : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 237
TrMDHc12 : CCTCTCTCTCTTCTCATGAAGCTCAATCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 234
TrMDHc13 : CCTCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTTCAACCCTATCTCTTTATGATATTGCT : 237
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

             320         *        340         *        360         *         3
TrMDHc1  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 374
TrMDHc2  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 371
TrMDHc3  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 357
TrMDHc4  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 343
TrMDHc5  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 340
TrMDHc6  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 339
TrMDHc7  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 342
TrMDHc8  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 341
TrMDHc9  : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 339
TrMDHc10 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 338
TrMDHc11 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 300
TrMDHc12 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 297
TrMDHc13 : GGAACCCCTGGTGTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACTGGGTAT : 300
TrMDHc14 : --------GNGTGTCGCCGCTGNNGTCAGCCACATCAACTCCANANCTGA-GTAACTGGGTAT :  54
TrMDHc15 : ------------------GNTGATGT-NGCC-CAT-AACTCC-GATCTGAGGTAACTGGGTAT :  41
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -
```

FIGURE 63 (cont.)

150/241

```
           80        *       400         *       420         *       440
TrMDHc1  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 437
TrMDHc2  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 434
TrMDHc3  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 420
TrMDHc4  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 406
TrMDHc5  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 403
TrMDHc6  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 402
TrMDHc7  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 405
TrMDHc8  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 404
TrMDHc9  : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 402
TrMDHc10 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 401
TrMDHc11 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCCGGT : 363
TrMDHc12 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 360
TrMDHc13 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 363
TrMDHc14 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 117
TrMDHc15 : GCAGGTGAAGAAGAGCTTGGAAAAGCTTTGGAGGGTGCTGATGTTGTTATAATTCCTGCTGGT : 104
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

                *       460         *       480         *       500
TrMDHc1  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 500
TrMDHc2  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 497
TrMDHc3  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTTAATATTAATGCTGGCATTGTCAAG : 483
TrMDHc4  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 469
TrMDHc5  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 466
TrMDHc6  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 465
TrMDHc7  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 468
TrMDHc8  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 467
TrMDHc9  : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTTAAG : 465
TrMDHc10 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 464
TrMDHc11 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 426
TrMDHc12 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 423
TrMDHc13 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 426
TrMDHc14 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 180
TrMDHc15 : GTGCCCAGAAAGCCTGGAATGACTCGTGATGATCTTTTCAATATTAACGCTGGCATTGTCAAG : 167
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

                *       520         *       540         *       560
TrMDHc1  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATG-------------------------- : 537
TrMDHc2  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 560
TrMDHc3  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 546
TrMDHc4  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 532
TrMDHc5  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 529
TrMDHc6  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 528
TrMDHc7  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 531
TrMDHc8  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 530
TrMDHc9  : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 528
TrMDHc10 : TCACTTGCCACTGGTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 527
TrMDHc11 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 489
TrMDHc12 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 486
TrMDHc13 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 489
TrMDHc14 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 243
TrMDHc15 : TCACTTGCCACTGCTATTTCTAAGTACTGCCCCCATGCCCTTGTTAACATGATAAGCAACCCT : 230
TrMDHc16 : -----------------------------------------------------------TTG--- :   3
TrMDHc17 : --------------------------------------------------------------- :   -
```

FIGURE 63 (cont.)

```
                  *        580         *        600         *        620         *
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGG--------------- : 608
TrMDHc3   : GTGAACTCCACCGTTCCCATTGCTGCAGG---------------------------------- : 575
TrMDHc4   : GTGAACTCCACCGTTCCCATTGCTGCAGAGG-------------------------------- : 563
TrMDHc5   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATAT-------- : 583
TrMDHc6   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 591
TrMDHc7   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 594
TrMDHc8   : GTGAACTCCACCGTTCCCATTGCTGC------------------------------------- : 556
TrMDHc9   : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 591
TrMDHc10  : GTGAACTCCACCGTTCCCATTGCTGNAGAGGTTTTCAAGAAGGCNGGGACATATGACNAGAAN : 590
TrMDHc11  : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 552
TrMDHc12  : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 549
TrMDHc13  : GTGAACTCCACCGTTCCCATTGCTGCANAGGTTTTCAAGAAGGCAGGGACATATGACNAGAAG : 552
TrMDHc14  : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 306
TrMDHc15  : GTGAACTCCACCGTTCCCATTGCTGCAGAGGTTTTCAAGAAGGCAGGGACATATGACGAGAAG : 293
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : --------------------------------------------------------------- :   -

                     640         *        660         *        680         *
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : AGATTGT-------------------------------------------------------- : 598
TrMDHc7   : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCGAAAACTTTTTATGCCGGGAAAGCT : 657
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCGAAAACTTTCTATGCCGGGAAAGCT : 654
TrMDHc10  : AAATTGTTTGGGGTT-CAACCCTTGATGTAGTCAGGGGGAAAACTTTTTTTTGCCGGGAAAGCT : 652
TrMDHc11  : AGATTGTTTGGGGTTACAACCCTTG-------------------------------------- : 577
TrMDHc12  : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACT------------------ : 594
TrMDHc13  : AGATTGTTTGGGGTTACAACCCTTGATGTAGNCAGGGCAAAAACTTTTTATGCTGGGAAAGCT : 615
TrMDHc14  : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACTTTCTATGCTGGGAAAGCT : 369
TrMDHc15  : AGATTGTTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAAACTTTCTATGCTGGGAAAGCT : 356
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : --------------------------------------------------------------- :   -

                     700         *        720         *        740         *
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTTTTGGAGGCCATGCAGGAGTTACTATTNTT : 720
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : AAAGTTCCAGTTGCCGAGGTCAATGTAC----------------------------------- : 682
TrMDHc10  : AAAGTTCCAGTTGCCGNGGCNAATGNNCCTGTTNTTGGAGGCC-TGC-NGAG-TNCTATT-NT : 711
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : AAAGTTCCAGTTGCCGAGGNCAATGCACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTN : 678
TrMDHc14  : AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTC : 432
TrMDHc15  : AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTC : 419
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : --------------------------------------------------------------- :   -
```

FIGURE 63 (cont.)

```
                 760         *         780         *         800         *         82
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : CCATTATTTTNTAAGG-AACACCTNAAGCCAATNTGGNTGATGAAACCCTTNAGGNTTTAACG : 782
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : CCGTTTTTTTTTTAGG-GANNCCT-NANCCANT-TNGGNGATNAAA-CCTTAAGGGTTT-ACG : 769
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : CCATTATTTTNTNAGGCAACACCTNAAGCCAATNTGGGTGANGATNCCCTTAAGGNTTTAACG : 741
TrMDHc14 : CCATTATTTTGTCAGGCAACACCTCAAGCCAATCTGGATGATGATACCATTAAGGGTCTAACG : 495
TrMDHc15 : CCATTATTTTGTCAGGCAACACCTCAAGCCAATCTGGATGATGATACCATTAAGGGTCTAACG : 482
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

             0         *         840         *         860         *         880
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : GNANGGGCNCAAGATGGGGGAACNGAA-TTGNGACCGCCAAGGGTT----------------- : 827
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : GG-NNGGCNCAAAANG-GGGAACAAAA-NTTNGAC---------------------------- : 801
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : GNANGGACCCAANANGGAGGAACANAANTTNNGACCCCCANGG-TGG-AAGGGTTNT-NNACT : 801
TrMDHc14 : GCAAGGACACAAGATGGAGGAACAGAAGTTGTGACCGCCAAGGCTGGAAAGGGTTCTGCAACT : 558
TrMDHc15 : GCAAGGACACAAGATGGAGGAACAGAAGTTGTGACCGCCAAGGCTGGAAAGGGTTCTGCAACT : 545
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : --------------------------------------------------------------- :   -

                       *         900         *         920         *         940
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : --------------------------------------------------------------- :   -
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : --------------------------------------------------------------- :   -
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : TT-NNAATGGN---------------------------------------------------- : 811
TrMDHc14 : TTGTCAATGGCTTATGCTGGAGCCATATTTGCTGATGCTTGCCTCAAAGGTCTGAATGGAGTT : 621
TrMDHc15 : TTGTCAATGGCT--------------------------------------------------- : 557
TrMDHc16 : -------------------------------CTGNTGCTNGCCT-NANGGNCTGAATGGAGTT :  34
TrMDHc17 : --------------------------------------------------------GNGNGTT :   7
```

FIGURE 63 (cont.)

```
                  *        960         *        980         *        1000
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : CCAGATGTTATTGAGTGCTCATATGTGCAATCCAATATCATCTCTGACCTTNCTTTCTTTGCT : 684
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : -CNGANGTTATTGAACTCTCATATGTGCAATCCAATATCATCTNTGACCTTCCTTTCTTTGCT :  96
TrMDHc17  : CCAGATGTTATNGAGTGCT-NTATGTGC-AT-CNATAT-NTCTCTGACCTTCCTTTCTTTGCT :  66

              *        1020        *        1040        *        1060        *
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : TCCAAGGTGAGGATTGGGAANAATGGTGTGGGAANAAT------------------------- : 722
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : TCCAAGGNNNGGATTGGGAAGAATGGTGTGGAAGAGATTCTG--------------------- : 138
TrMDHc17  : TCC-AGGTGAGGATTGGGAAGAATGGTGTGGAAGAAATTCTGGGCTTAGGTTCTCTCACAGAT : 128

                   1080         *        1100        *        1120        *
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : --------------------------------------------------------------- :   -
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : TTCGAGCAACAAGGCCTTGAAAACCTCAAGGCTGAACTCAAATCATCTATTGAAAAGGAATC : 191
```

FIGURE 63 (cont.)

```
                 1140         *      1160         *      1180         *      1
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : --------------------------------------------------------------- :   -
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : AAATTTGCCTCCCAGTAATCGAACATGTCATACATTACTGGATTTTTCCATTTAGAACCAGAT : 254

              200         *      1220         *      1240         *      1260
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : --------------------------------------------------------------- :   -
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : CAAATTTTGCAAATTCAGAACAATTGTTTGTAATGTTGCCGGTAGGTATACCCCTAGATTTAA : 317

                        *      1280         *      1300         *      1320
TrMDHc1   : --------------------------------------------------------------- :   -
TrMDHc2   : --------------------------------------------------------------- :   -
TrMDHc3   : --------------------------------------------------------------- :   -
TrMDHc4   : --------------------------------------------------------------- :   -
TrMDHc5   : --------------------------------------------------------------- :   -
TrMDHc6   : --------------------------------------------------------------- :   -
TrMDHc7   : --------------------------------------------------------------- :   -
TrMDHc8   : --------------------------------------------------------------- :   -
TrMDHc9   : --------------------------------------------------------------- :   -
TrMDHc10  : --------------------------------------------------------------- :   -
TrMDHc11  : --------------------------------------------------------------- :   -
TrMDHc12  : --------------------------------------------------------------- :   -
TrMDHc13  : --------------------------------------------------------------- :   -
TrMDHc14  : --------------------------------------------------------------- :   -
TrMDHc15  : --------------------------------------------------------------- :   -
TrMDHc16  : --------------------------------------------------------------- :   -
TrMDHc17  : TAAGTAAATCTGCGAGAGCAGTTTATTGCTGCAGGACTGAAATTAAAACCAGTTTTAGGTTG : 380
```

FIGURE 63 (cont.)

```
                     *        1340         *        1360         *        1380
TrMDHc1  : --------------------------------------------------------------- :   -
TrMDHc2  : --------------------------------------------------------------- :   -
TrMDHc3  : --------------------------------------------------------------- :   -
TrMDHc4  : --------------------------------------------------------------- :   -
TrMDHc5  : --------------------------------------------------------------- :   -
TrMDHc6  : --------------------------------------------------------------- :   -
TrMDHc7  : --------------------------------------------------------------- :   -
TrMDHc8  : --------------------------------------------------------------- :   -
TrMDHc9  : --------------------------------------------------------------- :   -
TrMDHc10 : --------------------------------------------------------------- :   -
TrMDHc11 : --------------------------------------------------------------- :   -
TrMDHc12 : --------------------------------------------------------------- :   -
TrMDHc13 : --------------------------------------------------------------- :   -
TrMDHc14 : --------------------------------------------------------------- :   -
TrMDHc15 : --------------------------------------------------------------- :   -
TrMDHc16 : --------------------------------------------------------------- :   -
TrMDHc17 : GCCTTTCCATTCGTAATGGCCCTTCATTGTTGCATGNTTTCATATAATGCAATTGAAGGGTGN : 443

                 *        1400
TrMDHc1  : ---------------------- :   -
TrMDHc2  : ---------------------- :   -
TrMDHc3  : ---------------------- :   -
TrMDHc4  : ---------------------- :   -
TrMDHc5  : ---------------------- :   -
TrMDHc6  : ---------------------- :   -
TrMDHc7  : ---------------------- :   -
TrMDHc8  : ---------------------- :   -
TrMDHc9  : ---------------------- :   -
TrMDHc10 : ---------------------- :   -
TrMDHc11 : ---------------------- :   -
TrMDHc12 : ---------------------- :   -
TrMDHc13 : ---------------------- :   -
TrMDHc14 : ---------------------- :   -
TrMDHc15 : ---------------------- :   -
TrMDHc16 : ---------------------- :   -
TrMDHc17 : TGGNCANCGATACACANCCCCC : 465
```

FIGURE 63 (cont.)

```
                   *        20         *        40         *        60
TrMDHd : GGGTAGGCGGAGATTTNAACCCATTTTCCTCTTAAATCTCTCTCAACTTCTCTTTCCATT :  60

                   *        80         *       100         *       120
TrMDHd : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 120

                   *       140         *       160         *       180
TrMDHd : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 180

                   *       200         *       220         *       240
TrMDHd : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 240

                   *       260         *       280         *       300
TrMDHd : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 300

                   *       320         *       340         *       360
TrMDHd : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACA : 360

                   *       380         *       400         *       420
TrMDHd : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 420

                   *       440         *       460         *       480
TrMDHd : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 480

                   *       500         *       520         *       540
TrMDHd : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 540

                   *       560         *       580         *
TrMDHd : TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTATACCTGCTGGTGTTCCCAGAAA : 598
```

FIGURE 64

```
                  *        20         *        40         *        60
TrMDHd : MAASAAATFTIGTAQTGRPLPQSNPFGLKVNSQVNFKTFSGLKAMSSLRCESESSFFGNE :  60

                  *        80         *       100         *       120
TrMDHd : TSAALRATFAPKAQKENQNINRNLHPQASYKVAVLGAAGGIGQPLALLIKMSPLVSDLHL : 120

                  *       140         *       160
TrMDHd : YDIANVKGVAADISHCNTPSKVLDFTGASELANCLKGVDVVVIPAGVPR : 169
```

FIGURE 65

```
                  *       20         *       40         *       60
TrMDHd1 : GNGTAGGCGGAGATTTNAACCCATTTTCCTCTTAAATCTCTCTNAACTTCTCTTTCCATT :  60
TrMDHd2 : -GTTAGGCGGAGATTNNAACCCATTTTCCTCTTAAATCTCTCTC-ACTTCTCTTTCCATT :  58
TrMDHd3 : -------GGGAGATTTNAACCCATTTTCCTCTTAAATCTCTC-CGACTTCTCCTTCCATT :  52

                  *       80         *      100         *      120
TrMDHd1 : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 120
TrMDHd2 : CCCATTACCATTCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 118
TrMDHd3 : CCCATTACCATTCATTCCCAGAGGTTGAGATGGCAGCATCAGCAGCAGCTACTTTTACTA : 112

                  *      140         *      160         *      180
TrMDHd1 : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 180
TrMDHd2 : TTGGAACTGCCCAAACAGGGAGGCCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 178
TrMDHd3 : TTGGAACTGCCCAAACAGGGAGGTCACTTCCTCAATCAAACCCTTTTGGTTTGAAAGTCA : 172

                  *      200         *      220         *      240
TrMDHd1 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 240
TrMDHd2 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAGATGCG : 238
TrMDHd3 : ATTCCCAGGTTAATTTTAAGACCTTCTCTGGTCTCAAGGCCATGTCGTCTCTAAGATGCG : 232

                  *      260         *      280         *      300
TrMDHd1 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 300
TrMDHd2 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTTGCAC : 298
TrMDHd3 : AGTCTGAATCATCTTTCTTTGGCAACGAAACTTGTGCTGCTCTGCGTGCAACTTTTGCAC : 292

                  *      320         *      340         *      360
TrMDHd1 : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACA : 360
TrMDHd2 : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTTGCATCCTCAGGCATCCTACA : 358
TrMDHd3 : CCAAAGCTCAAAAGGAAAACCGAAACATCAACCGCAATTTGCAGCCTCAGGCATCCTACA : 352

                  *      380         *      400         *      420
TrMDHd1 : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 420
TrMDHd2 : AAGTGGCGGTTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTTCTCATTAAGA : 418
TrMDHd3 : AAGTGGCGGTTCTCGGTGCTGCAGGAGGAATTGGTCAGCCACTTGCACTTCTCATTAAGA : 412

                  *      440         *      460         *      480
TrMDHd1 : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 480
TrMDHd2 : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 478
TrMDHd3 : TGTCGCCTTTGGTTTCCGACCTGCATCTTTATGACATTGCGAATGTTAAGGGAGTTGCTG : 472

                  *      500         *      520         *      540
TrMDHd1 : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 540
TrMDHd2 : CTGATATCAGTCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGT : 538
TrMDHd3 : CTGATATCAGCCATTGCAACACTCCTTCAAAGGTTTTGGATTTCACAGGTGCTTCTGAGC : 532

                  *      560         *      580         *
TrMDHd1 : TGGCAAATTGTTTG-------------------------------------------- : 554
TrMDHd2 : TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTATACCTGCTGGTGTTCCCAG--- : 593
TrMDHd3 : TAGCAAATTGTTTGAAAGGTGTGGATGTTGTTGTTATACCTGCTGGTGTTCCTAGAAA : 590
```

FIGURE 66

```
                     *        20         *        40         *        60
TrMDHe : TTNTNTTTATTTTATGTTTTTTNCCTCCTACATATAACTCTTNACTTNGCATACACTGTG :  60

                     *        80         *       100         *       120
TrMDHe : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG : 120

                     *       140         *       160         *       180
TrMDHe : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 180

                     *       200         *       220         *       240
TrMDHe : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 240

                     *       260         *       280         *       300
TrMDHe : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 300

                     *       320         *       340         *       360
TrMDHe : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 360

                     *       380         *       400         *       420
TrMDHe : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 420

                     *       440         *       460         *       480
TrMDHe : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 480

                     *       500         *       520         *       540
TrMDHe : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 540

                     *       560         *       580         *       600
TrMDHe : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 600

                     *       620         *       640         *       660
TrMDHe : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTAGGGGTTACA : 660

                     *       680         *       700         *       720
TrMDHe : ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA : 720

                     *       740         *       760         *       780
TrMDHe : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA : 780

                     *       800         *       820         *       840
TrMDHe : CAGGTTAAGCCTCCCAGTAGCTTCACCGCAGAAGAAACCGAATACCTGACAAANCGCATT : 840

                     *       860         *       880         *       900
TrMDHe : CAAAANGGCGGAACACAAGTTGTTGAGGCAAAGGCTGGGGCTGGTTCGGCAACACTANTN : 900

                     *       920         *       940         *       960
TrMDHe : ATGGCCTATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC : 960
```

FIGURE 67

```
                     *        980         *        1000         *        1020
TrMDHe : GGGATAGTGGAGTGTGCTTTTGTTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC : 1020

                     *       1040         *        1060         *        1080
TrMDHe : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG : 1080

                     *       1100         *        1120         *        1140
TrMDHe : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA : 1140

                     *       1160         *        1180         *        1200
TrMDHe : GTAGAATTCATCAAAAAAAAANAAAGATAAGGAAAAATTAGTTTTGTATTGNCTCTTTCT : 1200

                     *       1220         *
TrMDHe : ATATCTATAAAGAACTTGTGTAATAATTCC : 1230
```

FIGURE 67 (cont.)

```
                  *        20         *        40         *        60
TrMDHe : MEAHAAGANQRIARISAHLQPPNFQEGGDVAISKANCRAKGGAPGFKVAILGAAGGIGQS :  60

                  *        80         *       100         *       120
TrMDHe : LSLLLKINPLVSVLHLYDVVNTPGVTADVSHIDTGAVVRGFLGQAQLENALTGMDLVVIP : 120

                  *       140         *       160         *       180
TrMDHe : AGVPRKPGMTRDDLFKINAGIVRTLSEGIAKSCPNAIVNLISNPVNSTVPIAAEVFKKAG : 180

                  *       200         *       220         *       240
TrMDHe : TYDPKRLLGVTTLDVVRANTFVAEVLGVDPREVDVPVVGGHAGVTILPLLSQVKPPSSFT : 240

                  *       260         *       280         *       300
TrMDHe : AEETEYLTXRIQXGGTQVVEAKAGAGSATLMAYAAAKFANACLRGLKGEAGIVECAFVDS : 300

                  *       320         *       340         *
TrMDHe : QVTELPFFAAKVRLGRGGAEEIYQLGPLNEYERIGLEKAKKELAGSIQKGVEFIKKKXR : 359
```

FIGURE 68

```
                     *        20         *        40         *        60
TrMDHe1  : TTNTNTTTATTTTATGTTTTTTNCCTCCTACATATAACTCTTNACTTNGCATACACTGTG :  60
TrMDHe2  : ---------------------------------------------------------GNG :   3
TrMDHe3  : ---------------------------------------------------------GTG :   3
TrMDHe4  : ------------------------------------------------------------ :   -
TrMDHe5  : ------------------------------------------------------------ :   -
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                     *        80         *       100         *       120
TrMDHe1  : TCTCT-AATTATTATTAGTCCTTGGAAATGGAAGCACATGCAGCTGGTACCAATCAGAGG : 119
TrMDHe2  : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGTGCCAATCAGAGG :  63
TrMDHe3  : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCCCATGCAGCTGGAGCCAATCAGAGG :  63
TrMDHe4  : --------------GNAGTCCTTANAAATGGAAGCACATGCAGCTGGAGCC-ATC-GAGG :  44
TrMDHe5  : ----------------------GAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG :  38
TrMDHe6  : ----------------------------------CGANTGCAGCTGGTGCCANTNNGAGG :  26
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                     *       140         *       160         *       180
TrMDHe1  : ATTGCAAGAATCTCTGCTCATCTTCAGCCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 179
TrMDHe2  : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 123
TrMDHe3  : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA : 123
TrMDHe4  : ATTGCAAGAATCTCTGCTCATCTTC-GCCTCCAAATTTCCAGGAAGGAAGTGATGTCGCA : 103
TrMDHe5  : ATTGCAAGAATCTCTGCTCATCTTCAACCTCCAAATTTCCAGGAAGGAGGTGATGTTGCA :  98
TrMDHe6  : ATTGC-AGAATCTCTGCTCATCTT-NACCTCC-AATTTCCAGGAAGGAGGTGATGTTGCA :  83
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                     *       200         *       220         *       240
TrMDHe1  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 239
TrMDHe2  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 183
TrMDHe3  : ATTAGCAAAGCTAACTGCAGAGCGAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 183
TrMDHe4  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 163
TrMDHe5  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 158
TrMDHe6  : ATTAGCAAAGCTAACTGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 143
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -
```

FIGURE 69

```
                    *       260         *       280         *       300
TrMDHe1  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 299
TrMDHe2  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 243
TrMDHe3  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 243
TrMDHe4  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 223
TrMDHe5  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 218
TrMDHe6  : GGGGCTGCTGGTGGAATTGGTCAATCCCTTTCTTTGCTGTTGAAGATCAATCCATTGGTT : 203
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                    *       320         *       340         *       360
TrMDHe1  : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 359
TrMDHe2  : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 303
TrMDHe3  : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 303
TrMDHe4  : TCGGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 283
TrMDHe5  : TCGGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 278
TrMDHe6  : TCAGTTCTTCATCTTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 263
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                    *       380         *       400         *       420
TrMDHe1  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 419
TrMDHe2  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 363
TrMDHe3  : ATTGATACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 363
TrMDHe4  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 343
TrMDHe5  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 338
TrMDHe6  : ATTGACACCGGTGCTGTGGTTCGTGGCTTTCTAGGGCAGGCACAACTTGAGAATGCACTT : 323
TrMDHe7  : --------------------------------------GTTTCAACTTGAAAATGCACTT :  22
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                    *       440         *       460         *       480
TrMDHe1  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 479
TrMDHe2  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 423
TrMDHe3  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 423
TrMDHe4  : ACAGGCATGGACTTGGCCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 403
TrMDHe5  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 398
TrMDHe6  : ACAGGCATGGACTTGGTCGTTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 383
TrMDHe7  : ACAGGCATGGACTTGGTCGNTATACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG :  82
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                    *       500         *       520         *       540
TrMDHe1  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 539
TrMDHe2  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 483
TrMDHe3  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG : 483
TrMDHe4  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG : 463
TrMDHe5  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTTCTGAAGGAATTGTCAAG : 458
TrMDHe6  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 443
TrMDHe7  : GATGACTTATTTAAGATAAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG : 142
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -
```

FIGURE 69 (cont.)

```
                        *        560         *        580         *        600
TrMDHe1  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 599
TrMDHe2  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 543
TrMDHe3  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 543
TrMDHe4  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 523
TrMDHe5  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 518
TrMDHe6  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 503
TrMDHe7  : AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 202
TrMDHe8  : ------------------------------------------------------------ :   -
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                        *        620         *        640         *        660
TrMDHe1  : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTANGGGTAACA : 659
TrMDHe2  : GCTGCTGAGGTTTTCAAGAAAGCCGGTACAT----------------------------- : 574
TrMDHe3  : GCTGCTGAGGTCTTCAAGAAAGCCGGTACATAT--------------------------- : 576
TrMDHe4  : GCTGCTGAGGTCTTCAAGAAAGCCGGTACATATGATCCAAAACGACTTTTAGGAGTTACA : 583
TrMDHe5  : GCTGGTGAGGTGTTCAAGAAAGCCGGNACATATGATCCAAAACNACTTTTAAGGGTTACA : 578
TrMDHe6  : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTTAG-------- : 555
TrMDHe7  : GCTGCTGAGGTTTTCAAGAAAGCCGGTACATATGATTCAAAGCGACTTTTAGGGGTAACA : 262
TrMDHe8  : ------------------------------TATGATCC-ACGCGACTTTTAGG-GCTACA :  28
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                        *        680         *        700         *        720
TrMDHe1  : ACCCTCGATGNTGT---------------------------------------------- : 673
TrMDHe2  : ------------------------------------------------------------ :   -
TrMDHe3  : ------------------------------------------------------------ :   -
TrMDHe4  : ACCCTCGATG-------------------------------------------------- : 593
TrMDHe5  : ACCCTNGATGTTGNGAGGGCAAATACTTTTGTGGCANAAG-NCTTGGNGTTGANCCCAAA : 637
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA : 322
TrMDHe8  : ACCCTCGATGTTGTGAGGGCAAATACCTTTGTGGCAGAAGTACTTGGTGTTGATCCAAGA :  88
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                        *        740         *        760         *        780
TrMDHe1  : ------------------------------------------------------------ :   -
TrMDHe2  : ------------------------------------------------------------ :   -
TrMDHe3  : ------------------------------------------------------------ :   -
TrMDHe4  : ------------------------------------------------------------ :   -
TrMDHe5  : NAGGGTNATNTTCCANTGGTAGGAGGGCCCCCNGGANT-ACAANATTACC-CTTTTTT-- : 693
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : GAGGTTGATGTTCCAGNGGTAGGATGGCACGCANGAGT-ACAATATTACCTCTTTTGTCA : 381
TrMDHe8  : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTTGTCA : 148
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -

                        *        800         *        820         *        840
TrMDHe1  : ------------------------------------------------------------ :   -
TrMDHe2  : ------------------------------------------------------------ :   -
TrMDHe3  : ------------------------------------------------------------ :   -
TrMDHe4  : ------------------------------------------------------------ :   -
TrMDHe5  : ------------------------------------------------------------ :   -
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : CAGGTTAAGCCTNCCAGTANCTT-ACCGNAGAANAAACCGAATACCTGACANANCGNATT : 440
TrMDHe8  : CAGGTTAAGCCTCCCAGTAGCTTCACTGCAGAAGAAACCGAATACCTGACAAATCGCATT : 208
TrMDHe9  : ------------------------------------------------------------ :   -
TrMDHe10 : ------------------------------------------------------------ :   -
```

FIGURE 69 (cont.)

```
                 *        860         *        880         *        900
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : CAAAANGGCGGAACACAAGTGGTTGAGGCAAAG--------------------------- :  473
TrMDHe8  : CAAAANGGNGGAACANAAGTTGTTGAGGCAAAGGCTGGGGCTGGTTCGGCAACACTANTA :  268
TrMDHe9  : ------------------GTTGTTGAGGCAAAGGCTGGGGCTGGTTCGGCAACACTANTN :   42
TrMDHe10 : -------------------TTGTTGAGGNAAAGGCTGGGGCTGGTTCGG-NAC-CT-NTN :   38

                 *        920         *        940         *        960
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : ------------------------------------------------------------ :    -
TrMDHe8  : ATGGCNTATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC :  328
TrMDHe9  : ATGGCCTATGCAGCTGCCAAGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC :  102
TrMDHe10 : ATGGCCTATGCAGCTGCC-AGTTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAAGCC :   97

                 *        980         *        1000        *        1020
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : ------------------------------------------------------------ :    -
TrMDHe8  : GGGATAGTGGAGTGTGCTTTTGTTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC :  388
TrMDHe9  : GGGATAGTGGAGTGTGCTTTTGTTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC :  162
TrMDHe10 : GGGATAGTGGAGTGTGCTTTTGTTGATTCTCAGGTTACGGAACTTCCTTTCTTTGCAGCC :  157

                 *        1040        *        1060        *        1080
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : ------------------------------------------------------------ :    -
TrMDHe8  : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATACCAACTTGGTCCCCTTAATGAG :  448
TrMDHe9  : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG :  222
TrMDHe10 : AAGGTTCGTCTTGGTCGCGGTGGAGCAGAAGAGATATATCAACTTGGTCCCCTTAATGAG :  217

                 *        1100        *        1120        *        1140
TrMDHe1  : ------------------------------------------------------------ :    -
TrMDHe2  : ------------------------------------------------------------ :    -
TrMDHe3  : ------------------------------------------------------------ :    -
TrMDHe4  : ------------------------------------------------------------ :    -
TrMDHe5  : ------------------------------------------------------------ :    -
TrMDHe6  : ------------------------------------------------------------ :    -
TrMDHe7  : ------------------------------------------------------------ :    -
TrMDHe8  : TATGAGAGGATTGGGTTGGAAAAAGCGAAGAATGAGTTAGCGGGAAGCATCCAGAAGGGA :  508
TrMDHe9  : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA :  282
TrMDHe10 : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA :  277
```

FIGURE 69 (cont.)

```
                    *        1160         *        1180         *        1200
TrMDHe1  : ------------------------------------------------------------ :   -
TrMDHe2  : ------------------------------------------------------------ :   -
TrMDHe3  : ------------------------------------------------------------ :   -
TrMDHe4  : ------------------------------------------------------------ :   -
TrMDHe5  : ------------------------------------------------------------ :   -
TrMDHe6  : ------------------------------------------------------------ :   -
TrMDHe7  : ------------------------------------------------------------ :   -
TrMDHe8  : GTAGAATTCATCAGAAAATAAGTCAGATAAGGAAAAATTAGTTTTGTATTGNCTCTTTCT : 568
TrMDHe9  : GTAGAATTCATCACANAAAAAANAA----------------------------------- : 306
TrMDHe10 : GTAGAATTCATCAAAAAAAAAAN------------------------------------- : 299

                    *        1220         *
TrMDHe1  : ------------------------------ :   -
TrMDHe2  : ------------------------------ :   -
TrMDHe3  : ------------------------------ :   -
TrMDHe4  : ------------------------------ :   -
TrMDHe5  : ------------------------------ :   -
TrMDHe6  : ------------------------------ :   -
TrMDHe7  : ------------------------------ :   -
TrMDHe8  : ATATCTATAAAGAACTTGTGTAATAATTCC : 598
TrMDHe9  : ------------------------------ :   -
TrMDHe10 : ------------------------------ :   -
```

FIGURE 69 (cont.)

```
                          *        20         *        40         *        60
TrMDHf  : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA :  60

                          *        80         *       100         *       120
TrMDHf  : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120

                          *       140         *       160         *       180
TrMDHf  : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180

                          *       200         *       220         *       240
TrMDHf  : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240

                          *       260         *       280         *       300
TrMDHf  : AACCTCTTTCAATGTTGATGAAGATGAATCCTTTGGTTTNAGTTCTTCATCTTTATGATG : 300

                          *       320         *       340         *       360
TrMDHf  : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 360

                          *       380         *       400         *       420
TrMDHf  : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 420

                          *       440         *       460         *       480
TrMDHf  : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 480

                          *       500         *       520         *       540
TrMDHf  : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 540

                          *       560         *       580         *       600
TrMDHf  : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 600

                          *       620         *       640         *       660
TrMDHf  : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 660

                          *       680         *       700         *       720
TrMDHf  : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 720

                          *       740         *       760         *       780
TrMDHf  : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 780

                          *       800         *       820         *       840
TrMDHf  : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 840

                          *       860
TrMDHf  : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866
```

FIGURE 70

```
                    *        20         *        40         *        60
TrMDHf : MEPNSDANQRIARISGHLNPPNFKMNEHGDSSLTSFHCRAKGGAPGFKVAILGAAGGIGQ :  60

                    *        80         *       100         *       120
TrMDHf : PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII : 120

                    *       140         *       160         *       180
TrMDHf : PAGVPRKPGMTRDDLFNINAGIVKTLCEAIAKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180

                    *       200         *       220         *       240
TrMDHf : GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVDVPVVGGHAGITILPLLSQVKPHSSF : 240

                    *       260
TrMDHf : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268
```

FIGURE 71

```
                 *        20         *        40         *        60
TrMDHf1 : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA :  60
TrMDHf2 : ------------------------------------------------------------ :   -
TrMDHf3 : ------------------------------------------------------------ :   -

                 *        80         *       100         *       120
TrMDHf1 : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120
TrMDHf2 : ------------------------------------------------------------ :   -
TrMDHf3 : ------------------------------------------------------------ :   -

                 *       140         *       160         *       180
TrMDHf1 : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180
TrMDHf2 : ------------------------------------------------------------ :   -
TrMDHf3 : ------------------------------------------------------------ :   -

                 *       200         *       220         *       240
TrMDHf1 : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240
TrMDHf2 : ------------------------------------------------GTGNCATAGGTN :  12
TrMDHf3 : ------------------------------------------------------------ :   -

                 *       260         *       280         *       300
TrMDHf1 : AACCTCTTTCAATGTTGATGAAGATGAATCCGTTGGTTT-AGTTCTTCATCTTTATGATG : 299
TrMDHf2 : AGCCTCTTT-NATGTTGATGAAGATGAATCCTATGGTTT-AGTTCTTCATCTTTATGATG :  70
TrMDHf3 : -------------------------------TTTGGTTTNNGTTCTTATNCTTTATGATG :  29

                 *       320         *       340         *       360
TrMDHf1 : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCAGATGGATACTGGTGCTGTTGTTC : 359
TrMDHf2 : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 130
TrMDHf3 : TTG-TAATACTCCTGGTG-TACTTCTGATATTAGT-ATATGGATACTGCTGCTGTTGTTC :  86

                 *       380         *       400         *       420
TrMDHf1 : GAGGATTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 419
TrMDHf2 : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 190
TrMDHf3 : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 146

                 *       440         *       460         *       480
TrMDHf1 : TTCCTGCTGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 479
TrMDHf2 : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 250
TrMDHf3 : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 206

                 *       500         *       520         *       540
TrMDHf1 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCGAAGCGATGTCCTAAGGCGATTGTCA : 539
TrMDHf2 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 310
TrMDHf3 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGGTTGTCA : 266

                 *       560         *       580         *       600
TrMDHf1 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCC--------------------------- : 572
TrMDHf2 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 370
TrMDHf3 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 326
```

FIGURE 72

```
                  *       620         *       640         *       660
TrMDHf1 : ------------------------------------------------------------ :  -
TrMDHf2 : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 430
TrMDHf3 : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 386

                  *       680         *       700         *       720
TrMDHf1 : ------------------------------------------------------------ :  -
TrMDHf2 : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 490
TrMDHf3 : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 446

                  *       740         *       760         *       780
TrMDHf1 : ------------------------------------------------------------ :  -
TrMDHf2 : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 550
TrMDHf3 : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 506

                  *       800         *       820         *       840
TrMDHf1 : ------------------------------------------------------------ :  -
TrMDHf2 : TCACGACAAAGGAAATTGAGTACTTG---------------------------------- : 576
TrMDHf3 : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 566

                  *       860
TrMDHf1 : -------------------------- :  -
TrMDHf2 : -------------------------- :  -
TrMDHf3 : TTGAGGCCAAAGCTGGAGCTGGCTCT : 592
```

FIGURE 72 (cont.)

```
                  *        20         *        40         *        60
TrMDhg : GTAGGCAGCATCTAACAGCACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAA :  60

                  *        80         *       100         *       120
TrMDhg : TACGGTCCTTAAAAAATCTGTTCTTGTTTATTTGTACTTTTTTGTTTTGGAAGATCGT : 120

                  *       140         *       160         *       180
TrMDhg : TAGATACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGG : 180

                  *       200         *       220         *       240
TrMDhg : TGCTGCAGGACAAATTGGNTATGCTCTTGNTCCAATGATTGCAAGAGGGATGATGCTAGG : 240

                  *       260         *       280         *       300
TrMDhg : CCCAAATCAACCTGGAATTCTTCATATGCTNGATATTGAACCAGGATTAGAGGCCCTTAA : 300

                  *       320         *       340         *       360
TrMDhg : AGGGGTGAAGATGGAACTGATTGATGGTGCTTTCCCACTTCTTAGAGGTGTTGTTGCTAC : 360

                  *       380         *       400         *       420
TrMDhg : TACGGATGTTGTTGAAGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGTGGATCCCC : 420

                  *       440         *       460         *       480
TrMDhg : AAGGAAGGAAGGAATGGAAAGAAAAGATGTAATGTCTAAGAATGTTTCAATTTACAAGGC : 480

                  *       500         *       520         *       540
TrMDhg : TCAAGCTTCAGCTTTGGAGGAGCATGCTGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAA : 540

                  *       560         *       580         *
TrMDhg : TCCAGCAAACACAAATGCTCTAATATTGAAAGAATTTGCTCCATCAATCCCTGAGAAAA : 599
```

FIGURE 73

```
                    *        20         *        40         *        60
TrMDhg : MCGLLKVDKEPVTVLVTGAAGQIXYALXPMIARGMMLGPNQPGILHMXDIEPGLEALKGV :  60

                    *        80         *       100         *       120
TrMDhg : KMELIDGAFPLLRGVVATTDVVEACKDVNIAVMLGGSPRKEGMERKDVMSKNVSIYKAQA : 120

                    *       140         *
TrMDhg : SALEEHAAADCKVLVVANPANTNALILKEFAPSIPEK : 157
```

FIGURE 74

```
                    *        20         *        40         *        60
TrMDHg1 : GTAGGCATCA--TAACAGCACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAATA :  60
TrMDHg2 : ----GNNGGATCTAACAG-ACAATGAACATGGAAATGTTTGCTTTGGAAATTATGGACAATA :  57

                  *        80         *       100         *       120
TrMDHg1 : CGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTGTTTTGGAAGATCGTTAGA : 122
TrMDHg2 : CGGTCCTTAAAAAATCTGTTCTTGTTTTATTTTGTACTTTTTTGTTTTGGAAGATCGTTAGA : 119

                *       140         *       160         *       180
TrMDHg1 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 184
TrMDHg2 : TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCACTGGTGCTGC : 181

              *       200         *       220         *       240
TrMDHg1 : AGGACAAATTGGNTATGCTCTTGNTNCAATGATTGCNANAGGGATGATGCTANGNCCAAATC : 246
TrMDHg2 : AGGACAAATTGGTTATGCTCTTGTTCCAATGATTGCAAGAGGGATGATGCTAGGCCCAAATC : 243

            *       260         *       280         *       300         *
TrMDHg1 : NACCTGGNATTGTTGATATGCTNGNTNTTC-------------------------------- : 276
TrMDHg2 : AACCTGTAATTCTTCATATGCTTGATATTGAACCAGGATTAGAGGCCCTTAAAGGGGTGAAG : 305

                320         *       340         *       360         *
TrMDHg1 : -------------------------------------------------------------- :   -
TrMDHg2 : ATGGAACTGATTGATGGTGCTTTCCCACTTCTTAGAGGTGTTGTTGCTACTACGGATGTTGT : 367

              380         *       400         *       420         *
TrMDHg1 : -------------------------------------------------------------- :   -
TrMDHg2 : TGAAGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGTGGATCCCCAAGGAAGGAAGGAA : 429

            440         *       460         *       480         *
TrMDHg1 : -------------------------------------------------------------- :   -
TrMDHg2 : TGGAAAGAAAAGATGTAATGTCTAAGAATGTTTCAATTTACAAGGCTCAAGCTTCAGCTTTG : 491

          500         *       520         *       540         *       5
TrMDHg1 : -------------------------------------------------------------- :   -
TrMDHg2 : GAGGAGCATGCTGCTGCAGATTGTAAAGTGCTAGTGGTAGCCAATCCAGCAAACACAAATGC : 553

          60         *       580         *
TrMDHg1 : ----------------------------------------- :   -
TrMDHg2 : TCTAATATTGAAAGAATTTGCTCCATCAATCCCTGAGAAAA : 594
```

FIGURE 75

```
                     *        20         *        40         *        60
TrMDHh : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA :  60

                     *        80         *       100         *       120
TrMDHh : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120

                     *       140         *       160         *       180
TrMDHh : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180

                     *       200         *       220         *       240
TrMDHh : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240

                     *       260         *       280         *       300
TrMDHh : AACCTCTTTCAATGTTGATGAAGATGAATCCTTTGGTTTNAGTTCTTCATCTTTATGATG : 300

                     *       320         *       340         *       360
TrMDHh : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 360

                     *       380         *       400         *       420
TrMDHh : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 420

                     *       440         *       460         *       480
TrMDHh : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 480

                     *       500         *       520         *       540
TrMDHh : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 540

                     *       560         *       580         *       600
TrMDHh : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 600

                     *       620         *       640         *       660
TrMDHh : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 660

                     *       680         *       700         *       720
TrMDHh : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 720

                     *       740         *       760         *       780
TrMDHh : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 780

                     *       800         *       820         *       840
TrMDHh : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 840

                     *       860
TrMDHh : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866
```

FIGURE 76

```
                     *        20         *        40         *        60
TrMDHh : MEPNSDANQRIARISGHLNPPNFKMNEHGDSSLTSFHCRAKGGAPGFKVAILGAAGGIGQ :  60

                     *        80         *       100         *       120
TrMDHh : PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII : 120

                     *       140         *       160         *       180
TrMDHh : PAGVPRKPGMTRDDLFNINAGIVKTLCEAIAKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180

                     *       200         *       220         *       240
TrMDHh : GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVDVPVVGGHAGITILPLLSQVKPHSSF : 240

                     *       260
TrMDHh : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268
```

FIGURE 77

```
                *        20         *        40         *        60
TrMDHh1 : GNNTACNGCTATCNACCCTTCTTTCTTATACAATAATNATAGATAAATTCATCTGCTAAA :  60
TrMDHh2 : ------------------------------------------------------------ :   -
TrMDHh3 : ------------------------------------------------------------ :   -

                *        80         *       100         *       120
TrMDHh1 : TTATGGAGCCAAATTCAGATGCAAATCAACGAATCGCAAGAATCTCCGGCCACCTAAATC : 120
TrMDHh2 : ------------------------------------------------------------ :   -
TrMDHh3 : ------------------------------------------------------------ :   -

                *       140         *       160         *       180
TrMDHh1 : CTCCCAATTTCAAGATGAATGAACATGGTGATTCTTCTTTGACAAGTTTCCATTGCCGTG : 180
TrMDHh2 : ------------------------------------------------------------ :   -
TrMDHh3 : ------------------------------------------------------------ :   -

                *       200         *       220         *       240
TrMDHh1 : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTTTAGGTGCTGCTGGTGGCATAGGTC : 240
TrMDHh2 : ------------------------------------------------GTGNCATAGGTN :  12
TrMDHh3 : ------------------------------------------------------------ :   -

                *       260         *       280         *       300
TrMDHh1 : AACCTCTTTCAATGTTGATGAAGATGAATCCGTTGGTTT-AGTTCTTCATCTTTATGATG : 299
TrMDHh2 : AGCCTCTTT-NATGTTGATGAAGATGAATCCTATGGTTT-AGTTCTTCATCTTTATGATG :  70
TrMDHh3 : -------------------------------TTTGGTTTNNGTTCTTATNCTTTATGATG :  29

                *       320         *       340         *       360
TrMDHh1 : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCAGATGGATACTGGTGCTGTTGTTC : 359
TrMDHh2 : TTGTTAATACTCCTGGTGTTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTTC : 130
TrMDHh3 : TTG-TAATACTCCTGGTG-TACTTCTGATATTAGT-ATATGGATACTGCTGCTGTTGTTC :  86

                *       380         *       400         *       420
TrMDHh1 : GAGGATTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 419
TrMDHh2 : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 190
TrMDHh3 : GAGGGTTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTTGGTAATCA : 146

                *       440         *       460         *       480
TrMDHh1 : TTCCTGCTGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 479
TrMDHh2 : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 250
TrMDHh3 : TTCCTGCCGGTGTTCCCCGTAAACCTGGAATGACAAGAGATGATCTCTTCAATATAAATG : 206

                *       500         *       520         *       540
TrMDHh1 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCGAAGCGATGTCCTAAGGCGATTGTCA : 539
TrMDHh2 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGATTGTCA : 310
TrMDHh3 : CCGGGATCGTTAAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCGGTTGTCA : 266

                *       560         *       580         *       600
TrMDHh1 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCC--------------------------- : 572
TrMDHh2 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 370
TrMDHh3 : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTTCAAAAGAG : 326
```

FIGURE 78

```
                    *       620         *       640         *       660
TrMDHh1 : ------------------------------------------------------------ :   -
TrMDHh2 : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 430
TrMDHh3 : CCGGTACTTATGATCCCAAGAGACTTTTGGGAGTGACAATGCTTGATGTGGTTCGGGCCA : 386

                    *       680         *       700         *       720
TrMDHh1 : ------------------------------------------------------------ :   -
TrMDHh2 : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 490
TrMDHh3 : ATACGTTTGTGGCTGAAGTTCTTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 446

                    *       740         *       760         *       780
TrMDHh1 : ------------------------------------------------------------ :   -
TrMDHh2 : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 550
TrMDHh3 : GAGGACATGCCGGAATCACCATTTTACCTCTGCTTTCTCAGGTTAAACCACATTCCTCTT : 506

                    *       800         *       820         *       840
TrMDHh1 : ------------------------------------------------------------ :   -
TrMDHh2 : TCACGACAAAGGAAATTGAGTACTTG---------------------------------- : 576
TrMDHh3 : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG : 566

                    *       860
TrMDHh1 : -------------------------- :   -
TrMDHh2 : -------------------------- :   -
TrMDHh3 : TTGAGGCCAAAGCTGGAGCTGGCTCT : 592
```

FIGURE 78 (cont.)

```
                    *        20         *        40         *        60
TrMDHi : GNAATCCTCTTTGNCTCCCCTACCCTCCTTTTTTTTCCTTCCTTCTTACACCTTCTCTTA :  60

                    *        80         *       100         *       120
TrMDHi : TCAACTTTCCACCTCTGAACAAAACTTCAATCTTTTCTCATTTTCTTATACCCTTTTACA : 120

                    *       140         *       160         *       180
TrMDHi : AACTTCTTCATAAAGTGTTAGGTTTTTTTTTATTACTCTTTTCAAGAACCACAAAAAACAG : 180

                    *       200         *       220         *       240
TrMDHi : TGTTTCTTGAATTCTTTGGAATTTTTTTTTTCCTGCAACCATGGCCTTGGCACACTTAAA : 240

                    *       260         *       280         *       300
TrMDHi : CAACCCCACTTGCTCAAAAACTCAACTTCACTCATCACAACTCTCATTTCTCTCTAGGAC : 300

                    *       320         *       340         *       360
TrMDHi : TCTCCCTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAAT : 360

                    *       380         *       400         *       420
TrMDHi : TACTTGTTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAA : 420

                    *       440         *       460         *       480
TrMDHi : GAATAAGCCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTTGAAGGCTGAAGAGGA : 480

                    *       500         *       520         *       540
TrMDHi : GACAAAATCCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTC : 540

                    *       560         *       580         *       600
TrMDHi : CAATCATCTACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGCCCAAATCAACCTATTGC : 600

                    *       620         *       640
TrMDHi : GCTGAAATTATTAGGATCAGAAAGGTCCTTCCAAGCTCTTGAAGGTG : 647
```

FIGURE 79

```
                 *        20         *        40         *        60
TrMDHi : MALAHLNNPTCSKTQLHSSQLSFLSRTLPRQYHCTFAPLHRTQHGRITCSVAPNQVQAPA :  60

                 *        80         *       100         *       120
TrMDHi : VQSQDPKNKPDCYGVFCLTYDLKAEEETKSWKKLINIAVSGAAGMISNHLLFKLASGEVF : 120

                 *       140
TrMDHi : GPNQPIALKLLGSERSFQALEG : 142
```

FIGURE 80

```
                  *        20         *        40         *        60
TrMDHi1 : GNAATCCTCTTTGNCTCCCCTACCCTCCTTTTTTTTCCTTCCTTCTTACA-CTTCTCTTGT :  60
TrMDHi2 : -----------------------------------------TTCTTAGACCTTCTCTTAT :  19

                 *        80         *       100         *       120
TrMDHi1 : CAACTTTCCACCTCTGAACAAAACTTCTATCTTTTCTCATTTTCTTATACCCTTTTAGAAA : 121
TrMDHi2 : -AACTTTCNACCTCTGAACGAAA-TT-AATCTTTTCT-ATTTTCTTATACCCTTTTACAAA :  76

                *       140         *       160         *       180
TrMDHi1 : CTTCTTCATAAAGTGTTATTT--TTTTTTATTACTCTTTTCAAGAATCACAAAAACAGTGT : 180
TrMDHi2 : CTTCTTCATAAAGTGTTGGGTTTTTTTTATTACTCTTTTCAAGAACCACAAAAACAGTGT : 137

                *       200         *       220         *       240
TrMDHi1 : TTCTTGAATTCTTTGTAATTTTTTTTTCCTGCAACCATGGCCTTGGCACAGTTAAACAAT : 241
TrMDHi2 : TTCTTGAATTC-TTGGAA-TTTTTTTTCCTGCAACCATGGCTTTGGCACACTTAAACAAC : 196

               *       260         *       280         *       300
TrMDHi1 : CCCACTTGCTCAAAAACTCAACTTCACTCATCACAACTCTCATTTTTGTCTAGGACTCTCC : 302
TrMDHi2 : CCCACTTGCTCAAAAACTCAACTTCATTCATCACAGCTCTCATTTCTCTCTAGGACTCTCC : 257

              *       320         *       340         *       360
TrMDHi1 : CTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAATTACTTG : 363
TrMDHi2 : CTAGGCAATATCACTGTACTTTTGCACCACTTCACAGAACTCAACATGGCAGAATTACTTG : 318

             *       380         *       400         *       420
TrMDHi1 : TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAAGAATAAG : 424
TrMDHi2 : TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCCAAGAATAAG : 379

            *       440         *       460         *       480
TrMDHi1 : CCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTTGAAGGCTGAAGAGGAGACAAAAT : 485
TrMDHi2 : CCTGATTGCTATGGTGTCTTCTGCCTTACCTATGATTTGAAGGCTGAAGAGGAGACAAAAT : 440

           *       500         *       520         *       540
TrMDHi1 : CCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTCCAATCATCT : 546
TrMDHi2 : CCTGGAAGAAATTAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTCCAATCATCT : 501

          *       560         *       580         *       600         *
TrMDHi1 : ACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGTCCAAATCAACCTATTGCGCTGA----- : 602
TrMDHi2 : ACTTTTCAAGCTTGCATCTGGTGAAGTTTTTGGCCCAAATCAACCTATTGCGCTGAAATTA : 562

                620         *       640
TrMDHi1 : ------------------------------------- :  -
TrMDHi2 : TTAGGATCAGAAAGGTCCTTCCAAGCTCTTGAAGGTG : 599
```

FIGURE 81

```
                  *        20         *        40         *        60
TrMDHj : GCAAAGCNCTCNCNGACCTGGTGTGGAGCGAGCAGCTTTGCTAGACATAAATGGGCAGAT :  60

                  *        80         *       100         *       120
TrMDHj : TTTTGCGGAGCAGGGAAAAGCTCTAAATGCAGTCGCATCTCGCAATGTCAAAGTTATAGT : 120

                  *       140         *       160         *       180
TrMDHj : TGTGGGAAACCCTTGCAATACAAATGCATTAATATGCTTGAAGAATGCTCCAAATATTCC : 180

                  *       200         *       220         *       240
TrMDHj : TGCAAAAAATTTTCATGCTTTAACCCGTTTAGATGAGAACAGAGCAAAATGTCAGCTAGC : 240

                  *       260         *       280         *       300
TrMDHj : CCTCAAGGCAGGTGTCTTCTACGATAAAGTGTCGAATATGACGATATGGGGAAACCACTC : 300

                  *       320         *       340         *       360
TrMDHj : AACTACTCAGGTCCCCGATTTCTTAAATGCCAGAATCGATGGTTTGCCTGTCAAAGAAGT : 360

                  *       380         *       400         *       420
TrMDHj : GATTAAGGATCAAAAGTGGTTAGAGGAAGAGTTCACCGAAAAAGTTCAAAAGAGAGGTGG : 420

                  *       440         *       460         *       480
TrMDHj : CGTGCTTATTCAAAAGTGGGGAAGATCGTCTGCTGCATCAACTTCTGTGTCGATAGTTGA : 480

                  *       500         *       520         *       540
TrMDHj : TGCCATACGATCTTTGATCACTCCTACTCCGGAGGGTGATTGGTTTTCTACTGGTGTGTA : 540

                  *       560
TrMDHj : TACAGCTGGAAATCCTTATGGAATAGCTG : 569
```

FIGURE 82

```
                     *        20         *        40         *        60
TrMDHj  :  QSXXXPGVERAALLDINGQIFAEQGKALNAVASRNVKVIVVGNPCNTNALICLKNAPNIP  :   60

                     *        80         *       100         *       120
TrMDHj  :  AKNFHALTRLDENRAKCQLALKAGVFYDKVSNMTIWGNHSTTQVPDFLNARIDGLPVKEV  : 120

                     *       140         *       160         *       180
TrMDHj  :  IKDQKWLEEEFTEKVQKRGGVLIQKWGRSSAASTSVSIVDAIRSLITPTPEGDWFSTGVY  : 180

TrMDHj  :  TAGNPYGIA  : 189
```

FIGURE 83

```
                      *        20         *        40         *        60
TrMDHk : GNGTAGAACCCGTGAAGCCTTTTCCCTCCGGTCTCCCCGCTTGCGCCGTCGCCGTCAATT :  60

                      *        80         *       100         *       120
TrMDHk : GCTGCTTGTGTCGTCGCCTCCAGCTCCTCCTCCTCCACTGTGCCAACCGAATTACAAACC : 120

                      *       140         *       160         *       180
TrMDHk : AAAAAAATGGCGACTTGTTTGCAAACACAACTCCTCCACACAAGACCTTTTCAGTTTCGG : 180

                      *       200         *       220         *       240
TrMDHk : TCTTCCTCGTCGACAAGACCAACTTCCCTAAGATGTTCCGCCGCCACCCCATCCACCAAA : 240

                      *       260         *       280         *       300
TrMDHk : AAATCCTACAAAATCACTCTTCTTCCGGGTGATGGCATAGGTCCTGAAGTCGTTTCCGTC : 300

                      *       320         *       340         *       360
TrMDHk : GCTAAAGACGTTCTTCTCCTCACTGGATCCATCCATGGGATTAAACTTGAGTTTCAAGAG : 360

                      *       380         *       400         *       420
TrMDHk : AAGCTTTTGGGTGGTGCTGCTCTTGATGCTACTGGAGTTCCTTTACCTGATGATACTCTT : 420

                      *       440         *       460         *       480
TrMDHk : TCTGTTGCTAAGCAATCTGATGCTGTTCTTCTTGGTGCTATTGGAGGGTATAAATGGGAT : 480

                      *       500         *       520         *       540
TrMDHk : AAAAATGAGAAACAGCTGAAGCCAGAAACTGGATTGCTTCAGCTACGAGAAGGGCTTCAA : 540

                      *
TrMDHk : GTTTTTGCTAATCTCAGA : 558
```

FIGURE 84

```
                 *        20         *        40         *        60
TrMDHk : MATCLQTQLLHTRPFQFRSSSSTRPTSLRCSAATPSTKKSYKITLLPGDGIGPEVVSVAK :  60

                 *        80         *       100         *       120
TrMDHk : DVLLLTGSIHGIKLEFQEKLLGGAALDATGVPLPDDTLSVAKQSDAVLLGAIGGYKWDKN : 120

                 *       140
TrMDHk : EKQLKPETGLLQLREGLQVFANLR : 144
```

FIGURE 85

```
                    *        20         *        40         *        60
TrPEPCa : GNNACATTNCCGAATGCTGCTGAACTAGGGAGTGATTCCCTTGGAGCCTATGTCATCTCT :  60

                    *        80         *       100         *       120
TrPEPCa : ATGGCCTCAAGTGCAAGCGATGTCCTTGCAGTAGAGCTTTTACAGAAGGATGCACGTCTT : 120

                    *       140         *       160         *       180
TrPEPCa : ACAGTTTGTGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA : 180

                    *       200         *       220         *       240
TrPEPCa : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACTTTTATCAATC : 240

                    *       260         *       280         *       300
TrPEPCa : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 300

                    *       320         *       340         *       360
TrPEPCa : TATTCTGATTCTGGTAAAGATGCCGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 360

                    *       380         *       400         *       420
TrPEPCa : CAAGAGGATGTAGTGGCTGCTTGCAATAAGTACGATACTAAGGTTACTTTGTTCCACGGC : 420

                    *       440         *       460         *       480
TrPEPCa : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 480

                    *       500         *       520         *       540
TrPEPCa : CCTGGCTCTGTGATGGGAACCCTTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAG : 540

                    *       560         *       580         *       600
TrPEPCa : TTTGGGTTGCCACAGACAGCAGTTAGACAACTTGAAATATACACAACAGCTGTGCTACTT : 600

                    *       620         *       640         *       660
TrPEPCa : GCTACACGTCGTCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 660

                    *       680         *       700         *
TrPEPCa : ATNTCAAAAATCAGTTGTCAGTCCTACCGCAGTGTAGTCTATGAAAATCCAGN : 713
```

FIGURE 86

```
                    *        20         *        40         *        60
TrPEPCa : XTXPNAAELGSDSLGAYVISMASSASDVLAVELLQKDARLTVCGELGRACPGGTLRVVPL :  60

                    *        80         *       100         *       120
TrPEPCa : FETVQDLRGAGAVIRKLLSIDWYRQHIIKNHNGHQEVMVGYSDSGKDAGRFTAAWELYKA : 120

                    *       140         *       160         *       180
TrPEPCa : QEDVVAACNKYDTKVTLFHGRGGSIGRGGGPTYLAIQSQPPGSVMGTLRSTEQGEMVQAE : 180

                    *       200         *       220         *
TrPEPCa : FGLPQTAVRQLEIYTTAVLLATRRPPLPPREEKWRNLMEDXSKISCQSYRSVVYENP : 237
```

FIGURE 87

```
                  *        20         *        40         *        60
TrPEPCa1 : GNNACATTNCCGAATGCTGCTGAACTAGGGAGTGATTCCCTTGGAGCCTATGTCATCTCT :  60
TrPEPCa2 : ------------------------------------------------------------ :   -
TrPEPCa3 : ------------------------------------------------------------ :   -

                  *        80         *       100         *       120
TrPEPCa1 : ATGGCCTCAAGTGCAAGCGATGTCCTTGCAGTAGAGCTTTT-CAGAAGGATGCACGACTT : 119
TrPEPCa2 : ---------------------------------GNACTTTTACAGAAGGATGCACGTCTT :  27
TrPEPCa3 : ----------------------------------AGCTTTTACAGANGGATGCACGTCTT :  26

                  *       140         *       160         *       180
TrPEPCa1 : GCTGCTATTGGAGAGTTCGGAAGAGCATGTCCTGGTGGAACGTTGCGGGTTGTGCCTCTA : 179
TrPEPCa2 : ACAGTTTGTGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA :  87
TrPEPCa3 : ACAGTTTGTGGAGAATTAGGAAGAGCATGTCCGGGTGGAACGCTTCGGGTGGTTCCTCTA :  86

                  *       200         *       220         *       240
TrPEPCa1 : TTTGAAACTGTGAAGGACCTAAGAGGAGCTGGTTCAGTTATCGGGAAACTTTTATCGATA : 239
TrPEPCa2 : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACTTTTATCAATC : 147
TrPEPCa3 : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACTTTTATCAATC : 146

                  *       260         *       280         *       300
TrPEPCa1 : GAGTGGTACCGTGAACACATCATTAAGAACCAGAATGGACATCAAGAGGTTATGGTTGGA : 299
TrPEPCa2 : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 207
TrPEPCa3 : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 206

                  *       320         *       340         *       360
TrPEPCa1 : TATTCTGATTCGGGTAAAGATGCTGGCCGCTTCACTGCTGCTTGGGAACTTTACAAAGCT : 359
TrPEPCa2 : TATTCTGATTCTGGTAAAGATGCCGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 267
TrPEPCa3 : TATTCTGATTCTGGTAAAGATGCCGGGCGCTTTACTGCTGCTTGGGAACTTTACAAAGCT : 266

                  *       380         *       400         *       420
TrPEPCa1 : CAGGAGGATGTTGTAGCTGCTTGCAATGATTATGGTATTAAAGTTACAGTGTTTCATGGC : 419
TrPEPCa2 : CAAGAGGATGTAGTGGCTGCTTGCAATAAGTACGATACTAAGGTTACTTTGTTCCACGGC : 327
TrPEPCa3 : CAAGAGGATGTAGTGGCTGCTTGCAATAAGTACGATACTAAGGTTACTTTGTTCCACGGC : 326

                  *       440         *       460         *       480
TrPEPCa1 : CGTGGAGGGAGTATTGGTCGAGGTGGTGGCCCTACATATCTGGCTATTCAGTCCCAACCA : 479
TrPEPCa2 : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 387
TrPEPCa3 : CGCGGAGGGAGTATTGGACGTGGCGGAGGCCCAACATATCTGGCTATTCAGTCCCAGCCA : 386

                  *       500         *       520         *       540
TrPEPCa1 : CCTGGGTCTGTGATGGGAACACTTCGGTCTACTGAGCAGGGAGAAATGGTAGAGGCCAAG : 539
TrPEPCa2 : CCTGGCTCTGTGATGGGAACCCTTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAG : 447
TrPEPCa3 : CCTGGCTCTGTGATGGGAACCCTTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAG : 446

                  *       560         *       580         *       600
TrPEPCa1 : TTTGGGTTACCACAGATAGCTGTTAGACAACTTGANN----------------------- : 576
TrPEPCa2 : TTTGGGTTGCCACAGACAGCAGTTAGACAACTTGAAATATACACAACAGCTGTGCTACTT : 507
TrPEPCa3 : TTTGGGTTGCCACAGACAGCAGTTAGACAACTTGAAATATACACAACAGCTGTGCTACTT : 506
```

FIGURE 88

```
                  *        620         *        640         *        660
TrPEPCa1 : ------------------------------------------------------------ :   -
TrPEPCa2 : GCTACACGTCGTCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 567
TrPEPCa3 : GCTACACGTCGTCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 566

                  *        680         *        700         *
TrPEPCa1 : ----------------------------------------------------- :   -
TrPEPCa2 : ATN-------------------------------------------------- : 570
TrPEPCa3 : ATTTCAAAAATCAGTTGTCAGTCCTACCGCAGTGTAGTCTATGAAAATCCAGN : 619
```

FIGURE 88 (cont.)

```
                      *        20         *        40         *        60
TrPEPCb : GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT :  60

                      *        80         *       100         *       120
TrPEPCb : TCTGAAATTCCTGAAGAAGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA : 120

                      *       140         *       160         *       180
TrPEPCb : CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT : 180

                      *       200         *       220         *       240
TrPEPCb : GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA : 240

                      *       260         *       280         *       300
TrPEPCb : GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTTGGAAATTGGATCC : 300

                      *       320         *       340         *       360
TrPEPCb : TACCAAGACTGGTCTGAAGAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAAA : 360

                      *       380         *       400         *       420
TrPEPCb : AGGCCGCTTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTTAGAGACA : 420

                      *       440         *       460         *       480
TrPEPCb : TTTCATGTCATAGCAGAACTTCCATCAGACAACTTTGGAGCCTATATCATTTCGATGGCA : 480

                      *       500         *       520         *       540
TrPEPCb : ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT : 540

                      *       560         *       580         *
TrPEPCb : CCGTTAAGAGTTGTTCCGTTGTTTGAGAAACTTGCTGATCTCGAGTCTGCTCCTGCTG : 598
```

FIGURE 89

```
                     *        20         *        40         *        60
TrPEPCb : XRDKLYRTRERSRYLLAHGYSEIPEEATFTDVDEFLEPLELCYRSLCACGDRAIADGSLL :  60

                     *        80         *       100         *       120
TrPEPCb : DFLRQVSTFGLSLVRLDIRQESDRHTDVMDAITKHLEIGSYQDWSEEKRQEWLLSELVGK : 120

                     *       140         *       160         *       180
TrPEPCb : RPLFGPDLPQTDEIREVLETFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECKIKN : 180

                     *
TrPEPCb : PLRVVPLFEKLADLESAPA : 199
```

FIGURE 90

```
                 *        20         *        40         *        60
TrPEPCb1 : GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT :  60
TrPEPCb2 : GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT :  60

                 *        80         *       100         *       120
TrPEPCb1 : TCTGAAATTCCTGAAGAAGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA : 120
TrPEPCb2 : TCTGAAATTCCTGAAGAAGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA : 120

                 *       140         *       160         *       180
TrPEPCb1 : CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT : 180
TrPEPCb2 : CTATGCTACAGATCACTCTGTGCTTGTGGTGATCGTGCGATTGCCGATGGAAGCCTTCTT : 180

                 *       200         *       220         *       240
TrPEPCb1 : GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA : 240
TrPEPCb2 : GATTTCTTGAGGCAAGTTTCCACTTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA : 240

                 *       260         *       280         *       300
TrPEPCb1 : GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTTGGAAATTGGATCC : 300
TrPEPCb2 : GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTTGGAAATTGGATCC : 300

                 *       320         *       340         *       360
TrPEPCb1 : TACCAAGACTGGTCTGAAGAAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAAA : 360
TrPEPCb2 : TACCAAGACTGGTCTGAAGAAAAAAGACAGGAATGGCTTTTGTCTGAGTTGGTTGGCAAA : 360

                 *       380         *       400         *       420
TrPEPCb1 : AGGCCGCTTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTTAGAGACA : 420
TrPEPCb2 : AGGCCGCTTTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTTAGAGACA : 420

                 *       440         *       460         *       480
TrPEPCb1 : TTTCATGTCATAGCAGAACTTCCATCAGACAACTTTGGAGCCTATATCATTTCGATGGCA : 480
TrPEPCb2 : TTTCATGTCATAGCAGAACTTCCATCAGACAACTTTGGAGCCTATATCATTTCGATGGCA : 480

                 *       500         *       520         *       540
TrPEPCb1 : ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT : 540
TrPEPCb2 : ACTGCCCCGTCTGATGTGCTAGCGGTTGAACTTCTTCAACGTGAATGCAAAATCAAGAAT : 540

                 *       560         *       580         *
TrPEPCb1 : CCGTTAAGAGTTGTTCCGTTGTTTGAGAAACTTGCTGATCTCGAGTCTGCTCCTGCTG : 598
TrPEPCb2 : CCGTTAAGAGTTGTTCCGTTGTTTGAGAAACTTGCTGATCTCGN-------------- : 584
```

FIGURE 91

```
                 *        20         *        40         *        60
TrPEPCc : GTCACATGACAAACNATATCTCCCTTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA :  60

                 *        80         *       100         *       120
TrPEPCc : CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA : 120

                 *       140         *       160         *       180
TrPEPCc : CAAACTAGATTTTCCACCTAGGTCGTCACGAGATTTTCCTCTTCACTATTTTTCTTTTTC : 180

                 *       200         *       220         *       240
TrPEPCc : ATATAATAACTCAACACTTTTTCTAGCTACTTACTAGTACTGTGTAACACAAATTTTATT : 240

                 *       260         *       280         *       300
TrPEPCc : CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT : 300

                 *       320         *       340         *       360
TrPEPCc : ACTAGCACCAAGGAAAGTTTCTGATGATGATAAACTTGTCGAGTATGATGCTTTGTTATT : 360

                 *       380         *       400         *       420
TrPEPCc : GGATCGATTCCTTGACATTCTTCAAGATTTGCATGGAGAAGATATCAGACAAACTGTTCA : 420

                 *       440         *       460         *       480
TrPEPCc : AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTAAGCCGGAGAAATTGGAGGA : 480

                 *       500         *       520         *       540
TrPEPCc : ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAAATCATT : 540

                 *       560         *
TrPEPCc : TTCTCATATGCTTAATTTGGCAAACTTGGCAGAGN : 575
```

FIGURE 92

```
                      *        20         *        40         *        60
TrPEPCc : MATPRNIEKMASIDAQLRLLAPRKVSDDDKLVEYDALLLDRFLDILQDLHGEDIRQTVQD :  60

                      *        80         *       100         *
TrPEPCc : CYELSAEYEGELKPEKLEELGNMLTGLDAGDSIVIAKSFSHMLNLANLAE : 110
```

FIGURE 93

```
                         *        20         *        40         *        60
TrPEPCc1 : GTCACATGACTNACTATATCTCCCTTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA :  60
TrPEPCc2 : ------TGACAAACNATATCTCCCTTTCTCTAACTCCGTGATCAAGGCGTTAGTTAGTTA :  54

                         *        80         *       100         *       120
TrPEPCc1 : CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA : 120
TrPEPCc2 : CACAAATTGCTGTTAGGTTTCGTTGTACTTTCCCGTGCAATCCATAGTATCTTGGAGGAA : 114

                         *       140         *       160         *       180
TrPEPCc1 : CAAACTAGATTTTCCACCTAGGTCGTCACGAGATTTTCCTCTTCACTATTTTTCTTTTTC : 180
TrPEPCc2 : CAAACTAGATTTTCCACCTAGGTTGTCACGAGATTTTCCTCTTCACTATTTTTCTTTTTC : 174

                         *       200         *       220         *       240
TrPEPCc1 : ATATAATAACTCAACACTTTTTCTAGCTACTTACTAGTACTGTGTAACACAAATTTTATT : 240
TrPEPCc2 : ATATAATAATTCAACACTTTTTCTAGCTACTTACTAGTACTGTGTAACACAAATTTTATT : 234

                         *       260         *       280         *       300
TrPEPCc1 : CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT : 300
TrPEPCc2 : CATTATGGCTACTCCTCGCAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT : 294

                         *       320         *       340         *       360
TrPEPCc1 : ACTAGCACCAAGGAAAGTTTCTGATGATGATAAACTTGTCGAGTATGATGCTTTGTTATT : 360
TrPEPCc2 : ACTAGCACCAAGGAAAGTTTCTGATGATGATAAACTTGTCGAGTATGATGCTTTGTTATT : 354

                         *       380         *       400         *       420
TrPEPCc1 : GGATCGATTCCTTGACATTCTTCAAGATTTGCATGGAGAAGATATCAGACAAACTGTTCA : 420
TrPEPCc2 : GGATCGATTCCTTGACATTCTTCAAGATTTGCATGGAGAAGATATCAGACAAACTGTTCA : 414

                         *       440         *       460         *       480
TrPEPCc1 : AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTATGCCGGAGAAATTGGAGGA : 480
TrPEPCc2 : AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTAAGCCGGAGAAATTGGAGGA : 474

                         *       500         *       520         *       540
TrPEPCc1 : ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAAATCATT : 540
TrPEPCc2 : ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAAATCATT : 534

                         *       560         *
TrPEPCc1 : TTCTCATATGCTTAATTTGGCAAACTTGGCAGAGN : 575
TrPEPCc2 : TTN-------------------------------- : 537
```

FIGURE 94

```
                     *        20         *        40         *        60
TrPEPCd : AGAAGATCTCATGTTTGAGTTGTCTATGTGGCGCTGCAACGACGAGCTCCGTGTTAGAGC :  60

                     *        80         *       100         *       120
TrPEPCd : TGAAGAGCTTCATAGATCCTCAAAGAAAGATGCAAAACATTATATTGAGTTTTGGAAACA : 120

                     *       140         *       160         *       180
TrPEPCd : GATTCCTCCAAACGAGCCATATCGTGTTATTCTTGGAGGTGTGAGGGACAAACTGTATAA : 180

                     *       200         *       220         *       240
TrPEPCd : TACACGTGAACGTGCTCGACAGTTATTAGCAAATGGAACCTCTGACATCCTTGAAGAGAC : 240

                     *       260         *       280         *       300
TrPEPCd : AACCTTCACGAATGTTGAGCAGTTTCTGGAGCCTCTTGAACTGTGTTATAGGTCACTTTG : 300

                     *       320         *       340         *       360
TrPEPCd : TGCATGTGGTGACCGATCAATAGCAGACGGAAGCCTTCTTGATTTCTTGCGACAAGTTTC : 360

                     *       380         *       400         *       420
TrPEPCd : TACATTTGGACTTTCACTTGTAAGACTCGACATCCGTCAAGAGTCAGACAGGCACACAGA : 420

                     *       440         *       460         *       480
TrPEPCd : CGTTATGGATGCAATTACAAAACACTTGGAGATTGGATCTTACCGAGAATGGTCGGAAGA : 480

                     *       500         *       520         *       540
TrPEPCd : ACGCAGGCAGGAATGGCTCTTGTCTGAGCTTAGTGGAAAACGCCCTCTCTTCGGCCATGA : 540

                     *       560         *       580         *       600
TrPEPCd : TCTTCCTAAGACAGAAGAAATTGCCGATGTTTTAGATACCTTNCACGTNATTTCANAACT : 600

                     *       620         *       640         *       660
TrPEPCd : TNCCTCANATAGCTTTGGTGCCTATATCATCTCAATGGCAACCTCCCCATCTGATGTGCT : 660

                     *       680         *       700         *       720
TrPEPCd : AGCTGTCGAGCTTTTACAACGTGAATGTCATGTGAAGCAGCCGTTAANAGTTGTTCCACT : 720

                     *       740         *       760         *       780
TrPEPCd : GTTTGAAAAGCTCGCCNGTCTTGAGTCTGCTCCTGCTGCGGNAGCGCGTTTTTTNTTAGA : 780

                     *       800         *       820         *       840
TrPEPCd : TTGGGNCANAACCGNNNTAATGGAAAGCAGAAGTTNTGATAGGTACTCANACTNGGGAAA : 840

                     *
TrPEPCd : AGATGCTGGCCGNN : 854
```

FIGURE 95

```
                     *        20         *        40         *        60
TrPEPCd : EDLMFELSMWRCNDELRVRAEELHRSSKKDAKHYIEFWKQIPPNEPYRVILGGVRDKLYN :  60

                     *        80         *       100         *       120
TrPEPCd : TRERARQLLANGTSDILEETTFTNVEQFLEPLELCYRSLCACGDRSIADGSLLDFLRQVS : 120

                     *       140         *       160         *       180
TrPEPCd : TFGLSLVRLDIRQESDRHTDVMDAITKHLEIGSYREWSEERRQEWLLSELSGKRPLFGHD : 180

                     *       200         *       220         *       240
TrPEPCd : LPKTEEIADVLDTXHXISXLXSXSFGAYIISMATSPSDVLAVELLQRECHVKQPLXVVPL : 240

                     *       260         *       280
TrPEPCd : FEKLAXLESAPAAXARFXLDWXXTXXMESRSXDRYSXXGKDAGX : 284
```

FIGURE 96

```
                      *        20         *        40         *        60
TrPEPCe : GTTCACTGTCTCTCTGNCCAATTTTCCTCCCTTGTCTTCTTTTTCTTCTTCTTCCTCGTA :  60

                      *        80         *       100         *       120
TrPEPCe : TCTTACTGCCTCATTACACGGGTGAGAAGGAGTGAATTGCTCCAATGGCAACAAACAAAA : 120

                      *       140         *       160         *       180
TrPEPCe : TGGAAAAAATGGCATCAATTGATGCACAGCTTAGACAATTAGTACCAGCAAAAGTTAGTG : 180

                      *       200         *       220         *       240
TrPEPCe : AAGATGATAAACTTATTGAGTATGATGCTTTGTTGTTGGATCGGTTTCTTGATATCCTTC : 240

                      *       260         *       280         *       300
TrPEPCe : AGGATTTACATGGAGAGGATCTGAAAGATTCTGTTCAAGAAGTGTATGAACTTTCTGCGG : 300

                      *       320         *       340         *       360
TrPEPCe : AGTATGAAAGAAAGCATGATCCTAAGAAACTTGAAGAGCTCGGAAATTTGATAACAAGTT : 360

                      *       380         *       400         *       420
TrPEPCe : TAGATGCAGGAGATTCAATTGTTGTTGCTAAGTCCTTTTCGCACATGCTTAACTTGGCCA : 420

                      *       440         *       460         *       480
TrPEPCe : ACTTAGCTGAAGAGGTTCAGATTGCTCATCGTCGAAGGAACAAGTTGAAGAAAGGAGATT : 480

                      *       500         *       520         *       540
TrPEPCe : TTAGGGATGAGAGCAATGCAACTACCGAATCAGACATCGAAGAAACTCTTAAGAGACTTG : 540

                      *       560         *       580         *       600
TrPEPCe : TGTTTAATATGAAGAAATCTCCTCAGGAAGTTNTTGATGCGTTGAAGAACCNNACCGTTG : 600

                      *       620         *       640         *       660
TrPEPCe : ATTTGGTTCTTACTGCTCATCCCACTCAGTCCGTTCGANGNCCNCTGCTTCCCNNNGCCT : 660

                      *       680         *
TrPEPCe : GGNACGGGNACCGCNCTGNCTATCNNACTGNNN : 693
```

FIGURE 97

```
                    *        20         *        40         *        60
TrPEPCe : MATNKMEKMASIDAQLRQLVPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKDSVQEV :  60

                    *        80         *       100         *       120
TrPEPCe : YELSAEYERKHDPKKLEELGNLITSLDAGDSIVVAKSFSHMLNLANLAEEVQIAHRRRNK : 120

                    *       140         *       160         *       180
TrPEPCe : LKKGDFRDESNATTESDIEETLKRLVFNMKKSPQEVXDALKNXTVDLVLTAHPTQSVRXX : 180

                    *
TrPEPCe : LLPXAWXGXRXXYXTX : 196
```

FIGURE 98

```
                 *        20         *        40         *        60
TrCSa : GNNNCNCNACCATTACATTAATNACACTTTCCNCTTTCGCCTTGTTCTTTCTCTTCTCAA :  60

                 *        80         *       100         *       120
TrCSa : TATAAAGACCAATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCATTCTACGCGTCT : 120

                 *       140         *       160         *       180
TrCSa : TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTAAATGGCGTTCTT : 180

                 *       200         *       220         *       240
TrCSa : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 240

                 *       260         *       280         *       300
TrCSa : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 300

                 *       320         *       340         *       360
TrCSa : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 360

                 *       380         *       400         *       420
TrCSa : TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC : 420

                 *       440         *       460         *       480
TrCSa : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 480

                 *       500         *       520         *       540
TrCSa : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 540

                 *       560         *       580         *       600
TrCSa : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 600

                 *       620         *       640         *       660
TrCSa : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 660

                 *       680         *       700         *       720
TrCSa : ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT : 720

                 *       740         *       760         *       780
TrCSa : GGAGAGTGAGTTTACAAAGGCATACGAGAGTGGGATACATAAGTCAAGGTATTGGGAGCC : 780

                 *       800         *       820         *       840
TrCSa : AACTTATGAGGATAGCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA : 840

                 *       860         *       880         *       900
TrCSa : TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGTGC : 900
```

FIGURE 99

```
                  *        920         *        940         *        960
TrCSa : AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA :  960

                  *        980         *       1000         *       1020
TrCSa : TATTTCTATCCATAGTGATCATGAAGGNGGCAACGTTAGTTCTCACACAGCTCACCTAGT : 1020

                  *       1040         *       1060         *       1080
TrCSa : TGCTAGTTCACTATCAGATCCTTATCTTGCATTCGCAGCTGCTCTGAATGGTTTAGCTGG : 1080

                  *       1100         *       1120         *       1140
TrCSa : CCCACTGCATGGTTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAACATAGTTAAGGA : 1140

                  *       1160         *       1180         *       1200
TrCSa : GTTTGGAACTCCAAACATAAGTACAGAACAATTGAGCGACTACATTCATAAAACATTGAA : 1200

                  *       1220         *       1240         *       1260
TrCSa : CAGTGGCCAGGTTGTGCCTGGATATGGACATGGAGTTTTGCGCAATACAGACCCAAGATA : 1260

                  *       1280         *       1300
TrCSa : CACTTGCCAGAGGGAGTTTGCATTGAAGCATTTGCCTAATGATCCAN : 1307
```

FIGURE 99 (cont.)

```
                    *        20         *        40         *        60
TrCSa : MAFFRSVSALSKLRSRVGQQPSLANSVRWLQTPSSSNTDLYSEMKELVPEYQERVKKLKK :  60

                    *        80         *       100         *       120
TrCSa : DHGSVELGKITADMVLGGMRGMTALVWLGSAVDPDEGIRFRGMTIPDCQKTLPGAFPGGE : 120

                    *       140         *       160         *       180
TrCSa : PLPEAILWLLLTGKVPSKEQVDSLAHELRSRAKIPEYAYKAIDALPVSAHPMTQFSTGVM : 180

                    *       200         *       220         *       240
TrCSa : ALQVESEFTKAYESGIHKSRYWEPTYEDSLNLIARLPGIAAYIYRRIYKDGKIIPLDDSL : 240

                    *       260         *       280         *       300
TrCSa : DYGANYAHMLGFDDPETLEFMRLYISIHSDHEGNVSSHTAHLVASSLSDPYLAFAAALNG : 300

                    *       320         *       340         *       360
TrCSa : LAGPLHGLANQEVLRWIRNIVKEFGTPNISTEQLSDYIHKTLNSGQVVPGYGHGVLRNTD : 360

                    *
TrCSa : PRYTCQREFALKHLPNDP : 378
```

FIGURE 100

```
                 *       20         *       40         *        60
TrCSa1 : GNNNCNCNACCATTACGTTAATTACATTTTCTNCTTTCGCCTTGTTCTTTCTCTTCTCAA :  60
TrCSa2 : --------------ACATTCGTNATNCTTTTCTCTTTCGCCTTGTTCTTTCTCTTCT-AA :  45
TrCSa3 : ------------------------------------------------------------ :   -
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                 *       80         *      100         *       120
TrCSa1 : TATAAAGACCAATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCATTCTACGCTTCT : 120
TrCSa2 : TATAAAGACC-ATTCAATTCCCAATTCTTTTGGATCCGAAATCATTCATTCTACGCTTCT : 104
TrCSa3 : -----------------TACCGNAAAC--TTNCTTNC-TACTTTTNCAACCNCTNCGNCT :  40
TrCSa4 : --------------------------------------------------GTNCCCGAAA :  10
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                 *      140         *      160         *       180
TrCSa1 : TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTTAATGGCGTTCTT : 180
TrCSa2 : TCTCTCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTTAATGGCGTTCTT : 164
TrCSa3 : TCTTNCTTCTCTGCGTTTCAAACCCTAGTTGTTTTGTTGATTGATCTAAATGGCGTTCTT : 100
TrCSa4 : TNNTTCCTTTCTAC-TTT-TNACCCT-GTTGTTTNGTTGATTGATCTAAATGGCGTTCTT :  67
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                 *      200         *      220         *       240
TrCSa1 : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 240
TrCSa2 : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 224
TrCSa3 : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTCGC : 160
TrCSa4 : TCGAAGCGTTTCTGCGCTTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 127
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                 *      260         *      280         *       300
TrCSa1 : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 300
TrCSa2 : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 284
TrCSa3 : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 220
TrCSa4 : TAATTCAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTTATTCTGAGAT : 187
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -

                 *      320         *      340         *       360
TrCSa1 : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 360
TrCSa2 : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 344
TrCSa3 : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGATCATGGAAG : 280
TrCSa4 : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 247
TrCSa5 : ------------------------------------------------------------ :   -
TrCSa6 : ------------------------------------------------------------ :   -
TrCSa7 : ------------------------------------------------------------ :   -
```

FIGURE 101

```
                 *       380         *       400         *       420
TrCSa1 : TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC : 420
TrCSa2 : TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC : 404
TrCSa3 : TGTTGAATTGGGAAAAGTCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACAGC : 340
TrCSa4 : TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC : 307
TrCSa5 : ---------GNGGAAAAATACAGCTGATATGGTACTTGGTGGAATGAGAGGAATGACTGC :  51
TrCSa6 : --------------------------------------------GNAGAGGAATGACTGC :  16
TrCSa7 : ------------------------------------------------------------ :   -

                 *       440         *       460         *       480
TrCSa1 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 480
TrCSa2 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 464
TrCSa3 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 400
TrCSa4 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCANATGAGGGAATTCGCTTTAGGGGCATGAC : 367
TrCSa5 : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC : 111
TrCSa6 : TTTAGTGTGGCT-GGCT-NGCTGTTGACCCAGATGAGGGAATTCGCTTTAGGGGCATGAC :  74
TrCSa7 : ------------------------------------------------------------ :   -

                 *       500         *       520         *       540
TrCSa1 : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 540
TrCSa2 : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 524
TrCSa3 : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 460
TrCSa4 : AATTCCTGACTGCCACAAAACACTTGCAGGTGCTTTTNCTGGCGGGGAGNCTTTGNCCNA : 427
TrCSa5 : AATTCCTGACTGCCAGAAAACACTTCCAGGTGCTGTTCCTGGTGGGGAGCCTTTGCCCGA : 171
TrCSa6 : AATTCCTGACTGCCAG-AAACACTTCCAGGTGCTTTTCCTGGTGGGGAGCCTTTGCCCGA : 133
TrCSa7 : ------------------------------------------------------------ :   -

                 *       560         *       580         *       600
TrCSa1 : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 600
TrCSa2 : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 584
TrCSa3 : GGCTATACTGTGGCTGCCATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 520
TrCSa4 : GGCTATACTGCGGNTTNTATTGACCGGNN------------------------------- : 456
TrCSa5 : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 231
TrCSa6 : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCATT : 193
TrCSa7 : ------------------------------------------------------------ :   -

                 *       620         *       640         *       660
TrCSa1 : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 660
TrCSa2 : AGCN-------------------------------------------------------- : 588
TrCSa3 : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 580
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 291
TrCSa6 : AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 253
TrCSa7 : ------------------------------------------------------------ :   -

                 *       680         *       700         *       720
TrCSa1 : ACTGCCTGTTTCTGCTCATCCAATGACACAAN---------------------------- : 692
TrCSa2 : ------------------------------------------------------------ :   -
TrCSa3 : ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT : 640
TrCSa4 : ------------------------------------------------------------ :   -
TrCSa5 : ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT : 351
TrCSa6 : ACTGCCTGTTTCTGCTCATCCAATGACACAATTTAGTACTGGTGTAATGGCCCTCCAGGT : 313
TrCSa7 : ------------------------------------------------------------ :   -
```

FIGURE 101 (cont.)

```
                 *        740         *        760         *        780
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : GGAGAGTGAGTTTACAAAGGCATATGAGAGTGGGATACATN------------------- :  681
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : GGAGAGTGAGTTTACAAAGGCATACGAGAGTGGGATACATAAGTCAAGGTATTGGGAGCC :  411
TrCSa6 : GGAGAGTGAGTTTACAAAGGCATACGAGAGTGGGATACATAAGTCAAGGTATTGGGAGCC :  373
TrCSa7 : ----------------------CNTCAGAGTGGGA-NCNT-AGT-AAGG-ATTGGGAGCC :   34

                 *        800         *        820         *        840
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : ------------------------------------------------------------ :    -
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : AACTTATGAGGATAGCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA :  471
TrCSa6 : AACTTATGAGGATAGCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA :  433
TrCSa7 : -ACTTATGAGGAT-GCTTGAATTTAATTGCTCGTTTGCCTGGAATTGCTGCCTATATTTA :   92

                 *        860         *        880         *        900
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : ------------------------------------------------------------ :    -
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGTGC :  531
TrCSa6 : TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGTGC :  493
TrCSa7 : TCGACGGATATACAAGGATGGAAAAATCATACCATTGGATGATTCTTTGGATTATGGTGC :  152

                 *        920         *        940         *        960
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : ------------------------------------------------------------ :    -
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA :  591
TrCSa6 : AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA :  553
TrCSa7 : AAACTATGCTCACATGTTAGGATTTGATGATCCAGAAACGCTGGAGTTTATGAGGCTGTA :  212

                 *        980         *       1000         *       1020
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : ------------------------------------------------------------ :    -
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : TATTTCTATN-------------------------------------------------- :  601
TrCSa6 : TATTTCTATCCATAGTGATCATGAAGGN-------------------------------- :  581
TrCSa7 : TATTTCTATCCATAGTGATCATGAAGGTGGCAACGTTAGTTCTCACACAGCTCACCTAGT :  272

                 *       1040         *       1060         *       1080
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : ------------------------------------------------------------ :    -
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : ------------------------------------------------------------ :    -
TrCSa6 : ------------------------------------------------------------ :    -
TrCSa7 : TGCTAGTTCACTATCAGATCCTTATCTTGCATTCGCAGCTGCTCTGAATGGTTTAGCTGG :  332
```

FIGURE 101 (cont.)

```
                    *        1100          *        1120          *        1140
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : ------------------------------------------------------------ :    -
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : ------------------------------------------------------------ :    -
TrCSa6 : ------------------------------------------------------------ :    -
TrCSa7 : CCCACTGCATGGTTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAACATAGTTAAGGA : 392

                    *        1160          *        1180          *        1200
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : ------------------------------------------------------------ :    -
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : ------------------------------------------------------------ :    -
TrCSa6 : ------------------------------------------------------------ :    -
TrCSa7 : GTTTGGAACTCCAAACATAAGTACAGAACAATTGAGCGACTACATTCATAAAACATTGAA : 452

                    *        1220          *        1240          *        1260
TrCSa1 : ------------------------------------------------------------ :    -
TrCSa2 : ------------------------------------------------------------ :    -
TrCSa3 : ------------------------------------------------------------ :    -
TrCSa4 : ------------------------------------------------------------ :    -
TrCSa5 : ------------------------------------------------------------ :    -
TrCSa6 : ------------------------------------------------------------ :    -
TrCSa7 : CAGTGGCCAGGTTGTGCCTGGATATGGACATGGAGTTTTGCGCAATACAGACCCAAGATA : 512

                    *        1280          *        1300
TrCSa1 : ----------------------------------------------- :    -
TrCSa2 : ----------------------------------------------- :    -
TrCSa3 : ----------------------------------------------- :    -
TrCSa4 : ----------------------------------------------- :    -
TrCSa5 : ----------------------------------------------- :    -
TrCSa6 : ----------------------------------------------- :    -
TrCSa7 : CACTTGCCAGAGGGAGTTTGCATTGAAGCATTTGCCTAATGATCCAN : 559
```

FIGURE 101 (cont.)

```
                 *        20         *        40         *        60
TrCSb : CNTTTCNTTTCCACAGCATCCTAATCCTAATCCTAATCCTAATCCTATTACTAATTACTA :   60

                 *        80         *       100         *       120
TrCSb : ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTTTCTCGAACCCATTCATTC :  120

                 *       140         *       160         *       180
TrCSb : AAGNAGAAGAAGGAAAAACAAAATCCACACAAACAAACATCTTACAACAATGTCAACGAC :  180

                 *       200         *       220         *       240
TrCSb : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT :  240

                 *       260         *       280         *       300
TrCSb : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT :  300

                 *       320         *       340         *       360
TrCSb : TTCTTCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA :  360

                 *       380         *       400         *       420
TrCSb : TGAACGTACCGGGAAGAAGTATACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA :  420

                 *       440         *       460         *       480
TrCSb : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGACTCAAACTTTATGATCCTGG :  480

                 *       500         *       520         *       540
TrCSb : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT :  540

                 *       560         *       580         *       600
TrCSb : CCTTAGATATAGAGGATACCCCATTGAGGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT :  600

                 *       620         *       640         *       660
TrCSb : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT :  660

                 *       680         *       700         *       720
TrCSb : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC :  720

                 *       740         *       760         *       780
TrCSb : TCAAGATGCACATCCTATGGGCGTCCTAGTGAATGCAATAAGCGCTCTGTCTGTTTTTCA :  780

                 *       800         *       820         *       840
TrCSb : TCCTGACGCAAATCCTGCTCTCAGAGGTCTTGACATCTACAACTCAAAGCAAGTGAGAGA :  840

                 *       860         *       880         *       900
TrCSb : CAAACAAATAGCACGGATTATTGGAAAGATAACAACAATTGCTGCTGCAATTAATCTTAG :  900
```

FIGURE 102

```
                    *        920         *        940         *        960
TrCSb : AATGGCAGGAAGGCCACCTGTGCTTCCATCCAACAAACTATCTTACACAGAGAACTTCCT :  960

                    *        980         *       1000         *       1020
TrCSb : ATACATGCTTGATTCTCTAGGCAATCGGTCATATAAACCCAACCCTCAGCTAACTCGTGC : 1020

                    *       1040         *       1060         *       1080
TrCSb : ACTAGACATCATCTTCATCCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 1080

                    *       1100         *       1120         *       1140
TrCSb : ACGACACCTTGCATCAAGCGGCGTCGATGTATACACTGCTATTGCTGGAGGTGTTGGAGC : 1140

                    *       1160         *       1180         *       1200
TrCSb : TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCGGTCCTTAAAATGCTGAGTGAAAT : 1200

                    *       1220         *       1240
TrCSb : TGGAAGTGTCGATAACATTCCAGAGTTCATTGAAGGTGTTAANN : 1244
```

FIGURE 102 (cont.)

```
                      *        20         *        40         *        60
TrCSb : MSTTTTTTDESKLHDAARNRLATLSAHLLPSSTTSAALLHPIHLSSSSGISPPSNVKGTL :  60

                      *        80         *       100         *       120
TrCSb : TVVDERTGKKYTIEVSPDGTVKANDFKKISTGKNDKGLKLYDPGYLNTAPVRSTISYIDG : 120

                      *       140         *       160         *       180
TrCSb : DEGILRYRGYPIEELAEKSTFPEVAYLILYGNLPSANQLQEWEFAISQHSALPQGVLDLI : 180

                      *       200         *       220         *       240
TrCSb : QSMPQDAHPMGVLVNAISALSVFHPDANPALRGLDIYNSKQVRDKQIARIIGKITTIAAA : 240

                      *       260         *       280         *       300
TrCSb : INLRMAGRPPVLPSNKLSYTENFLYMLDSLGNRSYKPNPQLTRALDIIFILHAEHEMNCS : 300

                      *       320         *       340         *
TrCSb : TSAVRHLASSGVDVYTAIAGGVGALYGPLHGGANEAVLKMLSEIGSVDNIPEFIEGVX : 358
```

FIGURE 103

```
                 *        20         *        40         *        60
TrCSb1 : CNTTTCNTTTCCACAGCATCCTAATCCTAATCCTAATCCTAATCCTATTACTAATTACTA :  60
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                 *        80         *       100         *       120
TrCSb1 : ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTTTCTCGAACCCATTCATTC : 120
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                 *       140         *       160         *       180
TrCSb1 : AATTCAAAGAAGGAAAAACAAAAT-CACACAAACAAACATCTTACAACAATGTCAACGAC : 179
TrCSb2 : --GNAGNAGAAGGAAAGNC-AAATCCACAAAC-AAAAC-TCTTACAACAATGTCAACCAC :  55
TrCSb3 : --GNNGNAGAAGGAAAGACAAAATNCACAAGAAAAACATCTTACAACAATGTCAACCAC :  58
TrCSb4 : ----GNAAAGAGGAAAAAC-AAAT--NCACAAAC-AACATCTTAC-ACAATGTC-ACGAC :  50
TrCSb5 : -------GNAAGGAAAAAC-AAAT--NC-CAAAC-AAC-TCTTAC-ACAATGTC-ACGAC :  45
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                 *       200         *       220         *       240
TrCSb1 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCTACCCT : 239
TrCSb2 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT : 115
TrCSb3 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCCACCCT : 118
TrCSb4 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTAGCCACCCT : 110
TrCSb5 : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTTGGCTACCCT : 105
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                 *       260         *       280         *       300
TrCSb1 : CTCAGCTCACTTGCTTCCTTCCTCCACAAACTCCGCTGCGCTTCTCCATCCTATCCACCT : 299
TrCSb2 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 175
TrCSb3 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 178
TrCSb4 : CTCAGCTCACTTGCTTCCTTCCTCCACAACCTCCGCCGCGCTCCTCCATCCTATTCACCT : 170
TrCSb5 : CTCAGCTCACTTGCTTCCTTCCTCCACAAACTCCGCTGCGCTTCTCCATCCTATCCACCT : 165
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                 *       320         *       340         *       360
TrCSb1 : TTCTTCTTCCTCTGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 359
TrCSb2 : TTCCGCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 235
TrCSb3 : TTCCGCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 238
TrCSb4 : TTCTTCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 230
TrCSb5 : TTCTTCTTCCTCTGGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 225
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -
```

FIGURE 104

```
                  *       380         *       400         *       420
TrCSb1 : TGAACGTACCGGGAAGAAGTATACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA : 419
TrCSb2 : TGAACGTACCGGGAAGAAGTATAACATTGAGGTCTCACCTGATGGCACCGTTAAAGCCAA : 295
TrCSb3 : TGAACGTACCGGGAAGAAGTATAACATTGAGGTCTCACCTGATGGCACCGTTAAAGCCAA : 298
TrCSb4 : TGAACGTACCGGGAAGAAGTATACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA : 290
TrCSb5 : TGAACGTACCGGGAAGAAGTATACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA : 285
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                  *       440         *       460         *       480
TrCSb1 : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGGCTCAAACTTTATGATCCTGG : 479
TrCSb2 : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGACTCAAACTTTATGATCCTGG : 355
TrCSb3 : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGACTCAAACTTTATGATCCTGG : 358
TrCSb4 : TGATTTCAAGAAGATATCGACTGGGAAGAATGATAAGGGACTCAAACTTTATGATCCTGG : 350
TrCSb5 : TGATTTCAAGAAGATATCAACTGGGAAGAATGATAAGGGGCTCAAACTTTATGATCCTGG : 345
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : -------------------------------------------------A---------- :   1

                  *       500         *       520         *       540
TrCSb1 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 539
TrCSb2 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 415
TrCSb3 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 418
TrCSb4 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 410
TrCSb5 : ATATTTAAACACTGCTCCTGTGCGATCAACAATTTCTTATATTGATGGTGATGAGGGAAT : 405
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : ------------------------------------------------------------ :   -

                  *       560         *       580         *       600
TrCSb1 : CCTTAGATATAGAGGATACCCCATTGAAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 599
TrCSb2 : CCTTAGATATAGAGGATACCCCATTGAGGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 475
TrCSb3 : CCTTAGATATAGAGGATACCCCATTGAGGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 478
TrCSb4 : CCTTAGATATAGAGGATACCCCATTGAGGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 470
TrCSb5 : CCTTAGATATAGAGGATACCCCATTGAAGAGTTGGCCGAGAAAAGCACCTTTCCGGAAGT : 465
TrCSb6 : --------ATAGAGGGT--CCNATTGAGGAGTTGG-CGAGAAAAGCACTTTTATGGAAGT :  49
TrCSb7 : ------------------------------------------------------------ :   -

                  *       620         *       640         *       660
TrCSb1 : GGCATATCTN-------------------------------------------------- : 609
TrCSb2 : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT : 535
TrCSb3 : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT : 538
TrCSb4 : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT : 530
TrCSb5 : GGCATATCTCATATTGTATGGAAATTTGCCTTCTGCAAATCAGTTACAAGAATGGGAATT : 525
TrCSb6 : GTCCTATCT-ATAATGTATGGAAGTTTACCTACTGAAAGTAAGTTAGCTGAATGGAATTT : 108
TrCSb7 : -------------------------------------------------GAATGGGAATT :  12

                  *       680         *       700         *       720
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTGGATCTCATACAATN------ : 589
TrCSb3 : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCNN---- : 594
TrCSb4 : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTN-------------------- : 570
TrCSb5 : TGCTATATCTCAGCATTCAGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC : 585
TrCSb6 : CGCTATATCTCAGCATTCAGCTGTTCCAGAAGGAGTTTTGGATATCATACAATCAATGCC : 168
TrCSb7 : TGCTATATCT-AGCATT-AGCCTTACCTCAAGGAGTTTTGGATCTCATACAATCAATGCC :  70
```

FIGURE 104 (cont.)

```
                  *        740         *        760         *        780
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : TCAAGNN----------------------------------------------------- : 592
TrCSb6 : TCATGATGCACATCCTATGGGTGTCCTAGTGAATGCAATAAGCGCTCTATCTGTTTTTCA : 228
TrCSb7 : TCAAGATGCACATCCTATGGGCGTGCTTGTTAATGCTGTAAGTGCTTTGTCTGTTTTTCA : 130

                  *        800         *        820         *        840
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : TCCTGACGCGAATCCTGCTCTTAGAGGTCTTGATATTTACGACTCAAAGGAAGTGAGAGA : 288
TrCSb7 : TCCTGATGCAAATCCTGCTCTCAGAGGTCTTGACATCTACAACTCAAAGCAAGTGAGAGA : 190

                  *        860         *        880         *        900
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : CAAACAAATAGCACGGATTATTGGAAAGATTATAACAATTGCTGCTGCAGTTTATCTTAG : 348
TrCSb7 : CAAACAAATAGTGCGGATTATTGGAAAGATAACAACAATTGCTGCTGCGATTAATCTTAG : 250

                  *        920         *        940         *        960
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : AATGGCAGGAAGGCCACCTGTGCTTCCATCCAACCAACTATCTTACACTGAGAACTTCCT : 408
TrCSb7 : ATTGGGAGGAAGGCCACCTGTTCTTCCATCCAACAAACTTTCTTACACAGAGAACTTCCT : 310

                  *        980         *       1000         *       1020
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ATACATGCTTGATTCTTTAGGCAATCGGTCATATAAACCCAACCCTCAGCTAACTCGTGC : 468
TrCSb7 : TTACATGCTTGATTCTCTTGGCAATCGGTCATATAAACCTAATCCTCGTCTAACTCGTGC : 370

                  *       1040         *       1060         *       1080
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ACTAGACATTATCTTCATCCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 528
TrCSb7 : ACTGGACATCATCTTCATCCTTCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 430
```

FIGURE 104 (cont.)

```
                        *        1100         *        1120         *        1140
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : CCGACACCTTGCATCAAGCGGCGTTGATGTATATACTGCTATTGCTGGGGN--------- : 579
TrCSb7 : ACGCCACCTTGCATCAAGTGGTGTCGATGTATACACTGCTATTGCTGGAGGTGTTGGAGC : 490

                        *        1160         *        1180         *        1200
TrCSb1 : ------------------------------------------------------------ :   -
TrCSb2 : ------------------------------------------------------------ :   -
TrCSb3 : ------------------------------------------------------------ :   -
TrCSb4 : ------------------------------------------------------------ :   -
TrCSb5 : ------------------------------------------------------------ :   -
TrCSb6 : ------------------------------------------------------------ :   -
TrCSb7 : TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCGGTCCTTAAAATGCTGAGTGAAAT : 550

                        *        1220         *        1240
TrCSb1 : -------------------------------------------- :   -
TrCSb2 : -------------------------------------------- :   -
TrCSb3 : -------------------------------------------- :   -
TrCSb4 : -------------------------------------------- :   -
TrCSb5 : -------------------------------------------- :   -
TrCSb6 : -------------------------------------------- :   -
TrCSb7 : TGGAAGTGTCGATAACATTCCAGAGTTCATTGAAGGTGTTAANN : 594
```

FIGURE 104 (cont.)

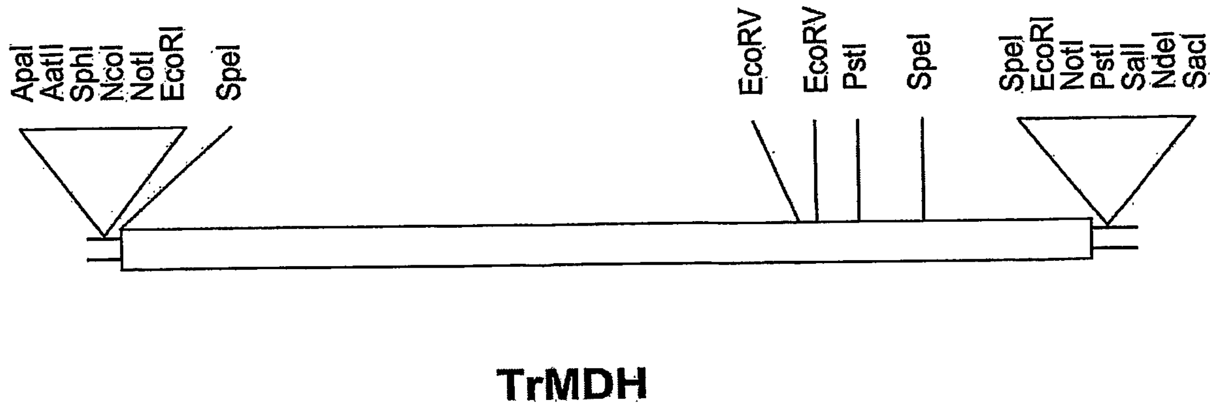

ApaI
AatII
SphI
NcoI
NotI
EcoRI
SpeI
EcoRV
EcoRV
PstI
SpeI
SpeI
EcoRI
NotI
PstI
SalI
NdeI
SacI
TrMDH

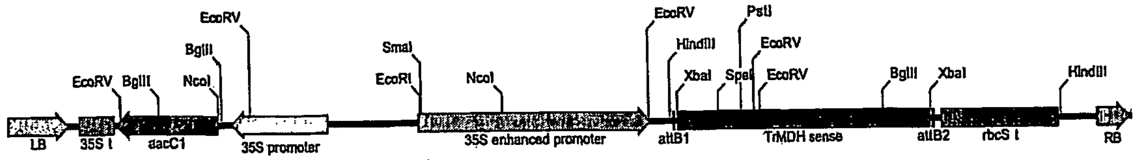
FIGURE 105

```
   1 GGCCGCGAAT TCACTAGTGA TTAAGCAGTG GTAACAACGC AGAGTACGCG
  51 GGGGTAGGCG GAGATTTCAA ACCCAATTTT CCTCTTAAAT CTCTCCCAAC
 101 TTCTCCTTCC AATTCCCATT ACCATTCATT CCCAGAGGTC GAGATGGCAG
 151 CATCAGCAGC AGCTACTTTT ACTATTGGAA CTGCCCAAAC AGGGAGGCCA
 201 CTTCCTCAAT CAAACCCTTT TGGTTTGAAA GTCAATTCCC AGGTTAATTT
 251 TAAGACCTTC TCTGGTCTCA AGGCCATGTC ATCTCTAAGA TGCGAGTCTG
 301 AATCATCTTT CTTTGGCAAC GAAACTAGTG CTGCTCTGCG TGCAACTTTT
 351 GCACCCAAAG CTCAAAAGGA AAACCAAAAC ATCAACCGCA ATTTGCATCC
 401 TCAGGCATCC TACAAAGTGG CGGTTCTTGG TGCTGCAGGA GGAATTGGTC
 451 AGCCACTGGC ACTTCTCATT AAGATGTCGC CTTTGGTTTC CGACCTGCAT
 501 CTTTATGATA TCGCGAATGT TAAGGGAGTT GCTGCTGATA TCAGTCATTG
 551 CAACACTCCT TCAAAGGTTT TGGATTTCAC AGGTGCTTCT GAGTTGGCAA
 601 ATTGTTTGAA AGGTGTGGAT GTAGTTGTTA TACCTGCTGG TGTTCCCAGA
 651 AAACCTGGCA TGACTCGTGA TGACCTTTTC AACATCAATG CCGGTATAGT
 701 CAGGGACTTG GTCACCGCTG TTGCAGATAA TTGCCCTGGT GCTTTTATTC
 751 ATGTTATCAG TAACCCGGTG AACTCTACAG TTCCTATTGC TGCTGAAATT
 801 CTGAAACAAA AGGGTGTTTA TGATCCTAAA AAGCTCTTTG GTGTTACTAC
 851 ACTTGATGTT GTGAGGGCAA ACACATTTGT TGCTCAGAAA AAGAACCTGA
 901 GGCTGATTGA TGTAGATGTT CCTGTTGTTG GTGGTCATGC CGGGATTACC
 951 ATTCTTCCTC TTCTGTCAAA GACAAGACCC TCAGCAAATT TCACTGATGA
1001 AGAAATTGAG GCGCTAACTG TCAGGATTCA AAATGCTGGA ACTGAAGTTG
1051 TTGAGGCCAA GGCTGGTGCA GGGTCTGCTA CTTTGTCAAT GGCCTATGCA
1101 GCAGCTAGAT TTGTTGAATC ATCTCTTCGT GCGCTTGACG GTGACGCTGA
1151 TGTGTATGAG TGCTCATTTG TACAGTCAGA TCTGACTGAC CTTCCGTTTT
1201 TTGCTTCAAG GGTGAAGATT GGTAGGAAAG GAGTCGAGGC TTTGATTCCA
1251 ACTGATCTCC AAGGGTTGAG TGAGTATGAG CAGAAGGCTT TGGAAGCACT
1301 TAAACCAGAA CTTAAGGCTA GCATTGAAAA GGGTATTGCT TTTGCTCAAA
1351 AGCAAACTGT TTCTGCTTAA CTTATTTTGT GAAAGCATAT ATTCTATACT
1401 CTCTAGCGTC CATGCGAGAG AATGTCAATG GGTGATTTCT TGGGTTATGG
1451 ATTTATTTGA GCATGAATAC TACTTAGAGG ACTTAGATTG CAGATTTATG
1501 TAGCATCATT TACTGCTTCC AGAACTTATG ATTTAAATTT TCCATAGTAT
1551 CATTTCTACT TACAGATTTG TTAGTAGAAC GGGAGGGGCT TCCATTTCTA
1601 TTCTCTATAT TGAGCTTTAG TTTTGATCAG AAATCTCAAT AGATTGTTAC
1651 TATCATGTAC TACTAGAATT GGAAAAATGT AAACGTTGCA TTTTGAATAA
1701 TACTGCCTTT GGACTAGTTT GTGTTTCGAA AAAAAAA
```

FIGURE 106

```
  1 MAASAAATFT IGTAQTGRPL PQSNPFGLKV NSQVNFKTFS GLKAMSSLRC
 51 ESESSFFGNE TSAALRATFA PKAQKENQNI NRNLHPQASY KVAVLGAAGG
101 IGQPLALLIK MSPLVSDLHL YDIANVKGVA ADISHCNTPS KVLDFTGASE
151 LANCLKGVDV VVIPAGVPRK PGMTRDDLFN INAGIVRDLV TAVADNCPGA
201 FIHVISNPVN STVPIAAEIL KQKGVYDPKK LFGVTTLDVV RANTFVAQKK
251 NLRLIDVDVP VVGGHAGITI LPLLSKTRPS ANFTDEEIEA LTVRIQNAGT
301 EVVEAKAGAG SATLSMAYAA ARFVESSLRA LDGDADVYEC SFVQSDLTDL
351 PFFASRVKIG RKGVEALIPT DLQGLSEYEQ KALEALKPEL KASIEKGIAF
401 AQKQTVSA
```

FIGURE 107



pPZP221:TrMDH sense

FIGURE 108

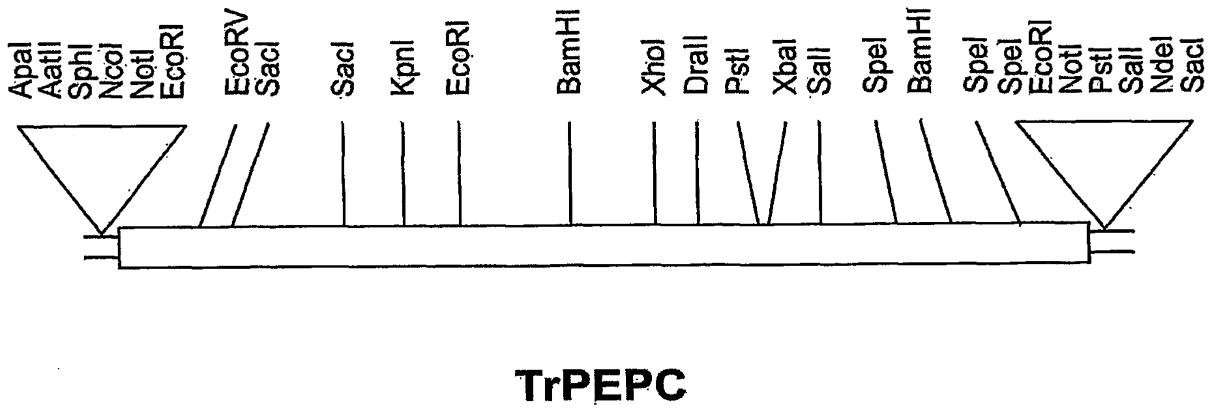

ApaI
AatII
SphI
NcoI
NotI
EcoRI
EcoRV
SacI
SacI
KpnI
EcoRI
BamHI
XhoI
DraII
PstI
XbaI
SalI
SpeI
BamHI
SpeI
SpeI
EcoRI
NotI
PstI
SalI
NdeI
SacI
TrPEPC

FIGURE 109

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GATAACACTG
  51 TCTCTCTGAT CCAAATTTTC CATCCCTTGT CTTCTTTTTC TTCTTCTTCC
 101 TCGTATCTTA CTGCCTCATT ACACGGGTGA GAAGGAGTGA ATTGCTCCAA
 151 TGGCAACAAA CAAAATGGAA AAAATGGCAT CAATTGATGC ACAGCTTAGA
 201 CAATTAGTAC CAGCAAAAGT TAGTGAAGAT GATAAACTTA TTGAGTATGA
 251 TGCTTTGTTG TTGGATCGGT TTCTTGATAT CCTTCAGGAT TTACATGGAG
 301 AGGATCTGAA AGATTCTGTT CAAGAAGTGT ATGAACTTTC TGCGGAGTAT
 351 GAAAGAAAGC ATGATCCTAA GAAACTTGAA GAGCTCGGAA ATTTGATAAC
 401 AAGTTTAGAT GCAGGAGATT CAATTGTTGT TGCTAAGTCC TTTTCGCACA
 451 TGCTTAACTT GGCCAACTTA GCTGAAGAGG TTCAGATTGC TCATCGTCGA
 501 AGGAACAAGT TGAAGAAAGG AGATTTTAGG GATGAGAGCA ATGCAACTAC
 551 CGAATCAGAC ATCGAAGAAA CTCTTAAGAG ACTTGTGTTT AATATGAAGA
 601 AATCTCCTCA GGAAGTTTTT GATGCGTTGA AGAACCAGAC CGTTGATTTG
 651 GTTCTTACTG CTCATCCTAC TCAGTCGGTT CGTAGGTCGT TGCTTCAAAA
 701 GCATGGAAGG GTAAGGAACT GTTTATCTCA ATTGTATGCT AAAGACATCA
 751 CTCCTGATGA TAAGCAAGAG CTCGACGAAG CTCTCCAGAG GGAGATTCAA
 801 GCTGCATTCC GTACCGATGA AATCAAGAGG ACACCTCCAA CACCACAAGA
 851 TGAGATGAGA GCAGGGATGA GTTACTTCCA CGAAACAATT TGGAAGGGTG
 901 TCCCTAAATT TCTTCGCCGT GTTGATACTG CGTTGAAGAA CATAGGGATT
 951 AACGAACGTG TTCCCTATAA TGCTCCTCTT ATTCAGTTTT CTTCATGGAT
1001 GGGGGGTGAT CGTGATGGTA ATCCGAGAGT GACTCCTGAA GTAACGAGAG
1051 ATGTTTGCTT ACTAGCTAGA ATGATGGCTG CAAATTTGTA TTATTCCCAG
1101 ATTGAAGATC TTATGTTTGA ACTGTCTATG TGGCGTTGCA ATGATGAGCT
1151 GCGTGATCGC GCAGAAGAAC TTCACAGGAA TTCCAAGAAA GATGAAGTTG
1201 CAAAACACTA CATAGAGTTT TGGAAAAAAA TTCCTTTGAA TGAACCGTAC
1251 CGTGTTATAC TTGGTGATGT AAGGGACAAG CTCTATCGTA CTCGTGAGCG
1301 GTCTCGCTAT CTCTTAGCTC ATGGCTATTC TGAAATTCCT GAGGAAGCCA
1351 CATTCACCAA TGTTGATGAG TTCTTGGAAC CTCTTGAACT ATGCTACAGA
1401 TCACTCTGTG CTTGTGGTGA TCGTGCGGTT GCCGATGGAA GCCTTCTTGA
1451 TTTCTTGAGG CAAGTTTCCA CTTTTGGACT GTCACTGGTA AGACTTGATA
1501 TAAGGCAGGA GTCAGATCGT CACACGGACG TGATGGATGC CATTACCAAA
1551 CATTTGGAAA TTGGATCCTA CCAAGATTGG TCTGAAGAAA AACGACAGGA
1601 ATGGCTTTTG TCTGAGTTGG TTGGCAAAAG GCCGCTTTTT GGACCTGATC
1651 TACCTCAAAC CGATGAAATT AGAGAAGTTT TAGAGACATT TCATGTCATA
1701 GCAGAACTTC CATCAGACAA CTTTGGAGCC TATATCATTT CGATGGCAAC
1751 TGCCCCGTCT GATGTGCTGG CGGTTGAACT TCTTCAACGT GAATGCAAAA
1801 TCAAGAATCC GTTAAGAGTT GTTCCATTGT TTGAGAAACT TGCTGATCTC
1851 GAGTCTGCTC CTGCTGCTTT GGCTCGGTTG TTTTCGATAG ACTGGTACAT
1901 AAACCGTATC GATGGGAAGC AAGAAGTTAT GATTGGATAT TCTGATTCAG
1951 GTAAAGATGC TGGAAGGTTT TCTGCCGCAT GGCAGCTATA TAAGGCTCAG
2001 GAGGACCTCA TAAATGTTGC TCAGAAATAC GGTGTTAAGC TAACAATGTT
2051 CCATGGTCGT GGTGGAACTG TTGGAAGAGG AGGTGGACCT ACTCATCTTG
2101 CTATCTTGTC TCAACCACCA GACACAATTC ACGGATCTCT TCGTGTGACG
2151 GTTCAAGGTG AAGTTATTGA ACAGTCGTTC GGAGAGGAGC ACTTGTGCTT
2201 TAGAACGCTG CAGCGTTTCA CTGCTGCCAC TCTAGAACAC GGAATGCGTC
2251 CCCCAAGTTC TCCAAAACCG GAATGGCGTG AATTGATGGA TCAGATGGCT
2301 GTCATTGCTA CCGAGGAGTA CCGTTCAATT GTGTTCAAGG AACCACGTTT
2351 TGTTGAGTAT TTCCGTCTGG CCACACCAGA GATGGAGTAC GGAAGGATGA
2401 ACATTGGAAG TCGACCGGCA AAAAGAAGGC CATGTGGAGG CATTGAAACA
2451 CTGCGTGCGA TACCATGGAT TTTTGCATGG ACACAGACAA GGTTTCATCT
2501 TCCAGTATGG CTTGGCTTTG GAGCAGCTTT TAAACAAGTT ATTGCGAAGG
2551 ATGTTAAGAA TCTTCATATG CTGCAAGAGA TGTACAATCA ATGGCCTTTC
2601 TTTAGGGTCA CTATTGATTT AGTCGAAATG GTGTTCGCTA AGGGTGACCC
2651 TGGTATTGCA GCCCTGAATG ATAGGCTACT AGTTTCTCAG GATCTTTGGC
2701 CATTTGGGGA ACAGTTGAGA AGCAAATATG AAGAAACTAA GAAACTCCTA
2751 CTTCAGGTGG CAACACACAA GGAAGTTCTT GAAGGAGATC CCTACTTGAA
2801 ACAAAGACTC AGACTCCGTG ATTCTTACAT TACAACCCTT AACGTTTTCC
2851 AAGCATACAC ATTGAAACGG ATCCGTGATC CAAACTATAA GGTGGAGGTG
```

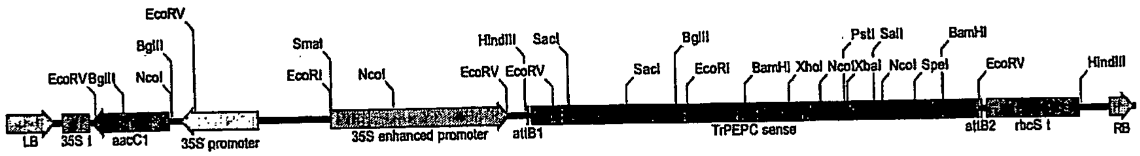
FIGURE 110

```
2901 CGCCCCCGCG TATCGAAAGA ATCTGCTGAA ACAAGTAAAT CGGCTGATGA
2951 ACTTGTAACA TTGAATCCAA CAAGTGAATA TGCTCCTGGT TTGGAAGACA
3001 CACTCATTCT CACCATGAAG GGTATTGCTG CTGGCATGCA AAACACTGGT
3051 TAATTTTTGG TGATTTTTTT CACTTGTATT TGTTTCTTTT ATGTTAAGTG
3101 TGTGCTAAGA TATCATAAAT ACTAGATGAA TCTAGTTGCA AGCACTTCAA
3151 GTGAGTGCTT TTTTTTTTCT TTTTCCTTTT CCTTTTTCAT AAGAAACTCA
3201 CATCAGGTTT TGTTGATGTT TTTCCTTACT TTGTTACCAT ACAAACGAGT
3251 TAATGCAATT GATGTTATGT TTCAATGCAT AGATTTTATC TCCTTTCTTC
3301 TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AGTACTCTGC GTTGTTACCA
3351 CTGCTTAATC ACTAGTGAAT TC
```

FIGURE 110 (cont.)

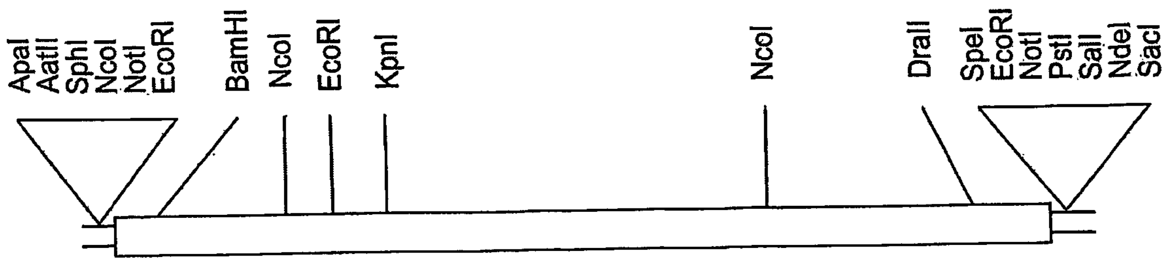
1 MATNKMEKMA SIDAQLRQLV PAKVSEDDKL IEYDALLLDR FLDILQDLHG
51 EDLKDSVQEV YELSAEYERK HDPKKLEELG NLITSLDAGD SIVVAKSFSH
101 MLNLANLAEE VQIAHRRRNK LKKGDFRDES NATTESDIEE TLKRLVFNMK
151 KSPQEVFDAL KNQTVDLVLT AHPTQSVRRS LLQKHGRVRN CLSQLYAKDI
201 TPDDKQELDE ALQREIQAAF RTDEIKRTPP TPQDEMRAGM SYFHETIWKG
251 VPKFLRRVDT ALKNIGINER VPYNAPLIQF SSWMGGDRDG NPRVTPEVTR
301 DVCLLARMMA ANLYYSQIED LMFELSMWRC NDELRDRAEE LHRNSKKDEV
351 AKHYIEFWKK IPLNEPYRVI LGDVRDKLYR TRERSRYLLA HGYSEIPEEA
401 TFTNVDEFLE PLELCYRSLC ACGDRAVADG SLLDFLRQVS TFGLSLVRLD
451 IRQESDRHTD VMDAITKHLE IGSYQDWSEE KRQEWLLSEL VGKRPLFGPD
501 LPQTDEIREV LETFHVIAEL PSDNFGAYII SMATAPSDVL AVELLQRECK
551 IKNPLRVVPL FEKLADLESA PAALARLFSI DWYINRIDGK QEVMIGYSDS
601 GKDAGRFSAA WQLYKAQEDL INVAQKYGVK LTMFHGRGGT VGRGGGPTHL
651 AILSQPPDTI HGSLRVTVQG EVIEQSFGEE HLCFRTLQRF TAATLEHGMR
701 PPSSPKPEWR ELMDQMAVIA TEEYRSIVFK EPRFVEYFRL ATPEMEYGRM
751 NIGSRPAKRR PCGGIETLRA IPWIFAWTQT RFHLPVWLGF GAAFKQVIAK
801 DVKNLHMLQE MYNQWPFFRV TIDLVEMVFA KGDPGIAALN DRLLVSQDLW
851 PFGEQLRSKY EETKKLLLQV ATHKEVLEGD PYLKQRLRLR DSYITTLNVF
901 QAYTLKRIRD PNYKVEVRPR VSKESAETSK SADELVTLNP TSEYAPGLED
951 TLILTMKGIA AGMQNTG

FIGURE 111



pPZP221:TrPEPC sense

FIGURE 112



TrCSa

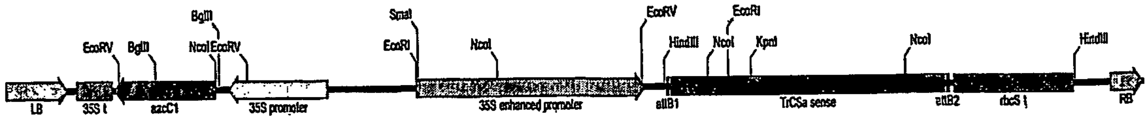
FIGURE 113

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GAGCACAACA
  51 TTACGTTAAT TACATTTTCT CTTTCGCCAT TGTTCTTTCT CTTCTCAATA
 101 TAAAGACCAA TTCAATTCCC AATTCTTTTG GATCCGAAAT CATTCATTCT
 151 ACGCTTCTTC TCTCTTCTCT GCGTTTCAAA CCCTAGTTGT TTTGTTGATT
 201 GATCTTAATG GCGTTCTTTC GAAGCGTTTC TGCGCTTTCA AAACTACGAT
 251 CTCGTGTGGG TCAACAACCT AGTCTTGCTA ATTCAGTTAG ATGGCTCCAA
 301 ACTCCAAGCT CCAGTAACAC TGATCTTTAT TCTGAGATGA AGGAGCTAGT
 351 TCCAGAGTAT CAGGAACGTG TTAAGAAGTT GAAGAAAGAC CATGGAAGTG
 401 TTGAATTGGG AAAAATCACA GCTGATATGG TACTTGGTGG AATGAGAGGA
 451 ATGACTGCTT TAGTGTGGCT AGGCTCAGCT GTTGACCCAG ATGAGGGAAT
 501 TCGCTTTAGG GGCATGACAA TTCCTGACTG CCAGAAAACA CTTCCAGGTG
 551 CTTTTCCTGG TGGGGAGCCT TTGCCCGAGG CTATACTGTG GCTTCTATTG
 601 ACCGGAAAGG TACCAAGTAA AGAGCAAGTA GATTCATTAG CTCACGAATT
 651 GCGAAGTCGT GCAAAAATCC CAGAGTATGC TTACAAGGCA ATTGATGCAC
 701 TGCCTGTTTC TGCTCATCCA ATGACACAAT TTAGTACTGG TGTAATGGCC
 751 CTCCAGGTGG AGAGTGAGTT TACAAAGGCA TACGAGGGTG GGATACATAA
 801 GTCAAGGTAT TGGGAGCCAA CTTATGAGGA TAGCTTGAAT TTAATTGCTC
 851 GTTTGCCTGG AATTGCTGCC TATATTTATC GACGGATATA CAAGGATGGA
 901 AAAATCATAC CATTGGATGA TTCTTTGGAT TATGGTGCAA ACTATGCTCA
 951 CATGTTAGGA TTTGATGATC CAGAAACGCT GGAGTTTATG AGGCTGTATA
1001 TTTCTATCCA TAGTGATCAT GAAGGTGGCA ACGTTAGTTC TCACACAGCT
1051 CACCTAGTTG CTAGTTCACT ATCAGATCCT TATCTTGCAT TCGCAGCTGC
1101 TCTGAATGGT TTAGCTGGCC CACTGCATGG TTTAGCCAAT CAGGAAGTTC
1151 TACGATGGAT CAGAAACATA GTTAAGGAGT TTGGAACTCC AAACATAAGT
1201 ACAGAACAAT TGAGCGACTA CATTCATAAA ACATTGAACA GTGGCCAGGT
1251 TGTGCCTGGA TATGGACATG GAGTTTTGCG CAATACAGAC CCAAGATACA
1301 CTTGCCAGAG GGAGTTTGCA TTGAAGCATT TGCCTAATGA TCCACTTTTC
1351 CAGCTGGTGT CCAAAATTAA AGAAGTCGTG CCTCCCATTC TGACCAAGTT
1401 AGGAAAGGTT AAAAATCCAT GGCCTAATGT TGATGCTCAT AGTGGAGTAC
1451 TACTAAACTA CTATGGTCTA ACTGAAGAAA ACTATTATAC CGTTCTTTTT
1501 GGTGTCGCGA GGAGTATTGG AGTTGGCCCT CAGCTGATAT GGGACCGTGC
1551 TCTTGGAATG CCACTTGAAA GGCCAAAAAG TGTCACACTG GAGAAACTTG
1601 AGAAACTGGT CGGCGCATCG TCCTAAAATT GAAAGCGCGG TTATCTGTGG
1651 ATTACTAAAA TACACTCTGC GGTTGTAGGT TGTTGGTAAC TCTAAACATT
1701 TGGTGCAATT GCAATGAGAA ATATTTTGCC CAAATCCCCC TTCCCTTATT
1751 TTTCTGGTTG TTTTGTCAGC ATTTTTTGAT TGAGGAGATT TTGGTATTTA
1801 GGAAAAGGGT GGGATTATCA CCCTCACAGT TGTCTTTCCA TTTTTCTACA
1851 CAGCATAAAT TAGGTCCCAA GGGAGCATCA GAATAAAGGC ATTATGTTTT
1901 GGGGGTAATC CCTCTGTATT CTTTCTAAAT AGGATTGACC CCTTTGACAA
1951 AAAATACAAA TTATCAATAT CACTCGTCTA CTTGAAGATT CGACTAAAAA
2001 AAAAAAAAAA AAAAAAAAAA AAAAAGTACT CTGCGTTGTT ACCACTGCTT
2051 AATCACTAGT GAATTC
```

FIGURE 114

1 MAFFRSVSAL SKLRSRVGQQ PSLANSVRWL QTPSSSNTDL YSEMKELVPE
51 YQERVKKLKK DHGSVELGKI TADMVLGGMR GMTALVWLGS AVDPDEGIRF
101 RGMTIPDCQK TLPGAFPGGE PLPEAILWLL LTGKVPSKEQ VDSLAHELRS
151 RAKIPEYAYK AIDALPVSAH PMTQFSTGVM ALQVESEFTK AYEGGIHKSR
201 YWEPTYEDSL NLIARLPGIA AYIYRRIYKD GKIIPLDDSL DYGANYAHML
251 GFDDPETLEF MRLYISIHSD HEGGNVSSHT AHLVASSLSD PYLAFAAALN
301 GLAGPLHGLA NQEVLRWIRN IVKEFGTPNI STEQLSDYIH KTLNSGQVVP
351 GYGHGVLRNT DPRYTCQREF ALKHLPNDPL FQLVSKIKEV VPPILTKLGK
401 VKNPWPNVDA HSGVLLNYYG LTEENYYTVL FGVARSIGVG PQLIWDRALG
451 MPLERPKSVT LEKLEKLVGA SS

FIGURE 115



pPZP221:TrCSa sense

FIGURE 116

TrCSb

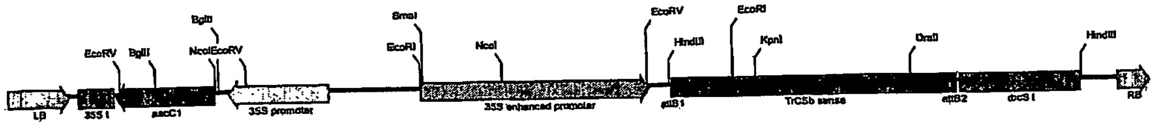
FIGURE 117

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GAGCACAACA
  51 TTACGTTAAT TACATTTTCT CTTTCGCCAT TGTTCTTTCT CTTCTCAATA
 101 TAAAGACCAA TTCAATTCCC AATTCTTTTG GATCCGAAAT CATTCATTCT
 151 ACGCTTCTTC TCTCTTCTCT GCGTTTCAAA CCCTAGTTGT TTTGTTGATT
 201 GATCTTAATG GCGTTCTTTC GAAGCGTTTC TGCGCTTTCA AAACTACGAT
 251 CTCGTGTGGG TCAACAACCT AGTCTTGCTA ATTCAGTTAG ATGGCTCCAA
 301 ACTCCAAGCT CCAGTAACAC TGATCTTTAT TCTGAGATGA AGGAGCTAGT
 351 TCCAGAGTAT CAGGAACGTG TTAAGAAGTT GAAGAAAGAC CATGGAAGTG
 401 TTGAATTGGG AAAAATCACA GCTGATATGG TACTTGGTGG AATGAGAGGA
 451 ATGACTGCTT TAGTGTGGCT AGGCTCAGCT GTTGACCCAG ATGAGGGAAT
 501 TCGCTTTAGG GGCATGACAA TTCCTGACTG CCAGAAAACA CTTCCAGGTG
 551 CTTTTCCTGG TGGGGAGCCT TTGCCCGAGG CTATACTGTG GCTTCTATTG
 601 ACCGGAAAGG TACCAAGTAA AGAGCAAGTA GATTCATTAG CTCACGAATT
 651 GCGAAGTCGT GCAAAAATCC CAGAGTATGC TTACAAGGCA ATTGATGCAC
 701 TGCCTGTTTC TGCTCATCCA ATGACACAAT TTAGTACTGG TGTAATGGCC
 751 CTCCAGGTGG AGAGTGAGTT TACAAAGGCA TACGAGGGTG GGATACATAA
 801 GTCAAGGTAT TGGGAGCCAA CTTATGAGGA TAGCTTGAAT TTAATTGCTC
 851 GTTTGCCTGG AATTGCTGCC TATATTTATC GACGGATATA CAAGGATGGA
 901 AAAATCATAC CATTGGATGA TTCTTTGGAT TATGGTGCAA ACTATGCTCA
 951 CATGTTAGGA TTTGATGATC CAGAAACGCT GGAGTTTATG AGGCTGTATA
1001 TTTCTATCCA TAGTGATCAT GAAGGTGGCA ACGTTAGTTC TCACACAGCT
1051 CACCTAGTTG CTAGTTCACT ATCAGATCCT TATCTTGCAT TCGCAGCTGC
1101 TCTGAATGGT TTAGCTGGCC CACTGCATGG TTTAGCCAAT CAGGAAGTTC
1151 TACGATGGAT CAGAAACATA GTTAAGGAGT TTGGAACTCC AAACATAAGT
1201 ACAGAACAAT TGAGCGACTA CATTCATAAA ACATTGAACA GTGGCCAGGT
1251 TGTGCCTGGA TATGGACATG GAGTTTTGCG CAATACAGAC CCAAGATACA
1301 CTTGCCAGAG GGAGTTTGCA TTGAAGCATT TGCCTAATGA TCCACTTTTC
1351 CAGCTGGTGT CCAAAATTAA AGAAGTCGTG CCTCCCATTC TGACCAAGTT
1401 AGGAAAGGTT AAAAATCCAT GGCCTAATGT TGATGCTCAT AGTGGAGTAC
1451 TACTAAACTA CTATGGTCTA ACTGAAGAAA ACTATTATAC CGTTCTTTTT
1501 GGTGTCGCGA GGAGTATTGG AGTTGGCCCT CAGCTGATAT GGGACCGTGC
1551 TCTTGGAATG CCACTTGAAA GGCCAAAAAG TGTCACACTG GAGAAACTTG
1601 AGAAACTGGT CGGCGCATCG TCCTAAAATT GAAAGCGCGG TTATCTGTGG
1651 ATTACTAAAA TACACTCTGC GGTTGTAGGT TGTTGGTAAC TCTAAACATT
1701 TGGTGCAATT GCAATGAGAA ATATTTTGCC CAAATCCCCC TTCCCTTATT
1751 TTTCTGGTTG TTTTGTCAGC ATTTTTTGAT TGAGGAGATT TTGGTATTTA
1801 GGAAAAGGGT GGGATTATCA CCCTCACAGT TGTCTTTCCA TTTTTCTACA
1851 CAGCATAAAT TAGGTCCCAA GGGAGCATCA GAATAAAGGC ATTATGTTTT
1901 GGGGGTAATC CCTCTGTATT CTTTCTAAAT AGGATTGACC CCTTTGACAA
1951 AAAATACAAA TTATCAATAT CACTCGTCTA CTTGAAGATT CGACTAAAAA
2001 AAAAAAAAAA AAAAAAAAAA AAAAAGTACT CTGCGTTGTT ACCACTGCTT
2051 AATCACTAGT GAATTC
```

FIGURE 118

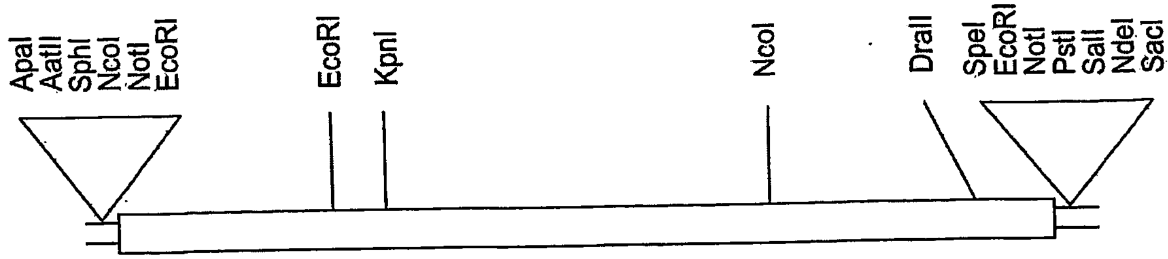
1 MAFFRSVSAL SKLRSRVGQQ PSLANSVRWL QTPSSSNTDL YSEMKELVPE
51 YQERVKKLKK DHGSVELGKI TADMVLGGMR GMTALVWLGS AVDPDEGIRF
101 RGMTIPDCQK TLPGAFPGGE PLPEAILWLL LTGKVPSKEQ VDSLAHELRS
151 RAKIPEYAYK AIDALPVSAH PMTQFSTGVM ALQVESEFTK AYEGGIHKSR
201 YWEPTYEDSL NLIARLPGIA AYIYRRIYKD GKIIPLDDSL DYGANYAHML
251 GFDDPETLEF MRLYISIHSD HEGGNVSSHT AHLVASSLSD PYLAFAAALN
301 GLAGPLHGLA NQEVLRWIRN IVKEFGTPNI STEQLSDYIH KTLNSGQVVP
351 GYGHGVLRNT DPRYTCQREF ALKHLPNDPL FQLVSKIKEV VPPILTKLGK
401 VKNPWPNVDA HSGVLLNYYG LTEENYYTVL FGVARSIGVG PQLIWDRALG
451 MPLERPKSVT LEKLEKLVGA SS

FIGURE 119



pPZP221:TrCSb sense

FIGURE 120



TrCSd

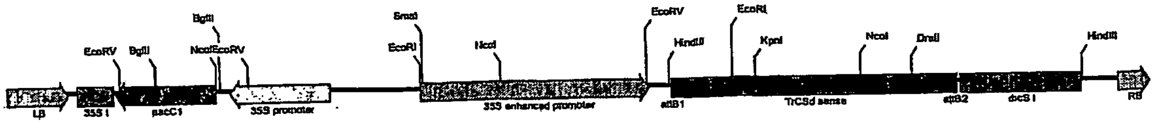
FIGURE 121

```
   1 GAATTCGATT AAGCAGTGGT AACAACGCAG AGTACGCGGG GATCCGAAAT
  51 CATTCATTCT ACTTTTCAAC CTGTTGTTTT GTTGATTGAT CTAAATGGCG
 101 TTCTTTCGAA GCGTTTCTGC GCTTTCAAAA CTACGATCTC GTGTGGGTCA
 151 ACAACCTAGT CTTGCTAATT CAGTTAGATG GCTCCAAACT CCAAGCTCCA
 201 GTAACACTGA TCTTTATTCT GAGATGAAGG AGCTAGTTCC AGAGTATCAG
 251 GAACGTGTTA AGAAGTTGAA GAAAGACCAT GGAAGTGTTG AATTGGGAAA
 301 AATCACAGCT GATATGGTAC TTGGTGGAAT GAGAGGAATG ACTGCTTTAG
 351 TGTGGCTAGG CTCAGCTGTT GACCCAGATG AGGGAATTCG CTTTAGGGGC
 401 ATGACAATTC CTGACTGCCA GAAAACACTT CCAGGTGCTT TTCCTGGTGG
 451 GGAGCCTTTG CCCGAGGCTA TACTGTGGCT TCTATTGACC GGAAAGGTAC
 501 CAAGTAAAGA GCAAGTAGAT TCATTAGCTC ACGAATTGCG AAGTCGTGCA
 551 AAAATCCCAG AGTATGCTTA CAAGGCAATT GATGCACTGC CTGTTTCTGC
 601 TCATCCAATG ACACAATTTA GTACTGGTGT AATGGCCCTC CAGGTGGAGA
 651 GTGAGTTTAC AAAGGCATAC GAGAGTGGGA TACATAAGTC AAGGTATTGG
 701 GAGCCAACTT ATGAGGATAG CTTGAATTTA ATTGCTCGTT TGCCTGGAAT
 751 TGCTGCCTAT ATTTATCGAC GGATATACAA GGATGGAAAA ATCATACCAT
 801 TGGATGATTC TTTGGATTAT GGTGCAAACT ATGCTCACAT GTTAGGATTT
 851 GATGATCCAG AAACGCTGGA GTTTATGAGG CTGTATATTT CTATCCATAG
 901 TGATCATGAA GGTGGCAACG TTAGTTCTCA CACAGCTCAC CTAGTTGCTA
 951 GTTCACTATC AGATCCTTAT CTTGCATTCG CAGCTGCTCT GAATGGTTTA
1001 GCTGGCCCAC TGCATGGTTT AGCCAATCAG GAAGTTCTAC GATGGATCAG
1051 AAACATAGTT ACGGAATTTG GAACTCCAAA CATAAGTACA GAACAATTGA
1101 GCGACTACAT TCATAAAACA TTGAACAGTG GCCAGGTTGT GCCTGGATAT
1151 GGACATGGAG TTTTGCGCAA TACAGACCCA AGATACACTT GCCAGAGGGA
1201 GTTTGCATTG AAGCATTTGC CTAATGATCC ACTTTTCCAG CTGGTGTCCA
1251 AAATTAAAGA AGTCGTGCCT CCCATTCTGA CCAAGTTAGG AAAGGTTAAA
1301 AATCCATGGC CTAATGTTGA TGCTCATAGT GGAGTACTAC TAAACTACTA
1351 TGGTCTAACT GAAGAAAACT ATTATACCGT TCTTTTTGGC GTCGCGAGGA
1401 GTATTGGAGT TGGCCCTCAG CTGATATGGG ACCGTGCTCT TGGAATGCCA
1451 CTTGAAAGGC CAAAAAGTGT CACACTGGAG AAACTTGAGA AACTCGTCGG
1501 TGCATCATCC TAAAATTGAA AGCACAGTTA CCTCTGGATT ACTAAAATAC
1551 ACACTGCGGT TGTAGGTTGT TGGTAACTCG AAACATTTGG TGCAATTGCA
1601 ATGAGAAATA TTCGTTGCCC ACATCCCCTT CCCTTATTTT TCTGGTTGTT
1651 TTGTCAGCAT TTTTTGATTG AGAAGATTTT GGTATTTAGG AAAGGGTGGG
1701 ATTATCACCC TCACAGTTGT CTTTCCATTT TTCTACACAG CATAAATTAG
1751 GTCCCAAGGG AGCATCAGAA TAAAGGCATT ATGTTTTGGG GGTAATCCCC
1801 CTGTATTCTT TCTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAGTACTC
1851 TGCGTTGTTA CCACTGCTTA ATCACTAGTG AATTC
```

FIGURE 122

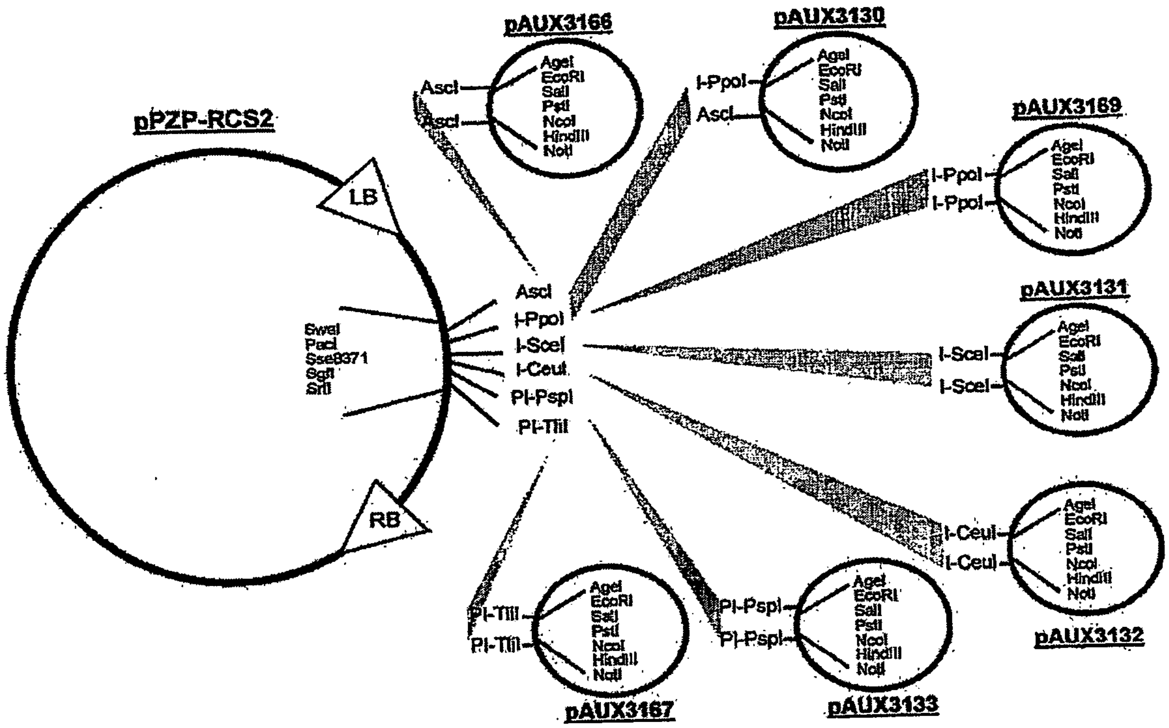
1 MAFFRSVSAL SKLRSRVGQQ PSLANSVRWL QTPSSSNTDL YSEMKELVPE
51 YQERVKKLKK DHGSVELGKI TADMVLGGMR GMTALVWLGS AVDPDEGIRF
101 RGMTIPDCQK TLPGAFPGGE PLPEAILWLL LTGKVPSKEQ VDSLAHELRS
151 RAKIPEYAYK AIDALPVSAH PMTQFSTGVM ALQVESEFTK AYESGIHKSR
201 YWEPTYEDSL NLIARLPGIA AYIYRRIYKD GKIIPLDDSL DYGANYAHML
251 GFDDPETLEF MRLYISIHSD HEGGNVSSHT AHLVASSLSD PYLAFAAALN
301 GLAGPLHGLA NQEVLRWIRN IVTEFGTPNI STEQLSDYIH KTLNSGQVVP
351 GYGHGVLRNT DPRYTCQREF ALKHLPNDPL FQLVSKIKEV VPPILTKLGK
401 VKNPWPNVDA HSGVLLNYYG LTEENYYTVL FGVARSIGVG PQLIWDRALG
451 MPLERPKSVT LEKLEKLVGA SS

FIGURE 123



pPZP221:TrCSd sense

FIGURE 124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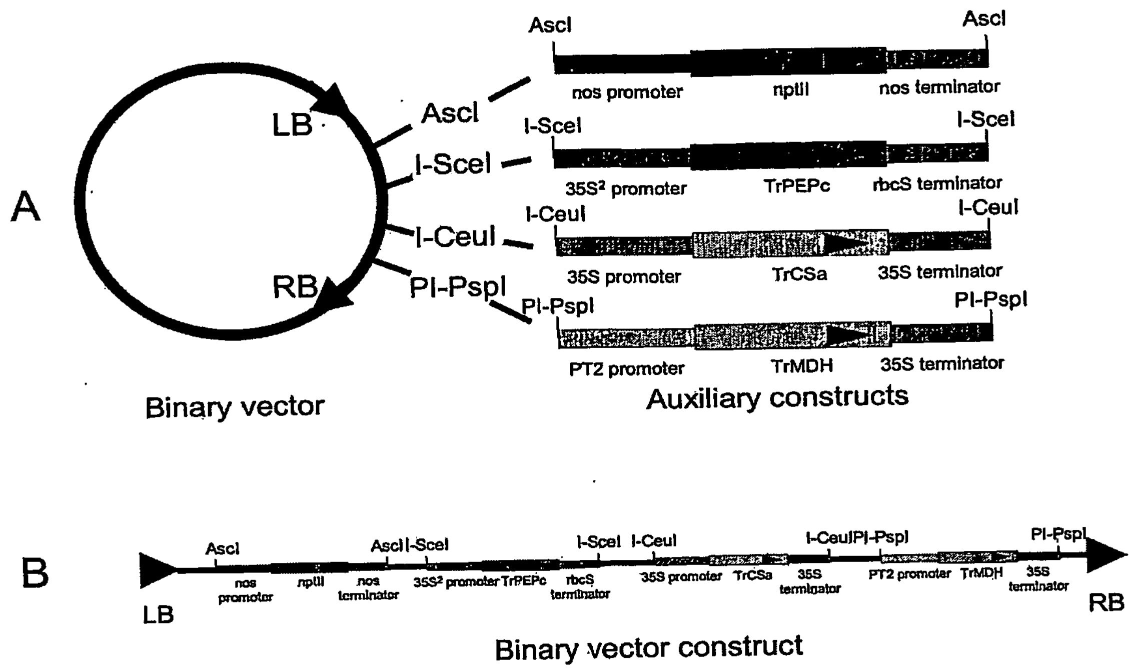
LB
RB
SwaI
PacI
Sse8371
SgfI
SrfI
AscI
I-PpoI
I-SceI
I-CeuI
PI-PspI
PI-TliI
pAUX3166
pAUX3130
pAUX3169
pAUX3131
pAUX3132
pAUX3133
pAUX3167
AgeI
EcoRI
SalI
PstI
NcoI
HindIII
NotI

FIGURE 125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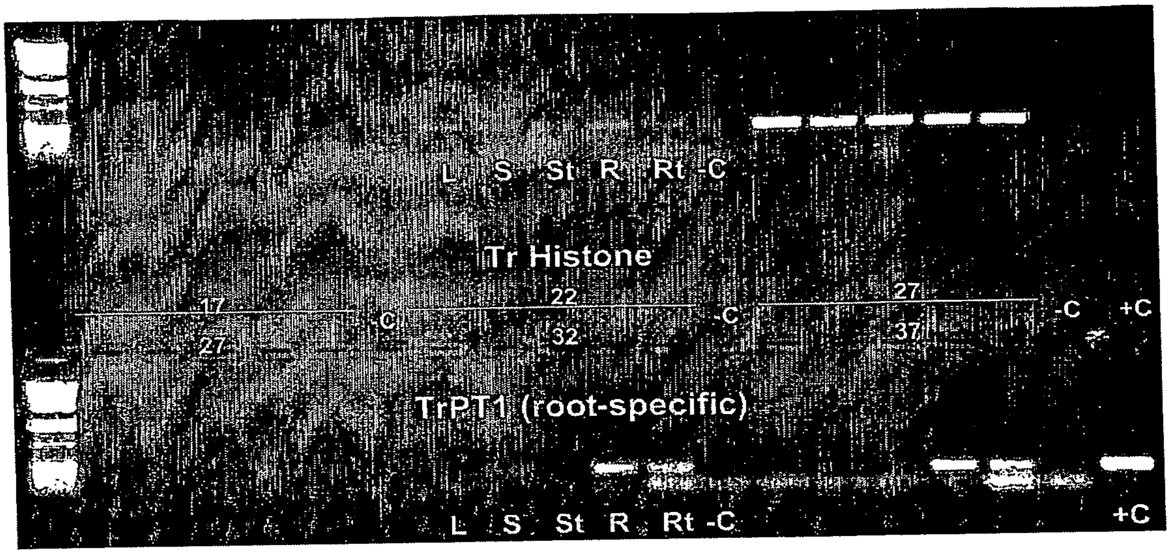
LB
RB
AscI
I-SceI
I-CeuI
PI-PspI
nos promoter
nptII
nos terminator
35S² promoter
TrPEPc
rbcS terminator
35S promoter
TrCSa
35S terminator
PT2 promoter
TrMDH
Binary vector
Auxiliary constructs
B
Binary vector construct

FIGURE 126

A



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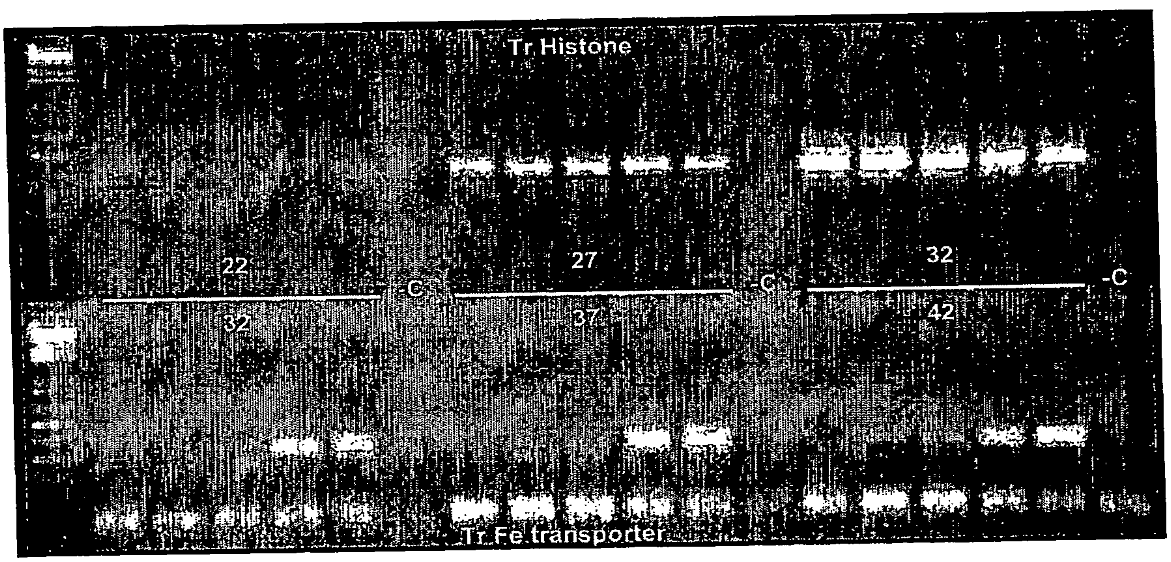
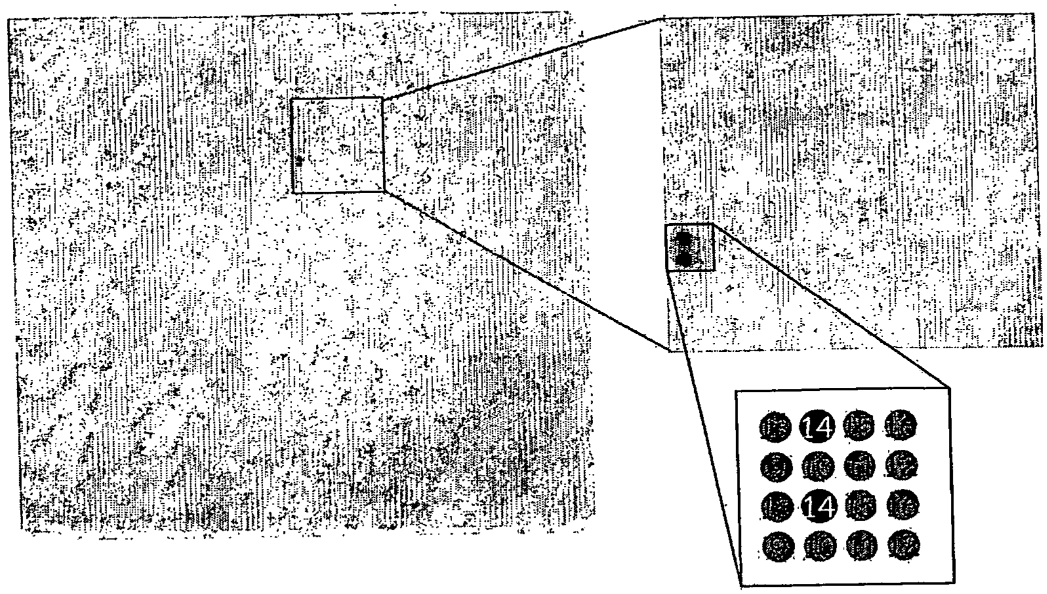


FIGURE 127

A



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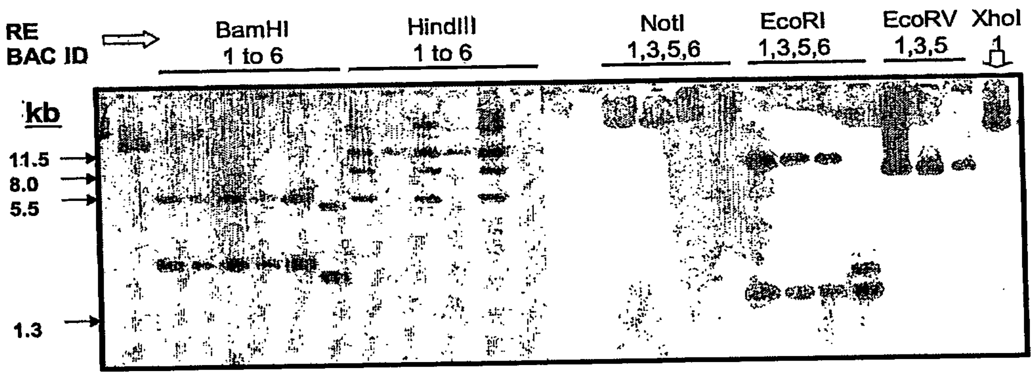


C

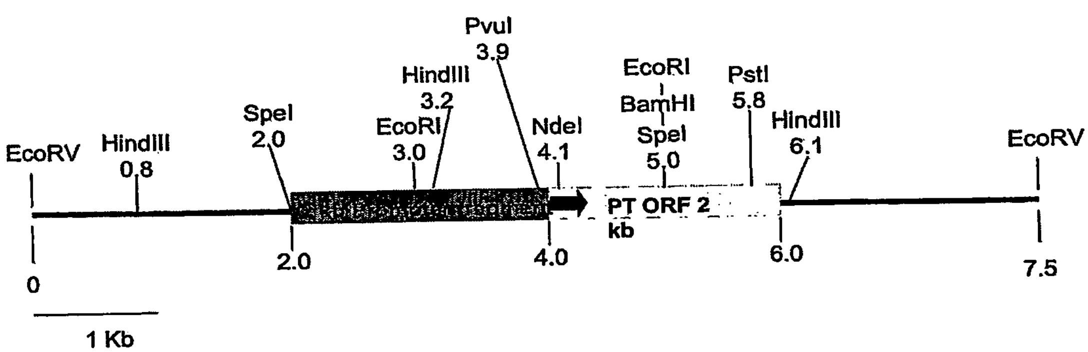


FIGURE 128

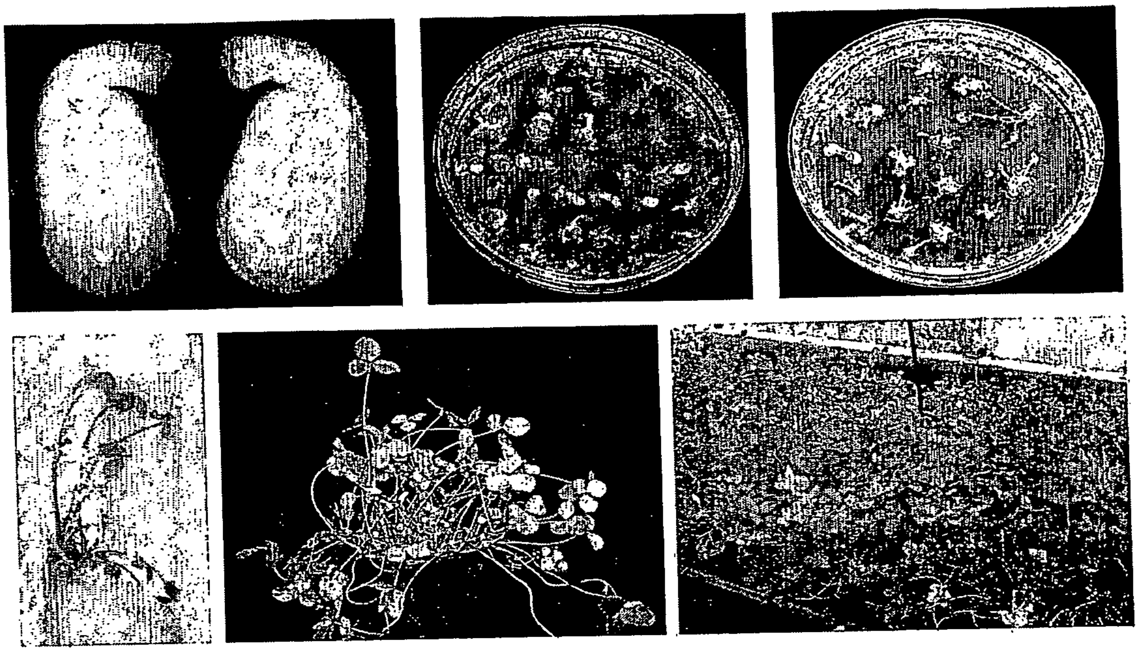
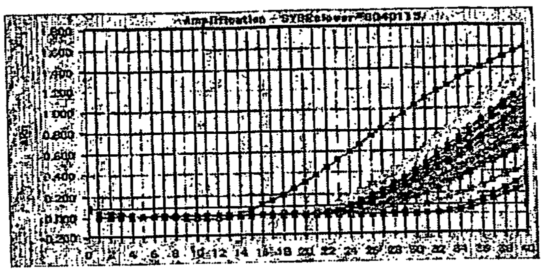
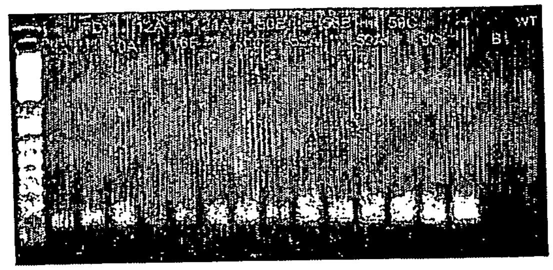


FIGURE 129

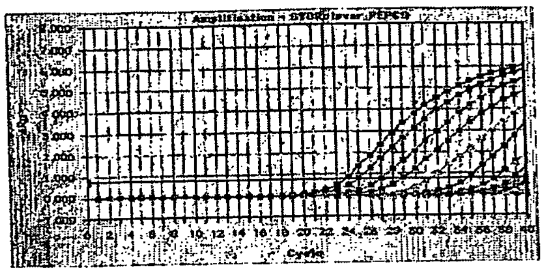


QPCR plots

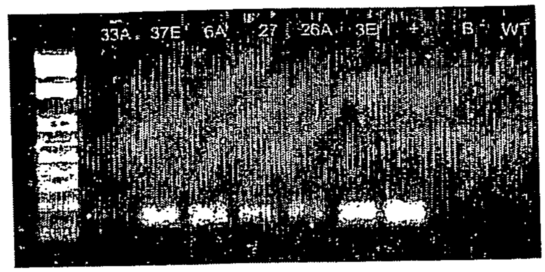


QPCR Result

FIGURE 130

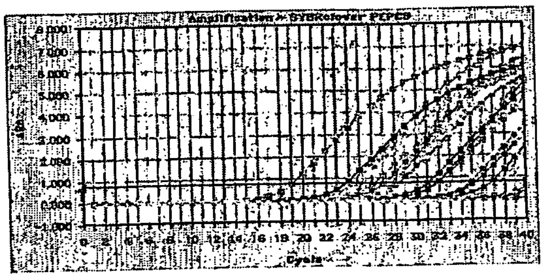


QPCR plots

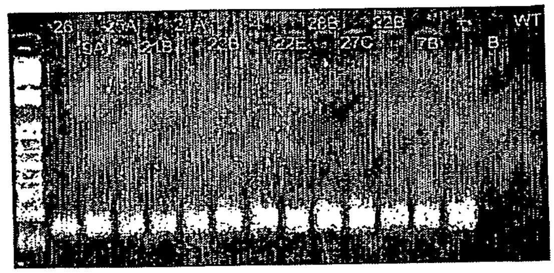


QPCR Result

FIGURE 131



QPCR plots



QPCR Result

FIGURE 132

SEQUENCE LISTING

<110> Agriculture Victoria Services Pty Ltd
AgResearch Limited

<120> Manipulation of organic acid biosynthesis and secretion

<130> M80678527:DLT:cl

<150> 2003901796
<151> 2003-04-14

<150> 2004901259
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<170> PatentIn version 3.2

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ccagagtcaa ctggcaggct gggagtttgc aatttcgcag cactctgctg ttcctcaagg 180

actcttggat ataatacaat caatgcctca tgatgcccac cccatgggtg tccttgccag 240

tgcaatgagc acactttcag tcttccatcc agatgcaaac cctgctctta gaggtcaaga 300

tctatacaag tcgaagcagg ttagggataa gcaaattgta cgagttcttg ggaaggcacc 360

agtaatagca gctgcagcct atctgagatt agcaggaagg ccctttgtcc ttccttcaaa 420

taatctctct tattcagaaa atttcttgta tatgctggac tctatgggtg acaaagatta 480

taagccaaat cccagacttg cccgggttct ggatgtcctt tttattcttc atgctgaaca 540

cgaaatgaac tgctcaacag ctgctgttag gcaccttgct tcaagtggtg tcgatgtctt 600

cactgctctt tctggtgctg ttggagctct atatggtcca ctgcatggtg gcgcaaatga 660

ggcggtactt aaaatgttaa atgagattgg aagtgtagag aatattccgg aattcattga 720

gggagtgaag aacaggaagc ggaaaatgtc tggttttggg caccgtgtgt ataagaatta 780

tgatcctcgt gctaaagtca tccggaagtt agcggaggag gttttcacga ttgtgggacg 840

ggatcctctt atcgaggtag ctgttgcttt ggagaaggca gcactgtcag acgagtattt 900

tatcaagagg aagctgtatc caaatgtgga tttttattct ggcctaatat atagggcaat 960

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agcacattgg aaggagtcac ttgatgaccc cgacaataaa attatgaggc cccaacaggt 1080

atacaccggt acttggctaa ggcattacac cccagtgaga gaacgggtgc catcaagcga 1140

cagtgagcag cttgggcaga tcgctacatc aaacgcgacg aggcgtcggc gtgctggctc 1200
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tatcttgaaa gtcttaatca tgtggaccaa tgaagacata gatcaagttc tttgcatggg 1500
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<212> PRT
<213> Lolium perenne

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20 25 30

Met Tyr Gly Asn Leu Pro Thr Gln Ser Gln Leu Ala Gly Trp Glu Phe
35 40 45

Ala Ile Ser Gln His Ser Ala Val Pro Gln Gly Leu Leu Asp Ile Ile
50 55 60

Gln Ser Met Pro His Asp Ala His Pro Met Gly Val Leu Ala Ser Ala
65 70 75 80

Met Ser Thr Leu Ser Val Phe His Pro Asp Ala Asn Pro Ala Leu Arg
85 90 95

Gly Gln Asp Leu Tyr Lys Ser Lys Gln Val Arg Asp Lys Gln Ile Val
100 105 110

Arg Val Leu Gly Lys Ala Pro Val Ile Ala Ala Ala Ala Tyr Leu Arg
115 120 125

Leu Ala Gly Arg Pro Phe Val Leu Pro Ser Asn Asn Leu Ser Tyr Ser
130 135 140

Glu Asn Phe Leu Tyr Met Leu Asp Ser Met Gly Asp Lys Asp Tyr Lys
145 150 155 160

Pro Asn Pro Arg Leu Ala Arg Val Leu Asp Val Leu Phe Ile Leu His
165 170 175

Ala Glu His Glu Met Asn Cys Ser Thr Ala Ala Val Arg His Leu Ala

180 185 190

Ser Ser Gly Val Asp Val Phe Thr Ala Leu Ser Gly Ala Val Gly Ala
195 200 205

Leu Tyr Gly Pro Leu His Gly Gly Ala Asn Glu Ala Val Leu Lys Met
210 215 220

Leu Asn Glu Ile Gly Ser Val Glu Asn Ile Pro Glu Phe Ile Glu Gly
225 230 235 240

Val Lys Asn Arg Lys Arg Lys Met Ser Gly Phe Gly His Arg Val Tyr
245 250 255

Lys Asn Tyr Asp Pro Arg Ala Lys Val Ile Arg Lys Leu Ala Glu Glu
260 265 270

Val Phe Thr Ile Val Gly Arg Asp Pro Leu Ile Glu Val Ala Val Ala
275 280 285

Leu Glu Lys Ala Ala Leu Ser Asp Glu Tyr Phe Ile Lys Arg Lys Leu
290 295 300

Tyr Pro Asn Val Asp Phe Tyr Ser Gly Leu Ile Tyr Arg Ala Met Gly
305 310 315 320

Phe Pro Thr Glu Phe Phe Pro Val Leu Phe Ala Val Pro Arg Met Ala
325 330 335

Gly Trp Leu Ala His Trp Lys Glu Ser Leu Asp Asp Pro Asp Asn Lys
340 345 350

Ile Met Arg Pro Gln Gln Val Tyr Thr Gly Thr Trp Leu Arg His Tyr
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Thr Pro Val Arg Glu Arg Val Pro Ser Ser Asp Ser Glu Gln Leu Gly
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Gln Ile Ala Thr Ser Asn Ala Thr Arg Arg Arg Arg Ala Gly Ser Ala
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<220>
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ccagagtcaa ctggcaggct gggagtttgc aatttcgcag cactctgctg ttcctcaagg 180

actcttggat ataatacaat caatgcctca tgatgcccac cccatgggtg tccttgccag 240

tgcaatgagc acactttcag tcttccatcc agatgcaaac cctgctctta gaggtcaaga 300

tctatacaag tcgaagcagg ttagggataa gcaaattgta cgagttcttg ggaaggcacc 360

agtaatagca gctgcagcct atctgagatt agcaggaagg ccttttgtcc ttccttcaaa 420

taatctctct tattcagaaa atttcttgta tatgctggac tctatgggtg acaaagatta 480

taagccaaat cccagacttg cccgggttct ggatgtcctt tttattcttc atgctgaaca 540

cgaaatgaac tgctcaacag ctgctgttag gcaccttgct tcaagtggtg tcgatgtctt 600

cactgctctt tctggtgctg ttggagctct atatggtcca ctgcatggng gcgcaaatga 660

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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tttcagtctt ccatccagat gcaaaccctg ctcttagagg tcaagatcta tacaagtcga 180

agcaggttag ggataagcaa attgtacgag ttcttgggaa ggcaccagta atagcagctg 240

cagcctatct gagattagca ggaaggccct ttgtccttcc ttcaaataat ctctcttatt 300

cagaaaattt cttgtatatg ctggactcta tgggtgacaa agattataag ccaaatccca 360

gacttgcccg ggttctggat gtccttttta ttcttcatgc tgaacacgaa atgaactgct 420

caacagctgc tgttaggcac cttgcttcaa gtggtgtcga tgtcttcact gctctttctg 480

gtgctgttgg agctctatat ggtccactgc atggtggcgc aaatgaggcg gtacttaaaa 540

tgttaaatga gattggaagt gtagagaata ttccggaatt cattgaggga gtgaagaaca 600

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tggcgcaaat gaggcggtac ttaaaatgtt aaatgagatt ggaagtgtag agaatattcc 180

ggaattcatt gagggagtga agaacaggaa gcggaaaatg tctggctttg ggcaccgtgt 240

gtataagaat tatgatcctc gtgctaaagt catccggaag ttagcggagg aggttttcac 300

gattgtggga cgggatcctc ttatcgaggt agctgttgct ttggagaagg tagcactgtc 360

agacgagtat tttatcaaga ggaagctgta tccaaatgtg gatttttatt ctggcctaat 420

atatagggca atgggattcc ctacagagtt tttccctgtt ctgtttgcag ttcctcgcat 480

ggctggttgg ttagcacatt ggaaggagtc acttgatgac cccgacaata aaattatgag 540

gccccaacag gtatacaccg gtacttggct aaggcattac accccagtga gagaacgggt 600

gccatcaagc gacagtgagc agcttgggca gatcactaca tcaaacgcga cgaggcgtcg 660

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accaagctgc caagggccac ggctgcttaa atn 753

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ttatcaagag gaagctgtat ccaaatgtgg atttttattc tggcctaata tatagggcaa 180

tgggattccc tgcagagttt ttccctgttc tgtttgcagt tcctcgcatg gctggttggt 240

tagcacattg gaaggagtca cttgatgacc ccgacaataa aattatgagg ccccaacagg 300

tatacaccgg tacttggcta aggcattaca ccccagtgag agaacgggtg ccatcaagcg 360

acagtgagca gcttgggcag atcgctacat caaacgcgac gaggcgtcgg cgtgctggct 420

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caataaacta ataatgccgc caggacactt cactggtggt catgtgaagt tggtagtaga 600

atgcacttgt aacgtgttgt taatttgtta tcctgcaatg tacgctctat aaactgttca 660

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atgtggattt ttattctggc ctaatatata gggcaatggg attccctaca gagtttttcc 180

ctgttctgtt tgcagttcct cgcatggctg gttggttagc acattggaag gagtcacttg 240

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attacacccc agtgagagaa cgggtgccat caagcgacag tgagcagctt gggcagatcg 360

ctacatcaaa cgcgacgagg cgtcggcgtg ctggctctgc cctgtagaac agtctgcatg 420

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acacttcact ggtggtcatg tgaagttggt agtagaatgc acttgtaacg tgttgttaat 600

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gcatggctgg ttggttagca cattggaagg agtcacttga tgaccccgac aataaaatta 180

tgaggcccca acaggtatac accggtactt ggctaaggca ttacacccca gtgagagaac 240

gggtgccatc aagcgacagt gagcagcttg ggcagatcgc tacatcaaac gcgacgaggc 300

gtcggcgtgc tggctctgcc ctgtagaaca gtctgcatga tacagcatac agtccacaca 360

ataaaccaag ctgccaaggg ccacggctgc ttaaatctgg gagctgctat acttgtgtta 420

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catggctggt tggttagcac attggaagga gtcacttgat gaccccgaca ataaaattat 180

gaggccccaa caggtataca ccggtacttg gctaaggcat tacaccccag tgagagaacg 240

ggtgccatca agcgacagtg agcagcttgg gcagatcgct acatcaaacg cgacgaggcg 300

tcggcgtgct ggctctgccc tgtagaacag tctgcatgat acagcataca gtccacacaa 360

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cacgtatata taggcaataa actaataatg ccgccaggac acttcactgg tggtcatgtg 480

aagttggtag tagaatgcac ttgtaacgtg ttgttaattt gttatcctgc aatgtacgct 540

ctataaactg ttcagtatct tgaaagtctt aatcatgtgg accaatcaaa aaaaaaa 597

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<211> 310
<212> DNA
<213> Lolium perenne

<400> 10
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tctgcatgat acagcataca gtccacacaa taaaccaagc tgccaagggc cacggctgct 120

taaatctggg agctgctata cttgtgttat cacgtatata taggcaataa actaataatg 180

ccgccaggac acttcactgg tggtcatgtg aagttggtag tagaatgcac ttgtaacgtg 240

ttgttaattt gttatcctgc aatgtacgct ctataaactg ttcagtatct tgaaagtctt 300

aaaaaaaaaa 310

<210> 11
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<213> Lolium perenne

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<223> n is a, c, g, or t

<220>
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<222> (457)..(457)
<223> n is a, c, g, or t

<220>
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<222> (1087)..(1087)
<223> n is a, c, g, or t

<220>
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<222> (1106)..(1106)
<223> n is a, c, g, or t

<400> 11
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ttgagagtga atttgcaaag gcttatgaga agggaattca taaatcaaag ttctgggagc 120

ctacatatga agatagctta aatttgattg ctcggcttcc acaagtggct tcatatgttt 180

accggagaat tttcaaggac gggaaaacta ttgcagctga taatacactg gactacgcag 240

ctaatttttc acacatgctt ggttttgatg accccaaaat gctggagttg atgcgcctat 300

acataacaat tcacactgat cacgaaggag ggaatgttag tgctcatgct gggcatctgg 360

ttggaagtgc tctgtcagat ccttatcttt cttttgcagc ggcactgaac ggtttagctg 420

gaccactgca cggcttggct aatcaggaag tgttgtnatg gatcaaatct gtgatggaag 480

aaaccgggag taacattaca actgatcagc ttaaagaata tgtttggaag acactgaaga 540

gtggaaaggt tgttcctggc tatggtcatg gagttctacg taatacagat ccacgatact 600

cgtgccaaag ggagtttgca ctgaagtatt tacccgaaga cccacttttc caactggtct 660

ccaagttgta cgaagttgtg cctcctatcc tcaccgagtt aggcaaggta aaaaacccat 720

ggcctaatgt tgatgctcac agtggagttt tgctcaacca cttcggatta gttgaagcac 780

ggtactacac tgtcttgttc ggcgtctcaa ggagcatggg aattggatct cagctcattt 840

gggaccgtgc cctcggcctg ccacttgaaa gaccgaagag tgtcaccatg gagtggctgg 900

aaaaccactg caagaaggct gcggcctgaa gctacaccaa tgcttcgttt tacaaatcag 960

gccgtctttg atgttaataa tgactgagca taagttaggc atggttagcc ttgttttacc 1020

atcttcgttt tcctggccaa taactggagc aagaggctca cagacggtag aattttgtaa 1080

ccaccgntac ttgaacaccg aatcanttaa atgtcatttg gcataaagag attaggacat 1140

gacacataag ttttatgtgt cgctcgg 1167

<210> 12
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<212> PRT
<213> Lolium perenne

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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (152)..(152)
<223> Xaa can be any naturally occurring amino acid

<400> 12

Ser Pro Cys Xaa Cys Ser Pro Met Thr Gln Phe Thr Thr Gly Val Met
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Ala Leu Gln Val Glu Ser Glu Phe Ala Lys Ala Tyr Glu Lys Gly Ile
20 25 30

His Lys Ser Lys Phe Trp Glu Pro Thr Tyr Glu Asp Ser Leu Asn Leu
35 40 45

Ile Ala Arg Leu Pro Gln Val Ala Ser Tyr Val Tyr Arg Arg Ile Phe
50 55 60

Lys Asp Gly Lys Thr Ile Ala Ala Asp Asn Thr Leu Asp Tyr Ala Ala
65 70 75 80

Asn Phe Ser His Met Leu Gly Phe Asp Asp Pro Lys Met Leu Glu Leu
85 90 95

Met Arg Leu Tyr Ile Thr Ile His Thr Asp His Glu Gly Gly Asn Val
100 105 110

Ser Ala His Ala Gly His Leu Val Gly Ser Ala Leu Ser Asp Pro Tyr
115 120 125

Leu Ser Phe Ala Ala Ala Leu Asn Gly Leu Ala Gly Pro Leu His Gly
130 135 140

Leu Ala Asn Gln Glu Val Leu Xaa Trp Ile Lys Ser Val Met Glu Glu
145 150 155 160

Thr Gly Ser Asn Ile Thr Thr Asp Gln Leu Lys Glu Tyr Val Trp Lys
165 170 175

Thr Leu Lys Ser Gly Lys Val Val Pro Gly Tyr Gly His Gly Val Leu
180 185 190

Arg Asn Thr Asp Pro Arg Tyr Ser Cys Gln Arg Glu Phe Ala Leu Lys
195 200 205

Tyr Leu Pro Glu Asp Pro Leu Phe Gln Leu Val Ser Lys Leu Tyr Glu
210 215 220

Val Val Pro Pro Ile Leu Thr Glu Leu Gly Lys Val Lys Asn Pro Trp
225 230 235 240

Pro Asn Val Asp Ala His Ser Gly Val Leu Leu Asn His Phe Gly Leu
245 250 255

Val Glu Ala Arg Tyr Tyr Thr Val Leu Phe Gly Val Ser Arg Ser Met
260 265 270

Gly Ile Gly Ser Gln Leu Ile Trp Asp Arg Ala Leu Gly Leu Pro Leu
275 280 285

Glu Arg Pro Lys Ser Val Thr Met Glu Trp Leu Glu Asn His Cys Lys
290 295 300

Lys Ala Ala Ala
305

<210> 13
<211> 802
<212> DNA
<213> Lolium perenne

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<222> (782)..(782)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (792)..(792)
<223> n is a, c, g, or t

<220>
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<222> (797)..(797)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (802)..(802)
<223> n is a, c, g, or t

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ttgagagtga atttgcaaag gcttatgaga agggaattca taaatcaaag ttctgggagc 120

ctacatatga agatagctta aatttgattg ctcggcttcc acaagtggct tcatatgttt 180

accggagaat tttcaaggac gggaaaacta ttgcagctga taatacactg gactacgcag 240

ctaatttttc acacatgctt ggttttgatg accccaaaat gctggagttg atgcgcctat 300

acataacaat tcacactgat cacgaaggag ggaatgttag tgctcatgct gggcatctgg 360

ttggaagtgc tctgtcagat ccttatcttt cttttgcagc ggcactgaac ggtttagctg 420

gaccactgca cggcttggct aatcaggaag tgttgttatg gatcaaatct gtgatggaag 480

aaaccgggag taacattaca actgatcagc ttaaagaata tgtttggaag acactgaaga 540

gtggaaaggt tgttcctggc tatggtcatg gagttctacg taatacagat ccacgatact 600

cgtgccaaag ggagtttgca ctgaagtatt tacctgaaga cccacttttc caactggtct 660

ccaagttgta tgaagttgtg cctcctatcc tcactgagtt aggcaaggta aaaaacccat 720

ggcctaatgt tgatgctcac agnggagttt tgctcaacca cttcggatta gttgaacacg 780

gnactacact gncttgntcg gn 802

<210> 14
<211> 710
<212> DNA
<213> Lolium perenne

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<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
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<222> (630)..(630)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (649)..(649)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (703)..(703)
<223> n is a, c, g, or t

<220>
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<222> (706)..(706)
<223> n is a, c, g, or t

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atatgtttgg aagacactga agagtggaaa ggttgttcct ggctatggtc atggagttct 120

acgtaataca gatccacgat actcgtgcca aagggagttt gcactgaagt atttacccga 180

agacccactt ttccaactgg tctccaagtt gtacgaagtt gtgcctccta tcctcaccga 240

gttaggcaag gtaaaaaacc catgccctaa tgttgatgct cacagtggag ttttgctcaa 300

ccacttcgga ttagttgaag cacggtacta cactgtcttg ttcggcgtct caaggagcat 360

gggaattgga tctcagccca tttgggaccg tgccctcggc ctgccacttg aaagaccgaa 420

gagtgtcacc atggagtggc tggaaaacca ctgcaagaag gctgcggcct gaagctacac 480

caatgcttcg ttttacaaat caggccgtct ttgatgttaa taatgactga gcataagtta 540

ggcatggtta gccttgtttt accatcttcg ttttcctggc caataactgg agcaagaggc 600

ttacagacgg tagaattttg taaccaccgn tacttgaaca ccgaatcant taaatgtcat 660

ttggcataaa gagattagga catgacacat aagttttatg tgncgntcgg 710

<210> 15
<211> 633
<212> DNA
<213> Lolium perenne

<220>
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<222> (83)..(83)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (86)..(86)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (413)..(413)
<223> n is a, c, g, or t

<220>
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<222> (427)..(427)
<223> n is a, c, g, or t

<220>
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<222> (490)..(490)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (570)..(570)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (572)..(573)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (581)..(581)
<223> n is a, c, g, or t

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cgatactcgt gccaaaggga gtnggnactg aagtatttac ccgaagaccc acttttccaa 120

ctggtctcca agttgtacga agttgtgcct cctatcctca ccgagttagg caaggtaaaa 180

aacccatggc ctaatgttga tgctcacagt ggagttttgc tcaaccactt cggattagtt 240

gaagcacggt actacactgt cttgttcggc gtctcaagga gcatgggaat tggatctcag 300

ctcatttggg accgtgccct cggcctgcca cttgaaagac cgaagagtgt caccatggag 360

tggctggaaa accactgcaa gaaggctgcg gcctgaagct acaccaatgc ttngttttac 420

aaatcangcc gtctttgatg ttaataatga ctgagcataa gttaggcatg ggtagccttg 480

ttttaccatn ttcgttttcc tggccaataa ctggagcaag aggctcacag acggtagaat 540

tttgtaacca ccggtacttg acaccgaatn anntaaatgg natttggcat aaagagatta 600

ggacatgaca cataagtttt atgtgtcgct cgg 633

<210> 16
<211> 349
<212> DNA
<213> Lolium perenne

<400> 16
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agtgtcacca tggagtggct ggaaaaccac tgcaagaagg ctgcggcctg aagctacacc 120

aatgcttcgt tttacaaatc aggccgtctt tgatgttaat aatgactgag cataagttag 180

gcatggttag ccttgtttta ccatcttcgt tttcctggcc aataactgga gcaagaggct 240

cacagacggt agaattttgt aaccaccgtt acttgaacac cgaatcagtt aaatgtcatt 300

tggcataaag agattaggac atgacacata agttttatgt gtcgctcga 349

<210> 17
<211> 635
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
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<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (107)..(107)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (635)..(635)
<223> n is a, c, g, or t

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cttcttattt ccaccccaac cgcccaacat gtgtcctccc accgaanaaa cacctgctac 120

caacggccat agcaacggca ccaacggcgc caatggctcc aaggaaggct tcacaggcgt 180

cacgaccaga cagaaccctc accctacaca caagagccca tatgcacctg ttggcgactt 240

tttgtcaaat gtcggccgct tcaagattat cgagagcaca ttaagagagg gcgagcaatt 300

cgccaacgcc tacttcgacc ttgaggctaa aatcaagatc gccagagctc tcgacaactt 360

tggtgttgac tacattgaag ttaccagccc tgctgcctct gagcagtcaa gaagggactg 420

cgaagccctc tgcaagctcg gattgaaagc caagatcctt acccacgtac gatgccacat 480

ggacgatgcc agaatcgctg tcgagactgg tgttgacggc ctcgatgtcg tcattggaac 540

ctctgcgtac ctccgcgagc acagccatgg caaggacatg acatacatca aaaacacagc 600

gctggaggtg attgagtttg tcaagagcaa gggan 635

<210> 18
<211> 211
<212> PRT
<213> Lolium perenne

<220>
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<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (6)..(6)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (8)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (36)..(36)
<223> Xaa can be any naturally occurring amino acid

<400> 18

Xaa Arg Gly Xaa Asn Xaa Pro Xaa Phe Lys Tyr Arg Pro Ser Ala Thr
1 5 10 15

Asn Pro Pro Thr Phe Leu Phe Pro Pro Gln Pro Pro Asn Met Cys Pro
20 25 30

Pro Thr Glu Xaa Thr Pro Ala Thr Asn Gly His Ser Asn Gly Thr Asn
35 40 45

Gly Ala Asn Gly Ser Lys Glu Gly Phe Thr Gly Val Thr Thr Arg Gln
50 55 60

Asn Pro His Pro Thr His Lys Ser Pro Tyr Ala Pro Val Gly Asp Phe
65 70 75 80

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Leu Ser Asn Val Gly Arg Phe Lys Ile Ile Glu Ser Thr Leu Arg Glu
                85                  90                  95

Gly Glu Gln Phe Ala Asn Ala Tyr Phe Asp Leu Glu Ala Lys Ile Lys
            100                 105                 110

Ile Ala Arg Ala Leu Asp Asn Phe Gly Val Asp Tyr Ile Glu Val Thr
        115                 120                 125

Ser Pro Ala Ala Ser Glu Gln Ser Arg Arg Asp Cys Glu Ala Leu Cys
    130                 135                 140

Lys Leu Gly Leu Lys Ala Lys Ile Leu Thr His Val Arg Cys His Met
145                 150                 155                 160

Asp Asp Ala Arg Ile Ala Val Glu Thr Gly Val Asp Gly Leu Asp Val
                165                 170                 175

Val Ile Gly Thr Ser Ala Tyr Leu Arg Glu His Ser His Gly Lys Asp
            180                 185                 190

Met Thr Tyr Ile Lys Asn Thr Ala Leu Glu Val Ile Glu Phe Val Lys
        195                 200                 205

Ser Lys Gly
    210
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<210> 19
<211> 636
<212> DNA
<213> Lolium perenne

<220>
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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<220>
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<222> (19)..(19)
<223> n is a, c, g, or t

<220>
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<222> (21)..(21)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

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<222> (30)..(30)
<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<221> misc_feature
<222> (47)..(47)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (50)..(50)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (636)..(636)
<223> n is a, c, g, or t

<400> 19
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caacgacctc agcgatcagg ccatcaagga ctacctgtgg tccaccctca aggctggcca 120

agtcgttccc ggttacggac acgccgttct ccgcaagacc gacccccgct acgtctccca 180

gcgcgagttc gcccagaagc accttcccga cgacccaatg ttcaagctcg tcagtcaggt 240

ctacaagatc gcccctggtg ttctcaccga gcacggcaag accaagaacc cctaccccaa 300

cgtcgacgcc cactccggtg tcctcctcca gtactacggc ctcactgagc agaactacta 360

caccgttctc ttcggtgtat cccgtgcgct cggtgtcctt ccccagctta tcattgaccg 420

tgccgtcggt gcccccattg agaggcccaa gtctttcagc actgaggctt acgccaagtt 480

ggttggtgct aagttgtaag cgcgttactg caacgtgctc tacagccagg agaatgtgga 540

ggaatttgtt taacattcag agataccttg tcctgtgtag aattgcaatg taaggatagg 600

gaatgggagc gttacggcgc tacatcacta catttn 636

<210> 20
<211> 165
<212> PRT
<213> Lolium perenne

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (4)..(7)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (12)..(12)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (14)..(17)
<223> Xaa can be any naturally occurring amino acid

<400> 20

Xaa Tyr Gly Xaa Xaa Xaa Xaa Pro Xaa Xaa Trp Xaa Pro Xaa Xaa Xaa
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Xaa Ala Ile Gly Asn Asp Leu Ser Asp Gln Ala Ile Lys Asp Tyr Leu
20 25 30

Trp Ser Thr Leu Lys Ala Gly Gln Val Val Pro Gly Tyr Gly His Ala
35 40 45

Val Leu Arg Lys Thr Asp Pro Arg Tyr Val Ser Gln Arg Glu Phe Ala
50 55 60

Gln Lys His Leu Pro Asp Asp Pro Met Phe Lys Leu Val Ser Gln Val
65 70 75 80

Tyr Lys Ile Ala Pro Gly Val Leu Thr Glu His Gly Lys Thr Lys Asn
85 90 95

Pro Tyr Pro Asn Val Asp Ala His Ser Gly Val Leu Leu Gln Tyr Tyr
100 105 110

Gly Leu Thr Glu Gln Asn Tyr Tyr Thr Val Leu Phe Gly Val Ser Arg
115 120 125

Ala Leu Gly Val Leu Pro Gln Leu Ile Ile Asp Arg Ala Val Gly Ala
130 135 140

Pro Ile Glu Arg Pro Lys Ser Phe Ser Thr Glu Ala Tyr Ala Lys Leu
145 150 155 160

Val Gly Ala Lys Leu
165

<210> 21
<211> 696
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (665)..(665)
<223> n is a, c, g, or t

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attgtctagt gaagacatca aggctctcac caagaggaca caggagggtg ggacagaagt 120

tgttgaggca aaggctggaa agggatctgc aaccttgtcc atggcgtatg ctggcgcagt 180

tttggtgat gcatgcttga agggtctgaa cggagttcct gacattgttg aatgctccta 240

cgtgcaatca actatcacag aactgccatt ctttgcctcc aaggtgaggc tcgggaagaa 300

tggagtcgag gaagtgcttg gtttgggtga gctgtcggcc tttgagaagg aaggtttgga 360

aagtctcaag ggtgagctca agtcttcaat tgacaagggc atcgcgttcg ccaatgcgag 420

ttaattaatt ttgcagatta tagcaaacca ggtctagtta aggggtctgt ttttgacttt 480

ttgttcagtg ctttttctgc ccatcacgtg ggcatggaag atttgagctt cacaataaaa 540

atccggcggc gtaatgccac agaacattac ttgtacaaga gggaactagt tcgtgtcaag 600

ttttgaactg gtacattaaa cgaacaattg ctgatgcact ttgagaaaaa aaaattgggg 660

gtgantccat tggcctcaag ccaaaaaaaa aaaaaa 696

<210> 22
<211> 140
<212> PRT
<213> Lolium perenne

<400> 22

Val Gly Cys Trp Tyr His His Ser Ala Leu Phe Ser Gln Ala Thr Pro
1 5 10 15

Ser Thr Asn Ala Leu Ser Ser Glu Asp Ile Lys Ala Leu Thr Lys Arg
20 25 30

Thr Gln Glu Gly Gly Thr Glu Val Val Glu Ala Lys Ala Gly Lys Gly
35 40 45

Ser Ala Thr Leu Ser Met Ala Tyr Ala Gly Ala Val Phe Gly Asp Ala
50 55 60

Cys Leu Lys Gly Leu Asn Gly Val Pro Asp Ile Val Glu Cys Ser Tyr
65 70 75 80

Val Gln Ser Thr Ile Thr Glu Leu Pro Phe Phe Ala Ser Lys Val Arg
85 90 95

Leu Gly Lys Asn Gly Val Glu Glu Val Leu Gly Leu Gly Glu Leu Ser
100 105 110

Ala Phe Glu Lys Glu Gly Leu Glu Ser Leu Lys Gly Glu Leu Lys Ser
115 120 125

Ser Ile Asp Lys Gly Ile Ala Phe Ala Asn Ala Ser
130 135 140

<210> 23
<211> 650
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (650)..(650)
<223> n is a, c, g, or t

<400> 23
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attgtctagt gaagacatca aggctctcac caagaggaca caggagggtg ggacagaagt 120

tgttgaggca aaggctggaa agggatctgc aaccttgtcc atggcgtatg ctggcgcagt 180

ttttggtgat gcatgcttga agggtctgaa cggagttcct gacattgttg aatgctccta 240

cgtgcaatca actatcacag aactgccatt ctttgcctcc aaggtgaggc tcgggaagaa 300

tggagtcgag gaagtgcttg gtttgggtga gctgtcggcc tttgagaagg aaggtttgga 360

aagtctcaag ggtgagctca agtcttcaat tgacaagggc atcgcgttcg ccaatgcgag 420

ttaattaatt ttgcagatta tagcaaacca ggtctagtta aggggtctgt tgtttttgtt 480

cagtgctttt tctgcccatc acgtgggcat ggaagatttg agcttcacaa taaaaatccg 540

gcggcgtaat gccacagaac attacttgta caagagggaa ctagttcgtg tcaagttttg 600

aactggtaca ttaaacgaac aattgctgat gcactttgag aaaaaaaaan 650

<210> 24
<211> 649
<212> DNA
<213> Lolium perenne

<400> 24
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ttgtctagtg aagacatcaa ggctctcacc aagaggacac aggagggtgg gacagaagtt 120

gttgaggcaa aggctggaaa gggatctgca accttgtcca tggcgtatgc tggcgcagtt 180

tttggtgatg catgcttgaa gggtctgaac ggagttcctg acattgttga atgctcctac 240

gtgcaatcaa ctatcacaga actgccattc tttgcctcca aggtgaggct cgggaagaat 300

ggagtcgagg aagtgcttgg tttgggtgag ctgtcggcct ttgagaagga aggtttggaa 360

agtctcaagg gtgagctcaa gtcttcaatt gacaagggca tcgcgttcgc caatgcgagt 420
taattaattt tgcagattat agcaaaccag gtctagttaa ggggtctgtt gtttttgttc 480
agtgcttttt ctgcccatca cgtgggcatg gaagatttga gcttcacaat aaaaatccgg 540
cggcgtaatg ccacagaaca ttacttgtac aagagggaac tagttcgtgt caagttttga 600
actggtacat taaacgaaca attgctgatg cactttgaga aaaaaaaa 649

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<213> Lolium perenne

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ttgtctagtg aagacatcaa ggctctcacc aagaggacac aggagggtgg gacagaagtt 120
gttgaggcaa aggctggaaa gggatctgca accttgtcca tggcgtatgc tggcgcagtt 180
tttggtgatg catgcttgaa gggtctgaac ggagttcctg acattgttga atgctcctac 240
gtgcaatcaa ctatcacaga actgccattc tttgcctcca aggtgaggct cgggaagaat 300
ggagtcgagg aagtgcttgg tttgggtgag ctgtcggcct ttgagaagga aggtttggaa 360
agtctcaagg gtgagctcaa gtcttcaatt gacaagggca tcgcgttcgc caatgcgagt 420
taattaattt tgcagattat agcaaaccag gtctagttaa ggggtctgtt gtttttgttc 480
agtgcttttt ctgcccatca cgtgggcatg gaagatttga gcttcacaat aaaaatccgg 540
cggcgtaatg ccacagaaca ttacttgtac aagagggaac tagttcgtgt caagttttga 600
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gaggcaaagg ctggaaaggg atctgcaacc ttgtccatgg cgtatgctgg cgcagttttt     180

ggtgatgcat gcttgaaggg tctgaacgga gttcctgaca ttgttgaatg ctcctacgtg     240

caatcaacta tcacagaact gccattcttt gcctccaagg tgaggctcgg gaagaatgga     300

gtcgaggaag tgcttggttt gggtgagctg tcggcctttg agaaggaagg tttggaaagt     360

ctcaagggtg agctcaagtc ttcaattgac aagggcatcg cgttcgccaa tgcgagttaa     420

ttaattttgc agattatagc aaaccaggtc tagttaaggg gtctgttgnt tttgntcann     480

gctttttctg cccatcacgt gngcatgnaa gatttgagct tnacantann tatnccngcg     540

cgnn                                                                  544


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attgttgaat gctcctatgt gcaatcaact atcacagaac tgccattctt tgcctccaag 180

gtgaggctcg ggaagaatgg agtcgaggaa gtgcttggtt tgggtgagct gtcggccttt 240

ganaaggaag gtttggaaag tctcaagggt gagctcaagt cttcaattga caagggcatc 300

gcgttcgcca atgcgagttg attaaatttg cagattatag caatccaggt ctagttgagg 360

ggtctgtttt tgactttttg ttcagngctt tttctgccca tcacgtgggc atggaagatt 420

tgagcttcac aataaaaatc cggcggcgta atgccacana acattacttg gacaagaggg 480

aactagttcg ggtnaagttt tgaactggna cattaaacaa ccaattgttg tgcccctttg 540

ngaaccgccc tttgggggtg antccattgg nctnaagccn aaaaaaaaa 589

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gagaaggaag gtttggaaag tctcaagggt gagctcaagt cttcaattga caagggcatc     120

gcgttcgcca atgcgagttg attaaatttg cagattatag caatccaggt ctagttgagg     180

ggtctgtttt tgactttttg ttcagtgctt tttctgccca tcacgtgggc atggaagatt     240

tgagcttcac aataaaaatc cggcggcgta atgccacaga acattacttg tacaagaggg     300

aactagttcg tgtcaagttt tgaactggta cattaaacga acaattgttg atgcactttg     360

tgaaccgtcc tttggtgttg attccattgt cttcaagtta acgaanaana aaa            413


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gaaagtctca agggtgagnt caagtcttca attgacaagg gcatcgcgtt cgccaatgcg     120

agttgattaa atttgcagat tatagcaatc caggtctagt tgaggggtct gtttttgact     180

ttttgttcag tgctttttct gcccatcacg tgggcatgga agatttgagc ttcacaataa     240

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agttttgaac tggtacatta aacgaacaat tgttgaaaaa aaaaa                     345
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taaaactttc tacgctggga aggcaaacgt gccagtcact ggggtgaatg ttcctgttgt 120

tggtggccat gctggtgtta ctatcctgcc acagttctca caggctactc ctgcaagtaa 180

tgcattgtcc catgaggacc ttaaggccct caccaagagg acacaagatg gtgggacgga 240

agttgttgaa gcaaaggctg gaaagggctc agcaacattg tcaatggcat atgctggtgc 300

agtatttgga gatgcatgct tgaaggggct caatggagtt cctgacattg tagagtgctc 360

ctttgtgcaa tcaaccgtaa cagagctgcc attctttgcc tccaaggtaa ggctcggcaa 420

gaacggagtg gaggaagtga ttgggctggg cgagctgtct gccttcgaga aggagggtct 480

ggagagcctc aagggcgagc tgntgncctc catcgagaag ggtatcaagt tcgcgcagga 540

gagctagtca acctgctcag attctaacac tccgcacatg aactcggtgg gatctgatga 600

atttttggta cgactccttt cactgccccc ttctcctggg gacattgagg cgtcgngctc 660

cacaataaaa tggcgtgnct tgttgccata ctgaactgaa cttgtaatac cagaaagagt 720

gaaaccctgt gccttatgta ccacagtacg gtgaacccga aaatcatgaa ggtagcagaa 780

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<210> 31
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20 25 30

Thr Gly Val Asn Val Pro Val Val Gly Gly His Ala Gly Val Thr Ile
35 40 45

Leu Pro Gln Phe Ser Gln Ala Thr Pro Ala Ser Asn Ala Leu Ser His
50 55 60

Glu Asp Leu Lys Ala Leu Thr Lys Arg Thr Gln Asp Gly Gly Thr Glu
65 70 75 80

Val Val Glu Ala Lys Ala Gly Lys Gly Ser Ala Thr Leu Ser Met Ala
85 90 95

Tyr Ala Gly Ala Val Phe Gly Asp Ala Cys Leu Lys Gly Leu Asn Gly
100 105 110

Val Pro Asp Ile Val Glu Cys Ser Phe Val Gln Ser Thr Val Thr Glu
115 120 125

Leu Pro Phe Phe Ala Ser Lys Val Arg Leu Gly Lys Asn Gly Val Glu
130 135 140

Glu Val Ile Gly Leu Gly Glu Leu Ser Ala Phe Glu Lys Glu Gly Leu
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Glu Ser Leu Lys Gly Glu Leu Xaa Xaa Ser Ile Glu Lys Gly Ile Lys
165 170 175

Phe Ala Gln Glu Ser
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<210> 32
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aaaactttct acgctgggaa ggcaaacgtg ccagtcactg gggtgaatgt tcctgttgtt 120
ggtggccatg ctggtgttac tatcctgcca ctgttctcac aggctactcc tgcaagtaat 180
gcattgtccc atgaggatct taaggccctc accaagagga cacaagatgg tgggacggaa 240
gttgttgaag caaaggctgg aaagggctca gcaacattgt caatggcata tgctggtgca 300
gtatttggag atgcatgctt gaaggggctc aatggagttc ctgacattgt agagtgctcc 360
tttgtgcaat caactgtaac agagctgcca ttctttgcct ccaaggtaag gctcggcaag 420
aacggagtgg aggaagtgat tgggctgggc gagctgtctg ccttcgagaa ggagggtctg 480
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tttttggtac gactcctttc tctgcccctt tttcgtgggg acattgaggc gttgngcttc 660
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<210> 33
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<213> Lolium perenne

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ttactatcct gccacagttc tcacaggcta ctcctgcaag taatgcattg tcccatgagg 180
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gcttgaaggg gctcaatgga gttcctgaca ttgtagagtg ctcctttgtg caatcaaccg 360
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cagattctaa cactccgcac atgaactcgg tgggatctga tgaatttttg gttcgactcc 600
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tcttgttgcc atactgaact gaacttgtaa taccagaaag agtgaaaccc tgtgccttat 720
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gttaatcctc cctgctcatt caccatgagg aaattagtat ctcaccttca cagcatacag 180

aatggtggga cagaagtngt cgaggcgaaa gctggagcag gatcggnnac tntttctatg 240

gcgnatgcgg cagctaaatt tgcagatgct tgctngagag gattgcatgg tgatgctggg 300

atagnggant gctcttatgt ggattctcag gtgacgganc tntctttntt tgcatccaaa 360

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<210> 35
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<223> Xaa can be any naturally occurring amino acid

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<400> 35

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Xaa Ile Leu Pro Leu Leu Ser Gln Val Asn Pro Pro Cys Ser Phe Thr
        35                  40                  45

Met Arg Lys Leu Val Ser His Leu His Ser Ile Gln Asn Gly Gly Thr
    50                  55                  60

Glu Xaa Val Glu Ala Lys Ala Gly Ala Gly Ser Xaa Thr Xaa Ser Met
65                  70                  75                  80

Ala Xaa Ala Ala Ala Lys Phe Ala Asp Ala Cys Xaa Arg Gly Leu His
                85                  90                  95

Gly Asp Ala Gly Ile Xaa Xaa Cys Ser Tyr Val Asp Ser Gln Val Thr
            100                 105                 110

Xaa Xaa Ser Xaa Phe Ala Ser Lys Val Arg Leu Gly Cys Ser Gly Val
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Xaa Glu Ile Leu Pro Leu Gly Pro Leu Asn Glu
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<210> 36
<211> 774
<212> DNA
<213> Lolium perenne

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cgatccagat cccacacacc gccgcagcca gcaacgatga ggccgtcggc gatgagatcc 120

gccgcgcagc tcctccgccg ccgcagctac tcgtccgcgt ccggccagcc ggagcggaag 180
gtggccatcc tcggcgcggc cggcgggatc gggcagccgc tggcgctcct catgaagctg 240
aacccgctcg tctcctccct ctccctctac gacatcgccg ccaccccggg cgtcgccgcc 300
gacgtctccc acatcaactc cccggccctg gtgaaggggt tcatgggcga cgatcagctc 360
gcggaggcgt tggagggggc cgacctcgtc atcatcccgg ccggcgttcc gaggaagccc 420
ggcatgacca gggacgatct cttcaacatc aacgccggca tcgttaagaa cctctgcacc 480
gccatcgcca agtactgccc caacgctctt atcaacatga tcagcaaccc tgtgaactca 540
actgttccaa ttgctgctga agttttcaag aaggctggaa cctatgatga gaagaagttg 600
tttggtgtga ccactcttga tgttgttcgt gccaggactt tctatgctgg gaaggctaat 660
gtacctgtta ctggtgtgaa cgttcctgtt gttggtggtc atgctggtat caccattctg 720
ccactgttct cacaggcaac tccttcgact aatgcattgt ctagtgaaga catn 774

<210> 37
<211> 258
<212> PRT
<213> Lolium perenne

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>
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<223> Xaa can be any naturally occurring amino acid

<400> 37

Xaa Xaa Pro Pro Thr Gln His His Arg Ser Pro Val Arg Ile Ser Pro
1 5 10 15

Phe Arg Leu His Arg Ser Arg Ser His Thr Pro Pro Gln Pro Ala Thr
20 25 30

Met Arg Pro Ser Ala Met Arg Ser Ala Ala Gln Leu Leu Arg Arg Arg
35 40 45

Ser Tyr Ser Ser Ala Ser Gly Gln Pro Glu Arg Lys Val Ala Ile Leu
50 55 60

Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Leu Leu Met Lys Leu
65 70 75 80

Asn Pro Leu Val Ser Ser Leu Ser Leu Tyr Asp Ile Ala Ala Thr Pro
85 90 95

Gly Val Ala Ala Asp Val Ser His Ile Asn Ser Pro Ala Leu Val Lys
100 105 110

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Gly Phe Met Gly Asp Asp Gln Leu Ala Glu Ala Leu Glu Gly Ala Asp
        115                 120                 125

Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg
    130                 135                 140

Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys Asn Leu Cys Thr
145                 150                 155                 160

Ala Ile Ala Lys Tyr Cys Pro Asn Ala Leu Ile Asn Met Ile Ser Asn
                165                 170                 175

Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val Phe Lys Lys Ala
            180                 185                 190

Gly Thr Tyr Asp Glu Lys Lys Leu Phe Gly Val Thr Thr Leu Asp Val
        195                 200                 205

Val Arg Ala Arg Thr Phe Tyr Ala Gly Lys Ala Asn Val Pro Val Thr
    210                 215                 220

Gly Val Asn Val Pro Val Val Gly Gly His Ala Gly Ile Thr Ile Leu
225                 230                 235                 240

Pro Leu Phe Ser Gln Ala Thr Pro Ser Thr Asn Ala Leu Ser Ser Glu
                245                 250                 255

Asp Xaa


<210>  38
<211>  816
<212>  DNA
<213>  Lolium perenne


<220>
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<223> n is a, c, g, or t

<220>
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<222> (816)..(816)
<223> n is a, c, g, or t

<400> 38
tccgtacnat tgctgctgaa gtatttaaaa aagctgggac atacaatcct aagagattgt 60

tgggggtgac aacacttgat gtagtgagag ccaatacttt tgtgggtgag gttcttggac 120

ttgaccccag agatgtcaat gttcctgttg ttggcgggca tgccggagtt acgatattac 180

cactcctttc gcaggttagt cctccctgct cgttcacccc tgaggaaatt agttatctca 240

cctcacgcat acagaatggt gggacagaag ttgtggaggc gaaagcagga gcaggatcgg 300

caactctttc tatggcgtat gcggcagcta aatttgcaga tgcttgcttg agaggattgc 360

atggtgatgc tgggatagtg gagtgctctt atgtggattc tcaggtgacc ggaactgcct 420

tctttgcatc caaagttcgc ctaggtcgtt ctggcgtcga ggagatcttg caacttgggt 480

ccactgaacc aggttttgaa aganctggac tggaanaagg cgaaanaang agctatcccg 540

agagccttcc agaaaggntg tgtcatttcg tncaacaaag tgagttacat gccatcatct 600

ttgttggatg tgcttcccca aagttccaac acaccgtcgn aattggcata tanatattgc 660

tggtttgggg ccttttgcnt tnatgcaaac aggctacctt ntgggtgggg ggggtccgtt 720

ntgaaaaact cttaacattt ttttttacgg ttggnaacaa aatntntgaa aagcctgaga 780

antatatgat aantgaanaa agtttnnaaa aaaaan 816

<210> 39
<211> 271
<212> PRT
<213> Lolium perenne

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<223> Xaa can be any naturally occurring amino acid

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<222> (168)..(168)
<223> Xaa can be any naturally occurring amino acid

<220>
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<223> Xaa can be any naturally occurring amino acid

<220>

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<222> (175)..(176)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (186)..(186)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (190)..(190)
<223> Xaa can be any naturally occurring amino acid

<220>
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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (268)..(269)
<223> Xaa can be any naturally occurring amino acid

<400> 39

Arg Xaa Ile Ala Ala Glu Val Phe Lys Lys Ala Gly Thr Tyr Asn Pro
1 5 10 15

Lys Arg Leu Leu Gly Val Thr Thr Leu Asp Val Val Arg Ala Asn Thr
20 25 30

Phe Val Gly Glu Val Leu Gly Leu Asp Pro Arg Asp Val Asn Val Pro
35 40 45

Val Val Gly Gly His Ala Gly Val Thr Ile Leu Pro Leu Leu Ser Gln
50 55 60

Val Ser Pro Pro Cys Ser Phe Thr Pro Glu Glu Ile Ser Tyr Leu Thr
65 70 75 80

Ser Arg Ile Gln Asn Gly Gly Thr Glu Val Val Glu Ala Lys Ala Gly
85 90 95

Ala Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Ala Ala Lys Phe Ala
100 105 110

Asp Ala Cys Leu Arg Gly Leu His Gly Asp Ala Gly Ile Val Glu Cys
115 120 125

Ser Tyr Val Asp Ser Gln Val Thr Gly Thr Ala Phe Phe Ala Ser Lys
130 135 140

Val Arg Leu Gly Arg Ser Gly Val Glu Glu Ile Leu Gln Leu Gly Ser
145 150 155 160

Thr Glu Pro Gly Phe Glu Arg Xaa Gly Leu Glu Xaa Gly Glu Xaa Xaa
165 170 175

Ser Tyr Pro Glu Ser Leu Pro Glu Arg Xaa Cys His Phe Xaa Gln Gln
180 185 190

Ser Glu Leu His Ala Ile Ile Phe Val Gly Cys Ala Ser Pro Lys Phe
195 200 205

Gln His Thr Val Xaa Ile Gly Ile Xaa Ile Leu Leu Val Trp Gly Leu
210 215 220

Leu Xaa Xaa Cys Lys Gln Ala Thr Xaa Trp Val Gly Gly Val Arg Xaa
225 230 235 240

Glu Lys Leu Leu Thr Phe Phe Phe Thr Val Xaa Asn Lys Xaa Xaa Glu
245 250 255

Lys Pro Glu Xaa Tyr Met Ile Xaa Glu Xaa Ser Xaa Xaa Lys Lys

260 265 270

<210> 40
<211> 798
<212> DNA
<213> Lolium perenne

<220>
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<223> n is a, c, g, or t

<220>
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<222> (13)..(13)
<223> n is a, c, g, or t

<220>
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<222> (134)..(134)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

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<222> (248)..(248)
<223> n is a, c, g, or t

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<222> (260)..(260)
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<222> (301)..(301)
<223> n is a, c, g, or t

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<222> (499)..(499)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (633)..(633)
<223> n is a, c, g, or t

<400> 40
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aagagctgtc ctaatgcaat agtgaatttg atcagcaacc ctgtgaactc aactgtcccc 120

attgcggcag aagntttcaa gagggctgga acttactgcc ccaaacgtct ccttggagtg 180

acaactcttg atgtagcgag ggctaacacc tttgtggctg aagtgcttgg agntgatcct 240

agagaagnca gtgttccggn tgttggcggg catgcaggga tcactatatt gcccctcctg 300

ncccaggtca gcccccgtg ctcattcact ccagatgaaa tcagctattt gactaaccgc 360

atacagaatg gcggtaccga agttgttgag gcaaaggctg gagcaggctc tgcaactttg 420

tcaatggctt ttgctgctgc aaaattcgcc gatgcatgct tgcgtggaat gcgtggtgat 480
gctggcattg tggaatgtnc atacgttgca tctgaggtga cagagctgcc gttctttgca 540
acaaaagtga ggttaggtcg tggcggagct gaggagatcc tccctcttgg gccactgaat 600
gactttgaga gagctggcct ggagaaggcg aanaaggagc tcagcgagag catccagaag 660
ggtgtggcgt tcatgaacaa gtgagatcat atgaatggat ggataccccg caacctatac 720
atagatgatg caaagactaa agaaagagtg tgatatagtg ctcctatata cctgtaaaat 780
ctctcctgcc tgtaagaa 798

<210> 41
<211> 220
<212> PRT
<213> Lolium perenne

<220>
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<222> (38)..(38)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (71)..(71)
<223> Xaa can be any naturally occurring amino acid

<220>
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<223> Xaa can be any naturally occurring amino acid

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<222> (80)..(80)
<223> Xaa can be any naturally occurring amino acid

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<222> (94)..(94)
<223> Xaa can be any naturally occurring amino acid

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<222> (160)..(160)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (204)..(204)
<223> Xaa can be any naturally occurring amino acid

<400> 41

Met Leu Gly Ile Val Arg Ser Ile Cys Glu Gly Val Ala Lys Ser Cys
1 5 10 15

Pro Asn Ala Ile Val Asn Leu Ile Ser Asn Pro Val Asn Ser Thr Val
20 25 30

Pro Ile Ala Ala Glu Xaa Phe Lys Arg Ala Gly Thr Tyr Cys Pro Lys

35 40 45

Arg Leu Leu Gly Val Thr Thr Leu Asp Val Ala Arg Ala Asn Thr Phe
50 55 60

Val Ala Glu Val Leu Gly Xaa Asp Pro Arg Glu Xaa Ser Val Pro Xaa
65 70 75 80

Val Gly Gly His Ala Gly Ile Thr Ile Leu Pro Leu Leu Xaa Gln Val
85 90 95

Ser Pro Pro Cys Ser Phe Thr Pro Asp Glu Ile Ser Tyr Leu Thr Asn
100 105 110

Arg Ile Gln Asn Gly Gly Thr Glu Val Val Glu Ala Lys Ala Gly Ala
115 120 125

Gly Ser Ala Thr Leu Ser Met Ala Phe Ala Ala Ala Lys Phe Ala Asp
130 135 140

Ala Cys Leu Arg Gly Met Arg Gly Asp Ala Gly Ile Val Glu Cys Xaa
145 150 155 160

Tyr Val Ala Ser Glu Val Thr Glu Leu Pro Phe Phe Ala Thr Lys Val
165 170 175

Arg Leu Gly Arg Gly Gly Ala Glu Glu Ile Leu Pro Leu Gly Pro Leu
180 185 190

Asn Asp Phe Glu Arg Ala Gly Leu Glu Lys Ala Xaa Lys Glu Leu Ser
195 200 205

Glu Ser Ile Gln Lys Gly Val Ala Phe Met Asn Lys
210 215 220

<210> 42
<211> 798
<212> DNA
<213> Lolium perenne

<220>
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<222> (2)..(4)
<223> n is a, c, g, or t

<220>
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<222> (10)..(10)
<223> n is a, c, g, or t

<220>
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<222> (13)..(13)
<223> n is a, c, g, or t

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<222> (130)..(130)
<223> n is a, c, g, or t

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<222> (134)..(134)
<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<222> (233)..(233)
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<222> (248)..(248)
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<222> (260)..(260)
<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<222> (301)..(301)
<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<400> 42
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aagagctgtc ctaatgcaat agtgaatttg atcagcaacc ctgtgaactc aactgtcccc 120

attgcggcan aagntttcaa gagggctgga acttactgcc ccaaacgtct ccttggagtg 180

acaactcttg atgtagcgag ggctaacacc tttgtggctg aagtgcttgn agntgatcct 240

agagaagnca gtgttccggn tgttggcggg catgcnggga tcactatatt gcccctcctg 300

ncccaggtca gcccccgtg ctcattcact ccagatgaaa tcagctattt gactaaccgc 360

atacagaatg gcggtaccga agttgttgag gcaaaggctg gagcaggctc tgcaactttg 420

tcaatggctt ttgctgctgc aaaattcgcc gatgcatgct tgcgtggaat gcgtggtgat 480

gctggcattg tggaatgttc atacgttgca tctgaggtga cagagctgcc gttctttgca 540

acaaaagtga ggttaggtcg tggcggagct gaggagatcc tccctcttgg gccactgaat 600

gactttgaga gagctggcct ggagaaggcg aanaaggagc tcagcgagag catccagaag 660

ggtgtggcgt tcatgaacaa gtgagatcat atgaatggat ggataccccg caacctatac 720

atagatgatg caaagactaa agaaagagtg tgatatagtg ctcctatata cctgtaaaat 780

ctctcctgcc tgtaagaa 798

<210> 43
<211> 497
<212> DNA
<213> Lolium perenne

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<222> (484)..(484)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (497)..(497)
<223> n is a, c, g, or t

<400> 43
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gagctgtcct aatgcaatag tgaatttgat cagcaaccct gtgaactcaa ctgtccccat 120

tgcggcagaa gttttcaaga gggctggaac ttactgcccc aaacgtctcc ttggagtgac 180

aactcttgat gtagcgaggg ctaacacctt tgtggctgaa gtgcttggag ttgatcctag 240

agaagtcagt gttccggttg ttggcgggca tgcagggatc actatattgc ccctcctgtc 300

ccaggtcagc cccccgtgct cattcactcc agatgaaatc agctatttga ctaaccgcat 360

acagaatggc ggtaccgaag ttgttgaggc aaaggctgga gcaggctctg caactttgtc 420

aatggctttt gctgctgcaa aattcgccga tgcatgcttg cgtggaatgc gtggtgatgc 480

tggnattgtg gaatgtn 497

<210> 44
<211> 667
<212> DNA
<213> Lolium perenne

<220>
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<222> (643)..(643)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (658)..(658)
<223> n is a, c, g, or t

<400> 44
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caaccgtcac tatggtcaag gctgtcgtcg caggtgctgc tggtggtatc ggccagcccc 120

tctctcttct actcaagacg agccccctca tcgatgagct tgccctctac gatgttgtca 180

acactcccgg tgttgccgct gatctttccc acatctcatc ccgcgctcaa atcgccggct 240

acctccccaa ggatgatggc gcaaaggctg cattcaaaga tgccgacatt atcgtcatcc 300
ccgccggcat tcctcgcaag cctggcatga cccgtgatga cctcttcaac atcaacgccg 360
gaattgtcaa gggtctgatt gaggttgccg ccgaagttgc cccaaggcc ttcattctgg 420
tcatctccaa ccctgtcaac tctaccgtcc ctatctctgc cgaggtcctc aaggccaagg 480
gcgtcttcaa ccctcagcgt cttttcggtg tcaccaccct cgacatcgtc cgtgccgaga 540
ctttcgtcgc cagcatcacc ggcgagaagc agccccagaa cttgaccgtc cccgtcattg 600
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ttcccgc 667

<210> 45
<211> 221
<212> PRT
<213> Lolium perenne

<220>
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<222> (214)..(214)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (219)..(219)
<223> Xaa can be any naturally occurring amino acid

<400> 45

Ile Ala Arg Ser Cys Ser Leu Gln His His Pro His Ala Ser Pro Thr
1 5 10 15

Gln Pro Leu Pro Thr Val Thr Met Val Lys Ala Val Val Ala Gly Ala
20 25 30

Ala Gly Gly Ile Gly Gln Pro Leu Ser Leu Leu Leu Lys Thr Ser Pro
35 40 45

Leu Ile Asp Glu Leu Ala Leu Tyr Asp Val Val Asn Thr Pro Gly Val
50 55 60

Ala Ala Asp Leu Ser His Ile Ser Ser Arg Ala Gln Ile Ala Gly Tyr
65 70 75 80

Leu Pro Lys Asp Asp Gly Ala Lys Ala Ala Phe Lys Asp Ala Asp Ile
85 90 95

Ile Val Ile Pro Ala Gly Ile Pro Arg Lys Pro Gly Met Thr Arg Asp
100 105 110

Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys Gly Leu Ile Glu Val
115 120 125

Ala Ala Glu Val Ala Pro Lys Ala Phe Ile Leu Val Ile Ser Asn Pro

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    130                 135                 140

Val Asn Ser Thr Val Pro Ile Ser Ala Glu Val Leu Lys Ala Lys Gly
145                 150                 155                 160

Val Phe Asn Pro Gln Arg Leu Phe Gly Val Thr Thr Leu Asp Ile Val
                165                 170                 175

Arg Ala Glu Thr Phe Val Ala Ser Ile Thr Gly Glu Lys Gln Pro Gln
            180                 185                 190

Asn Leu Thr Val Pro Val Ile Gly Gly His Ser Gly Glu Thr Ile Val
        195                 200                 205

Pro Leu Phe Ser Lys Xaa Gln Pro Ser Ala Xaa Ile Pro
    210                 215                 220
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<210> 46
<211> 1484
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<400> 46

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tgtcgtcgcc tcctcccgaa ccactctccc catccccgaa ctccagaacc ggctccaatg     120
gcggcgaagg aaccgatgcg cgtgctcgtc accggcgccg caggacaaat tggatatgct     180
cttgttccga tgattgctag ggggaattatg cttggtgcgg accagcctgt tattctgcat    240
atgctggata ttccaccagc tgctgaagct cttaatggtg ttaagatgga gttggttgat     300
gccgcatttc cacttctcaa gggagttgtt gcaacaactg atgttgttga ggcttgcact     360
ggtgtgaatg ttgcggttat ggttggtgga ttccccagga aggagggaat ggaaaggaag     420
gatgttatgt ctaagaatgt ttcaatctac aaatctcaag catctgccct tgaagcccat     480
gcagccccga attgcaaggt tctggttgtt gccaatccag caaacaccaa tgctcttatc     540
ttaaaggagt ttgctccatc tattcctgag aagaacatca gttgtttgac ccgcctagac     600
cataacaggg cacttggtca gatctctgag agacttgatg tccaagttag tgatgtgaag     660
aatgttatca tctggggcaa tcactcttcc agtcagtacc ctgatgtgaa ccacgccacc     720
gtgaagactt ccagtggcga gaagcctgtt cgcgaacttg ttaaagacga tgaatggcta     780
aatgcagggt tcattgccac tgtccagcag cgtggtgctg caatcatcaa agcgaggaag     840
ctctccagtg ctctctctgc tgccagctct gcttgtgacc acatccgtga ttgggttctc     900
ggaacccctg agggaacatt tgtttccatg ggtgtgtatt ctgatggttc atacggtgtg     960
cctgctgggc ttatctactc cttcccagta acttgctgcg gtggtgaatg gacaattgtt    1020
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gtagctctat tttcgcctga tgatttacag gacaggatat tggcaggaag attggaacaa 1320

tttgacgtct gattaaaacc aacctcttat tattcctgtg tgtatgaatg aggcttttgt 1380

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<400> 47

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35 40 45

Ala Glu Ala Leu Asn Gly Val Lys Met Glu Leu Val Asp Ala Ala Phe
50 55 60

Pro Leu Leu Lys Gly Val Val Ala Thr Thr Asp Val Val Glu Ala Cys
65 70 75 80

Thr Gly Val Asn Val Ala Val Met Val Gly Gly Phe Pro Arg Lys Glu
85 90 95

Gly Met Glu Arg Lys Asp Val Met Ser Lys Asn Val Ser Ile Tyr Lys
100 105 110

Ser Gln Ala Ser Ala Leu Glu Ala His Ala Ala Pro Asn Cys Lys Val
115 120 125

Leu Val Val Ala Asn Pro Ala Asn Thr Asn Ala Leu Ile Leu Lys Glu
130 135 140

Phe Ala Pro Ser Ile Pro Glu Lys Asn Ile Ser Cys Leu Thr Arg Leu
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Asp His Asn Arg Ala Leu Gly Gln Ile Ser Glu Arg Leu Asp Val Gln
165 170 175

Val Ser Asp Val Lys Asn Val Ile Ile Trp Gly Asn His Ser Ser Ser
180 185 190

Gln Tyr Pro Asp Val Asn His Ala Thr Val Lys Thr Ser Ser Gly Glu
195 200 205

Lys Pro Val Arg Glu Leu Val Lys Asp Asp Glu Trp Leu Asn Ala Gly
210 215 220

Phe Ile Ala Thr Val Gln Gln Arg Gly Ala Ala Ile Ile Lys Ala Arg
225 230 235 240

Lys Leu Ser Ser Ala Leu Ser Ala Ala Ser Ser Ala Cys Asp His Ile
245 250 255

Arg Asp Trp Val Leu Gly Thr Pro Glu Gly Thr Phe Val Ser Met Gly
260 265 270

Val Tyr Ser Asp Gly Ser Tyr Gly Val Pro Ala Gly Leu Ile Tyr Ser
275 280 285

Phe Pro Val Thr Cys Cys Gly Gly Glu Trp Thr Ile Val Gln Gly Leu
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tgttccgatg attgctaggg gaattatgct tggtgcggac cagcctgtta ttctgcatat     240
gctggatatt ccaccagctg ctgaagctct taatggtgtt aagatggagt tggttgatgc     300
cgcatttcca cttctcaagg gagttgttgc aacaactgat gttgttgagg cttgcactgg     360
tgtgaatgtt gcggttatgg ttggtggatt ccccaggaag gagggaatgg aaaggaagga     420
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agccccgaat tgcaaggttc tggttgttgc caatccagca aacaccaatg ctcttatctt     540
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taacagggca cttggtcaga tctctgagag acttgatgnc caagttagtg atgtgaanaa     660
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gccgtaggac aaattggata tgctcttgtt ccgatgattg ctaggggaat tatgcttggt 180

gcggaccagc ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat 240

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cgcaggacaa attggatatg ctcttgttcc gatgattgct aggggaatta tgcttggtgc 180

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aggacaaatt ggatatgctc ttgttccgat gattgctagg cnaattatgc ttggngtgca 180

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ggacaaattg gatatgctct tgttccgatg attgctaggg gaattatgct tggtgtggac 180
cagcctgtta ttctgcatat gctggatatt ccaccagctg ctgaagctct taatggtgtt 240
aagatggagt tggttgatgc cgcatttcca cttctcaagg gagttgttgc aacaactgat 300
gttgttgagg cttgcactgg tgtgaatgtt gcggttatgg ttggtggatt ccccaggaag 360
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tctgcccttg aagcccatgc agccccgaat tgcaaggttc tggttgttgc caatccagca 480
aacaccaatg ctcttatctt aaaggagttt gctccatcta ttcctgagaa gaacatcagt 540
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gcctgttatt ctgcatatgc tggatattcc accagctgct gaagctctta atggtgttaa 240
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tgcccttgaa gcccatgcag ccccgaattg caaggttctg gttgttgcca atccagcaaa 480
caccaatgct cttatcttaa aggagtttgc tccatctatt cctgagaaga acatcagttg 540

tttgacccgc ctagaccata acagggcact tggtcagatc tctgagagac ttgatgtcca 600

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ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga 240
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atgtgaacca cgccaccgtg aagacttcca gtggcgagaa gcctgttcgc gaacttgtta 720
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<212> DNA
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gacaaattgg atatgctctt gttccgatga ttgctagggg aattatgctt ggtgcggacc 180

agcctgttat tctgcatatg ctggatattc caccagctgc tgaagctctt aatggtgtta 240

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ttgttgaggc ttgcactggt gtgaatgttg cgtttatggt tggtggattc cccaggaagg 360

agggaatgga aaggaaggat gttatgtcta agaatgtttc aatctacaaa tctcaagcat 420

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acaccaatgc tcttatctta aaggagtttg ctccatctat tcctgagaag aacatcagtt 540

gtttgacccg cctagaccat aacagggcac ttggtcagat ctctgagaga cttgatgtcc 600

aagttagtga tgtgaagaat gttatcatct ggggcaatca ctcttccagt cagtaccctg 660

atgtgaacca cgccaccgtg aagacttcca ggggcgagaa gcctgttcgc gaacttgtta 720

aagacgatga atggctaaat gcangggtca ttgccactgt ccagcagcgt ggngctgcaa 780

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caaattggat atgctcttgt tccgatgatt gctaggggaa ttatgcttgg tgcggaccag 180

cctgttattc tgcatatgct ggatattcca ccagccgctg aagctcttaa tggtgttaag 240

atggagttgg ttgatgccgc atttccactt ctcaagggag ttgttgcaac aactgatgtt 300

gttgaggctt gcactggtgt gaatgttgcg gttatggttg gtggattccc caggaaggag 360

ggaatggaaa ggaaggatgt tatgtctaag aatgtttcaa tctacaaatc tcaagcatct 420

gcccttgaag cccatgcagc cccgaattgc aaggttctgg ttgttgccaa tccagcaaac 480

accaatgctc ttatcttaaa ggagtttgct ccatctattc ctgagaagaa catcagttgt 540

ttgacccgcc tagaccataa cagggcactt ggtcagatct ctgagagact tgatgtccaa 600

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<210> 58
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gcctgttatt ctgcatatgc tggatattcc accagctgct gaagctctta atggtgttaa 240

gatggagttg gttgatgccg catttccact tctcaaggga gttgttgcaa caactgatgt 300

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gggaatggaa aggaaggatg ttatgtctaa gaatgtttca atctacaaat ctcaagcatc 420

tgcccttgaa gcccatgcag ccccgaattg caaggttctg gttgttgcca atccagcaaa 480

caccaatgct cttatcttaa aggagtttgc tccatctatt cctgagaaga acatcagttg 540

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<210> 59
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ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga 240

tggagttggt tgatgccgca tttccacttc tcaagggagt tgttgcaaca actgatgttg 300

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cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagcaaaca 480

ccaatgctct tatcttaaag gagtttgctc catctattcc tgagaagaac atcagttgtt 540

tgacccgcct agaccataac agggcacttg gtcagatctc tgagagactt gatgtccaag 600

ttagtgatgt gaagaatgtt atcatctggg gcaatcactc ttccagtcag taccctgatg 660

tgaaccacgc caccgtgaag acttncagtg gcgagaagcc tgttcgcgaa cttgttaaag 720

acgatgaatg gctaaatgca gggttcattg ccactgtcca gcagcgtggt gctgcaatca 780

tcaaagcgag gaagctctnc a 801

<210> 60
<211> 563
<212> DNA
<213> Lolium perenne

<400> 60
gatccttatc ccgttgtcgt cgcctcctcc cgaccactct ccccatcccc gaactccaga 60

accggctcca atggcggcga aggaaccgat gcgcgtgctc gtcaccggcg ccgcaggaca 120

aattggatat gctcttgttc cgatgattgc taggggaatt atgcttggtg cggaccagcc 180

tgttattctg catatgctgg atattccacc agctgctgaa gctcttaatg gtgttaagat 240

ggagttggtt gatgccgcat ttccacttct caagggagtt gttgcaacaa ctgatgttgt 300

tgaggcttgc actggtgtga atgttgcggt tatggttggt ggattcccca ggaaggaggg 360

aatggaaagg aaggatgtta tgtctaagaa tgtttcaatc tacaaatctc aagcatctgc 420

ccttgaagcc catgcagccc cgaattgcaa ggttctggtt gttgccaatc cagcaaacac 480

caatgctctt atcttaaagg agtttgctcc atctattcct gagaagaaca tcagttgttt 540

gacccgccta gaccataaca ggc 563

<210> 61
<211> 692
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (34)..(34)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (692)..(692)
<223> n is a, c, g, or t

<400> 61
gnnaccttct cccgttgtcg tcgcctcctc ccgnaccact ctcccctccc cgaactccag 60

aaccggctcc aatggcggcg aaggaaccga tgcgcgtgct cgtcaccggc gccgcaggac 120

aaattggata tgctcttgtt ccgatgattg ctaggggaat tatgcttggt gcggaccagc 180

ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga 240

tggagttggt tgatgccgca tttccacttc tcaagggagt tgttgcaaca actgatgttg 300

ttgaggcttg cactggtgtg aatgttgcgg ttatggttgg tggattcccc aggaaggagg 360

gaatggaaag gaaggatgtt atgtctaaga atgtttcaat ctacaaatct caagcatctg 420

cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagcaaaca 480

ccaatgctct tatcttaaag gagtttgctc catctattcc tgagaagaac atcagttgtt 540

tgacccgcct agaccataac agggcactcg gtcagatctc tgagagactt gatgtccaag 600

ttagtgatgt gaagaatgtt atcatctggg gtaatcactc ttccagtcaa taccctgatg 660

tgaaccacgc caccgtgaag acttccagtg gn 692

<210> 62
<211> 764
<212> DNA
<213> Lolium perenne

<400> 62
gatccttcat cccgttgtcg tcgcctcctc ccgaccactc tccccatccc cgaactccag 60

aaccggctcc aatggcggcg aaggaaccga tgcgcgtgct cgtcaccggc gccgcaggac 120

aaattggata tgctcttgtt ccgatgattg ctaggggaat tatgcttggt gcggaccagc 180

ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga 240

tggagttggt tgatgccgca tttccacttc tcaagggagt tgttgcaaca actgatgttg 300
ttgaggcttg cactggtgtg aatgttgcgg ttatggttgg tggattcccc aggaaggagg 360
gaatggaaag gaaggatgtt atgtctaaga atgtttcaat ctacaaatct caagcatctg 420
cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagcaaaca 480
ccaatgctct tatcttaaag gagttcgctc catctattcc tgagaagaac atcagttgtt 540
tgacccgcct agaccataac agggcacttg gtcagatctc tgagagactt gatgtccaag 600
ttagtgatgt gaagaatgtt atcatctggg gcaatcactc ttccagtcag taccctgatg 660
tgaaccacgc caccgtgaag acttccagtg gcgagaagcc tgttcgcgaa cttgttaaag 720
acgatgaatg gctaaatgca gggttcattg ccactgtcca gcag 764

<210> 63
<211> 769
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<400> 63
gntccttcat cccgttgtcg tcgcctcctc ccgaccactc tccccatccc cgaactccag 60
aaccggctcc aatggcggcg aaggaaccga tgcgcgtgct cgtcaccggc gccgcaggac 120
aaattggata tgctcttgtt ccgatgattg ctaggggaat tatgcttggt gcggaccagc 180
ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga 240
tggagttggt tgatgccgca tttccacttc tcaagggagt tgttgcaaca actgatgttg 300
ttgaggcttg cactggtgtg aatgttgcgg ttatggttgg tggattcccc aggaaggagg 360
gaatggaaag gaaggatgtt atgtctaaga atgtttcaat ctacaaatct caagcatctg 420
cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagcaaaca 480
ccaatgctct tatcttaaag gagtttgctc catctattcc tgagaagaac atcagttgtt 540
tgacccgcct agaccataac agggcactcg gtcagatctc tgagaggctt gatgtccaag 600
ttagtgatgt gaagaatgtt atcatctggg gtaatcactc ttccagtcaa taccctgatg 660
tgaaccacgc caccgtgaag acttccagtg gcgagaagcc tgttcgcgaa cttgttaaag 720
acgatgaatg gctaaatgca gggttcattg ccactgtcca gcagcgtgg 769

<210> 64
<211> 770
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (763)..(763)
<223> n is a, c, g, or t

<400> 64
gatccttatc ccgttgtcgt cgcctcctcc cgaccactct ccccatcccc gaactccaga 60
accggctcca atggcggcga aggaaccgat gcgcgtgctc gtcaccggcg ccgcaggaca 120
aattggatat gctcttgttc cgatgattgc taggggaatt atgcttggtg cggaccagcc 180
tgttattctg catatgctgg atattccacc agctgctgaa gctcttaatg gtgttaagat 240
ggagttggtt gatgccgcat ttccacttct caagggagtt gttgcaacaa ctgatgttgt 300
tgaggcttgc actggtgtga atgttgcggt tatggttggt ggattcccca ggaaggaggg 360
aatggaaagg aaggatgtta tgtctaagaa tgtttcaatc tacaaatctc aagcatctgc 420
ccttgaagcc catgcagccc cgaattgcaa ggttctggtt gttgccaatc cagcaaacac 480
caatgctctt atcttaaagg agtttgctcc atctattcct gagaagaaca tcagttgttt 540
gacccgccta gaccataaca gggcacttgg tcagatctct gagagacttg atgtccaagt 600
tagtgatgtg aagaatgtta tcatctgggg caatcactct tccagtcagt accctgatgt 660
gaaccacgcc accgtgaaga cttccagtgg cgagaagcct gttcgcgaac ttgttaaaga 720
cgatgaatgg ctaaatgcag ggttcattgc cactgtccag cancgtggtg 770

<210> 65
<211> 779
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<400> 65
gntccctcat cccgttgtcg tcgcctcctc ccgaccactc tccccatccc cgaactccag 60
aaccggctcc aatggcggcg aaggaaccga tgcgcgtgct cgtcaccggc gccgcaggac 120
aaattggata tgctcttgtt ccgatgattg ctaggggaat tatgcttggt gcggaccagc 180
ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga 240
tggagttggt tgatgccgca tttccacttc tcaagggagt tgttgcgaca actgatgttg 300
ttgaggcttg cactggtgtg aatgttgcgg ttatggttgg tggattcccc aggaaggagg 360
gaatggaaag gaaggatgtt atgtctaaga atgtttcaat ctacaaatct caagcatctg 420
cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagtaaaca 480
ccaatgctct tatcctaaag gagtttgctc catctattcc tgagaagaac atcagttgtt 540
tgacccgcct agaccataac agggcactcg gtcagatctc tgagagactt gatgtccaag 600
ttagtgatgt gaagaatgtt atcatctggg gtaatcactc ttccagtcaa taccctgatg 660
tgaaccacgc caccgtgaag acttccagtg gcgagaagcc tgttcgcgaa cttgttaaag 720
acgatgaatg gctaaatgca gggttcattg ccactgtcca gcagcgtggt gctgcaatc 779

<210> 66
<211> 788
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (643)..(643)
<223> n is a, c, g, or t

<400> 66
gnnccttcat cccgttgtcg tcgcctcctc ccgaccactc tccccatccc cgaactccag 60

aaccggctcc aatggcggcg aaggaaccga tgcgcgtgct cgtcaccggc gccgcaggac 120

aaattggata tgctcttgtt ccgatgattg ctaggggaat tatgcttggt gcggaccagc 180

ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga 240

tggagttggt tgatgccgca tttccacttc tcaagggagt tgttgcaaca actgatgttg 300

ttgaggcttg cactggtgtg aatgttgcgg ttatggttgg tggattcccc aggaaggagg 360

gaatggaaag gaaggatgtt atgtctaaga atgtttcaat ctacaaatct caagcatccg 420

cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagcaaaca 480

ccaatgctct tatcttaaag gagtttgctc catctattcc tgagaagaac atcagttgtt 540

tgacccgcct agaccataac agggcacttg gtcagatctc tgagagactt gatgtccaag 600

ttagtgatgt gaagaatgtt atcatctggg gcaatcactc ttncagtcag taccctgatg 660

tgaaccacgc caccgtgaag acttccagtg gcgagaagcc tgttcgcgaa cttgttaaag 720

acgatgaatg gctaaatgca gggttcattg ccactgtcca acagcgtggt gctgcaatca 780

tcaaagcg 788

<210> 67
<211> 794
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<400> 67
gttccttntc ccgttgtcgt cgcctcctcc cgaccactct ccccatcccc gaactccaga 60

accggctcca atggcggcga aggaaccgat gcgcgtgctc gtcaccggcg ccgcaggaca 120

aattggatat gctcttgttc cgatgattgc taggggaatt atgcttggtg cggaccagcc 180

tgttattctg catatgctgg atattccacc agctgctgaa gctcttaatg gtgttaagat 240

ggagttggtt gatgccgcat ttccacttct caagggagtt gttgcaacaa ctgatgttgt 300

tgaggcttgc actggtgtga atgttgcggt tatggttggt ggattcccca ggaaggaggg 360

aatggaaagg aaggatgtta tgtctaagaa tgtttcaatc tacaaatctc aagcatctgc 420

ccttgaagcc catgcagccc cgaattgcaa ggttctggtt gttgccaatc cagcaaacac 480

caatgctctt atcttaaagg agtttgctcc atctattcct gagaagaaca tcagttgttt 540

gacccgccta gaccataaca gggcactcgg tcagatctct gagaggcttg atgtccaagt 600

tagtgatgtg aagaatgtta tcatctgggg taatcactct tccagtcaat accctgatgt 660

gaaccacgcc accgtgaaga cttccagtgg cgagaagcct gttcgcgaac ttgttaaaga 720

cgatgaatgg ctaaatgcag ggttcattgc cactgtccag cagcgtggtg ctgcaatcat 780

caaagcgagg aagc 794

<210> 68
<211> 797
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (489)..(489)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (734)..(734)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (757)..(757)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (776)..(776)
<223> n is a, c, g, or t

<400> 68
gntccttcat cccgttgtcg tcgcctcctc ccgaccactc tccccatccc cgaactccag 60

aaccggctcc aatggcggcg aaggaaccga tgcgcgtgct cgtcaccggc gccgcaggac 120

aaattggata tgctcttgtt ccgatgattg ctaggggaat tatgcttggt gcggaccagc 180

ctgttattct gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga 240

tggagttggt tgatgccgca tttccacttc tcaagggagt tgttgcaaca actgatgttg 300

ttgaggcttg cactggtgtg aatgttgcgg ttatggttgg tggattcccc aggaaggagg 360

gaatggaaag gaaggatgtt atgtctaaga atgtttcaat ctacaaatct caagcatccg 420

cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagcaaaca 480

ccaatgctnt tatcttaaag gagtttgctc catctattcc tgagaagaac atcagttgtt 540

tgacccgcct agaccataac agggcacttg gtcagatctc tgagagactt gatgtccaag 600
ttagtgatgt gaagaatgtt atcatctggg gcaatcactc ttccagtcag taccctgatg 660
tgaaccacgc caccgtgaag acttccagtg gcgagaagcc tgttcgcgaa cttgttaaag 720
acgatgaatg gctnaatgca gggttcattg ccactgncca gcagcgtggt gctgcnatca 780
tcaaagcgag gaagctt 797

<210> 69
<211> 802
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (222)..(222)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (685)..(685)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (770)..(770)
<223> n is a, c, g, or t

<400> 69
gatccttcat cccgttgtcg tcgcctcctc ccgaccactc tccccatccc cgaactccag 60
aaccggctcc aatggcggcg aaggaaccga tgcgcgtgct cgtcaccggc gccgcaggac 120
aaattggata tgctcttgtt ccgatgattg ctaggggaat tatgcttggt gcggaccagc 180
ctgttattct gcatatgctg gatattccac cagctgctga anctcttaat ggtgttaaga 240
tggagttggt tgatgccgca tttccacttc tcaagggagt tgttgcaaca actgatgttg 300
ttgaggcttg cactggtgtg aatgttgcgg ttatggttgg tggattcccc aggaaggagg 360
gaatggaaag gaaggatgtt atgtctaaga atgtttcaat ctacaaatct caagcatctg 420
cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagcaaaca 480
ccaatgctct tatcttaaag gagtttgctc catctattcc tgagaagaac atcagttgtt 540
tgacccgcct agaccataac agggcacttg gtcagatctc tgagagactt gatgtccaag 600
ttagtgatgt gaagaatgtt atcatctggg gcaatcactc ttccagtcag taccctgatg 660
tgaaccacgc caccgtgaag acttncagtg gcgagaagcc tgttcgcgaa cttgttaaag 720
acgatgaatg gctaaatgca gggttcattg ccactgtcca gcagcgtggn gctgcatcat 780
caaagcgagg aagctcttca gt 802

<210> 70
<211> 315
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (153)..(153)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (257)..(257)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (302)..(302)
<223> n is a, c, g, or t

<400> 70
gnccttnatc ccnttgtcgt cgcctcctcc cgaccactct ccccatcccc gaactccaga 60

accggctcca atggcggcca aggaaccgat gcgcgtgctc gtcaccggcg ccgcaggaca 120

aattggatat gctcttgttc cgatgattgc tangggaatt atgcttggtg cggaccagcc 180

tgttattctg catatgctgg atattccacc agctgctgaa gctcttaatg gtgttaagat 240

ggagttggtt gatgccncat ttccacttct caagggagtt gttgcaacaa ctgatgttgt 300

tnaggcttgc actgg 315

<210> 71
<211> 525
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (78)..(78)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (269)..(269)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (493)..(493)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (515)..(515)
<223> n is a, c, g, or t

<400> 71
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accggctcca atggcggnga aggaaccgat gcgcgtgctc gtcaccggcg ccgcaggaca 120

aattggatat gctcttgttc cgatgattgc taggggaatt atgcttggtg cggaccagcc 180

tgttattctg catatgctgg atattccacc agctgctgaa gctcttaatg gtgttaagat 240

ggagttggtt gatgccgcat ttccacttnt caagggagtt gttgcaacaa ctgatgttgt 300

tgaggcttgc actggtgtga atgttgcggt tatggttggt ggattcccca ggaaggaggg 360

aatggaaagg aaggatgtta tgtctaagaa tgtttcaatc tacaaatctc aagcatctgc 420

ccttgaagcc catgcagccc cgaattgcaa ggttctggtt gttgccaatc cagcaaacac 480

caatgctctt atnttaaagg agtttgctcc atctnttcct gagaa 525

<210> 72
<211> 696
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (547)..(547)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (603)..(603)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (613)..(613)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (632)..(632)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (642)..(642)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (646)..(646)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (674)..(674)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (681)..(681)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (683)..(683)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (691)..(691)
<223> n is a, c, g, or t

<400> 72
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accggctcca atggcggcga aggaaccgat gcgcgtgctc gtcaccggcg ccgcaggaca 120

aattggatat gctcttgttc cgatgattgc taggggaatt atgcttggtg cggaccagcc 180

tgttattctg catatgctgg atattccacc agctgctgaa gctcttaatg gtgttaagat 240

ggagttggtt gatgccgcat ttccacttct caagggagtt gttgcaacaa ctgatgttgt 300

tgaggcttgc actggtgtga atgttgcggt tatggttggt ggattcccca ggaaggaggg 360

aatggaaagg aaggatgtta tgtctaagaa tgtttcaatc tacaaatctc aagcatctgc 420

ccttgaagcc catgcagccc cgaattgcaa ggttctggtt gttgccaatc cagcaaacac 480

caatgctctt atcttaaagg agtttgctcc atctattcct gagaagaaca tcagatgttt 540

gacccgncta gaccataaca gggcactcgg tcagatctct gagagacttg atgtgcaagt 600

tancgatgtg aanaatgcta tcatctgggg anatcactct tncagncata ccctgatgtg 660

aaccacgcca ccgngaacac ntncactgcc nacaag 696

<210> 73
<211> 646
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<400> 73
tccttnatcc cgttgtcgtc gcctcctccc gaaccctctc cccatccccg aactccagaa 60

ccggctccaa tggcggcgaa ggaaccgatg cgcgtgctcg tcaccggcgc cgcaggacaa 120

attggatatg ctcttgttcc gatgattgct aggggaatta tgcttggtgc ggaccagcct 180

gttattctgc atatgctgga tattccacca gctgctgaag ctcttaatgg tgttaagatg 240

gagttggttg atgccgcatt tccacttctc aagggagttg ttgcaacaac tgatgttgtt 300

gaggcttgca ctggtgtgaa tgttgcggtt atggttggtg gattccccag gaaggaggga 360

atggaaagga aggatgttat gtctaagaat gtttcaatct acaaatctca agcatctgcc 420

cttgaagccc atgcagcccc gaattgcaag gttctggttg ttgccaatcc agcaaacacc 480

aatgctctta tcttaaagga gtttgctcca tctattcctg agaagaacat cagttgtttg 540

acccgcctag accataacag ggcacttggt cagatctctg agagacttga tgtccaagtt 600

agtgatgtga aaaatgttat catctggggc aatcactctt ccagtc 646

<210> 74
<211> 711
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (642)..(642)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (679)..(679)
<223> n is a, c, g, or t

<400> 74
accttctncc cgttgtcgtc gcctcctccc gaaccactct ccccatcccc gaactccaga 60

accggctcca atggcggcga aggaaccgat gcgcgtgctc gtcaccggcg ccgcaggaca 120

aattggatat gctcttgttc cgatgattgc taggggaatt atgcttggtg cggaccagcc 180

tgttattctg catatgctgg atattccacc agctgctgaa gctcttaatg gtgttaagat 240

ggagttggtt gatgccgcat ttccacttct caagggagtt gttgcaacaa ctgatgttgt 300

tgaggcttgc actggtgtga atgttgcggt tatggttggt ggattcccca ggaaggaggg 360

aatggaaagg aaggatgtta tgtctaagaa tgtttcaatc tacaaatctc aagcatctgc 420

ccttgaagcc catgcagccc cgaattgcaa ggttctggtt gttgccaatc cagcaaacac 480

caatgctctt atcttaaagg agtttgctcc atctattcct gagaagaaca tcagttgttt 540

gacccgccta gaccataaca gggcactcgg tcagatctct gagagacttg atgtccaagt 600

tagtgatgtg aagaatgtta tcatctgggg taatcactct tncagtcaat accctgatgt 660

gaaccacgcc accgtgaana ctttcagtgg cgagaagcct gttcgcgaac t 711

<210> 75
<211> 768
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<400> 75
tccttntccc gttgtcgtcg cctcctcccg accactctcc ccatccccga actccagaac 60

cggctccaat ggcggcgaag gaaccgatgc gcgtgctcgt caccggcgcc gcaggacaaa 120

ttggatatgc tcttgttccg atgattgcta ggggaattat gcttggtgcg gaccagcctg 180

ttattctgca tatgctggat attccaccag ctgctgaagc tcttaatggt gttaagatgg 240

agttggttga tgccgcattt ccacttctca agggagttgt tgcaacaact gatgttgttg 300

aggcttgcac tggtgtgaat gttgcggtta tggttggtgg attccccagg aaggagggaa 360

tggaaaggaa ggatgttatg tctaagaatg tttcaatcta caaatctcaa gcatctgccc 420

ttgaagccca tgcagccccg aattgcaagg ttctggttgt tgccaatcca gcaaacacca 480

atgctcttat cttaaaggag tttgctccat ctattcctga gaagaacatc agttgtttga 540

cccgcctaga ccataacagg gcacttggtc agatctctga gagacttgat gtccaagtta 600

gtgatgtgaa gaatgttatc atctggggca atcactcttc cagtcagtac cctgatgtga 660

accacgccac cgtgaagact tccagtggcg agaagcctgt tcgcgaactt gttaaagacg 720

atgaatggct aaatgcaggg ttcattgcca ctgtccagca gcgtggtg 768

<210> 76
<211> 783
<212> DNA
<213> Lolium perenne

<400> 76
tccttatccc gttgtcgtcg cctcctcccg accactctcc ccatccccga actccagaac 60

cggctccaat ggcggcgaag gaaccgatgc gcgtgctcgt caccggcgcc gcaggacaaa 120

ttggatatgc tcttgttccg atgattgcta ggggaattat gcttggtgcg gaccagcctg 180

ttattctgca tatgctggat attccaccag ctgctgaagc tcttaatggt gttaagatgg 240

agttggttga tgccgcattt ccacttctca agggagttgt tgcaacaact gatgttgttg 300

aggcttgcac tggtgtgaat gttgcggtta tggttggtgg attccccagg aaggagggaa 360

tggaaaggaa ggatgttatg tctaagaatg tttcaatcta caaatctcaa gcatctgccc 420

ttgaagccca tgcagccccg aattgcaagg ttctggttgt tgccaatcca gcaaacacca 480

atgctcttat cttaaaggag tttgctccat ctattcctga gaagaacatc agttgtttga 540

cccgcctaga ccataacagg gcacttggtc agatctctga gagacttgat gtccaagtta 600

gtgatgtgaa gaatgttatc atctggggca atcactcttc cagtcagtac cctgatgtga 660

accacgccac cgtgaagact tccagtggcg agaagcctgt tcgcgaactt gttaaagacg 720

atgaatggct aaatgcaggg ttcattgcca ctgtccagca gcgtggtgct gcaatcatca 780

aag 783

<210> 77
<211> 803
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (713)..(713)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (797)..(797)
<223> n is a, c, g, or t

<400> 77
tccttcntcc cgttgtcgtc gcctcctccc gaccactctc cccatccccg aactccagaa 60

ccggctccaa tggcggcgaa ggaaccgatg cgcgtgctcg tcaccggcgc cgcaggacaa 120

attggatatg ctcttgttcc gatgattgct aggggaatta tgcttggtgc ggaccagcct 180

gttattctgc atatgctgga tattccacca gctgctgaag ctcttaatgg tgttaagatg 240

gagttggttg atgccgcatt tccacttctc aagggagttg ttgcaacaac tgatgttgtt 300

gaggcttgca ctggtgtgaa tgttgcggtt atggttggtg gattccccag gaaggaggga 360

atggaaagga aggatgttat gtctaagaat gtttcaatct acaaatctca agcatctgcc 420

cttgaagccc atgcagcccc gaattgcaag gttctggttg ttgccaatcc agcaaacacc 480

aatgctctta tcttaaagga gtttgctcca tctattcctg agaagaacat cagttgtttg 540

acccgcctag accataacag ggcactcggt cagatctctg agaggcttga tgtccaagtt 600

agtgatgtga agaatgttat catctggggt aatcactctt ccagtcaata ccctgatgtg 660

aaccacgcca ccgtgaagac ttccagtggc gagaagcctg ttcgcgaact tgntaaagac 720

gatgaatggc taaatgcagg gttcattgcc actgtccagc agcgtggtgc tgcaatcatc 780

aaagcgagga agctctncag tgc 803

<210> 78
<211> 595
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature

<222> (386)..(386)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (439)..(439)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (496)..(496)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (510)..(510)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (520)..(520)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (529)..(529)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (531)..(531)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (558)..(558)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (561)..(562)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (567)..(567)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (578)..(578)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (580)..(580)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (588)..(588)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (590)..(590)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (595)..(595)
<223> n is a, c, g, or t

<400> 78
ccttcatccc gttgtcgtcg cctcctcccg accactctcc ccatccccga actccagaac 60

cggctccaat ggcggcgaag gaaccgatgc gcgtgctcgt caccggcgcc gcaggacaaa 120

ttggatatgc tcttgttccg atgattgcta ggggaattat gcttggtgcg gaccagcctg 180

ttattctgca tatgctggat attccaccag ctgctgaagc tcttaatggt gttaagatgg 240

agttggttga tgccgcattt ccacttctca agggagttgt tgcaacaact gatgttgttg 300

aggcttgcac tggtgtgaat gttgcggtta tggttggtgg attccccagg aaggagggaa 360

tggaaaggaa ggatgttatg tctaanaatg tttcaatcta caaatcttaa gcatctgccc 420

ttgaagccca tgcaccccna attgcaaggg tctggttgtt gccaatccag caaacaccaa 480

tgcttttatt ttaaangagt ttgctccatn tattcctgan aagaacatna nttgtttgac 540

ccgcctagac cataacangg nncttgncaa aatctttnan agacttgntn tcaan 595

<210> 79
<211> 696
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (120)..(120)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (335)..(335)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (387)..(387)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (482)..(482)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (603)..(603)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (608)..(608)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (612)..(612)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (674)..(674)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (689)..(689)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (695)..(696)
<223> n is a, c, g, or t

<400> 79
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ccggctccaa tggcggcgaa ggaaccgatg cgcgtgctcg tcaccggcgc cgcaggacan 120
attggatatg ctcttgttcc gatgattgct aggggaatta tgcttggtgc ggaccagcct 180
gttattctgc atatgctgga tattccacca gctgctgaag ctcttaatgg tgttaagatg 240
gagttggttg atgccgcatt tccacttctc aagggagttg ttgcaacaac tgatgttgtt 300
gaggcttgca ctggtgtgaa tgttgcggtt atggntggtg gattccccag gaaggaggga 360
atggaaagga aggatgttat gtctaanaat gtttcaatct acaaatctca agcatctgcc 420
cttgaagccc atgcagcccc gaattgcaag gttctggttg ttgccaatcc agcaaacacc 480
antgctctta tcttaaagga gtttgctcca tctatccctg agaagaacat cagttgtttg 540
acccgcctag accataacag ggcacttggt cagatctctg agagacttga tgtccaagtt 600
agngatgnga anaatgttat catctggggc aatcactctt ccagtcagta ccctgatgtg 660
aaccacgcca ccgngaagac ttccagtgnc gagann 696

<210> 80
<211> 779
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (77)..(77)
<223> n is a, c, g, or t

<400> 80
accttatccc gttgtcgtcg cctcctcccg accactctcc ccatccccga actccagaac 60
cggctccaac ggcggcnaag gaaccgatgc gcgtgctcgt caccggcgcc gcaggacaaa 120
ttggatatgc tcttgttccg atgattgcta ggggaattat gcttggtgcg gaccagcctg 180

ttattctgca tatgctggat attccaccag ctgctgaagc tcttaatggt gttaagatgg 240
agttggttga tgccgcattt ccacttctca agggagttgt tgcaacgact gatgttgttg 300
aggcttgcac tggtgtgaat gttgcggtta tggttggtgg attccccagg aaggagggaa 360
tggaaaggaa ggatgttatg tctaagaatg tttcaatcta caaatctcaa gcatctgccc 420
ttgaagccca tgcagccccg aattgcaagg ttctggttgt tgccaatcca gcaaacacca 480
atgctcttat cttaaaggag tttgctccat ctattcctga gaagaacatc agttgtttga 540
cccgcctaga ccataacagg gcacttggtc agatctctga gagacttgat gtccaagtta 600
gtgatgtgaa gaatgttatc atctggggca atcactcttc cagtcagtac cctgatgtga 660
accacgccac cgtgaagact tccagtggcg agaagcctgt tcgcgaactt gttaaagacg 720
atgaatggct aaatgcaggg ttcattgcca ctgtccagca gcgtggtgct gcaatcata 779

<210> 81
<211> 470
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (4)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (44)..(44)
<223> n is a, c, g, or t

<400> 81
cttnctcccg ttgtcgtcgc ctcctcccga accactctcc cctnccccga actccagaac 60
cggctccaat ggcggcgaag gaaccgatgc gcgtgctcgt caccggcgcc gcaggacaaa 120
ttggatatgc tcttgttccg atgattgcta ggggaattat gcttggtgcg gaccagcctg 180
ttattctgca tatgctggat attccaccag ctgctgaagc tcttaatggt gttaagatgg 240
agttggttga tgccgcattt ccacttctca agggagttgt tgcaacaact gatgttgttg 300
aggcttgcac tggtgtgaat gttgcggtta tggttggtgg attccccagg aaggagggaa 360
tggaaaggaa ggatgttatg tctaagaatg tttcaatcta caaatctcaa gcatctgccc 420
ttgaagccca tgcagccccg aattgcaagg ttctggttgt tgccaatcca 470

<210> 82
<211> 599
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (44)..(44)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (580)..(580)
<223> n is a, c, g, or t

<400> 82
ttnctnccgn ctgtcgtcgc ctcctcccga accactctcc cctnccccga actccaaacc 60

ggctccaatg gcggcgaagg aaccgatgcg cgtgctcgtc accggcgccg caggacaaat 120

tggatatgct cttgttccga tgattgctag gggaattatg cttggtgcgg accagcctgt 180

tattctgcat atgctggata ttccaccagc tgctgaagct cttaatggtg ttaagatgga 240

gttggttgat gccgcatttc cacttctcaa gggagttgtt gcaacaactg atgttgttga 300

ggcttgcact ggtgtgaatg ttgcggttat ggttggtgga ttccccagga aggagggaat 360

ggaaaggaag gatgttatgt ctaagaatgt ttcaatctac aaatctcaag catctgccct 420

tgaagcccat gcagccccga attgcaaggt tctggttgtt gccaatccag caaacaccaa 480

tgctcttatc ttaaaggagt ttgctccatc tattcctgag aagaacatca gttgtttgac 540

ccgcctagac cataacaggg cacttggtca gatctctgan agacttgatg tccaagtta 599

<210> 83
<211> 606
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (43)..(44)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (545)..(545)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (569)..(569)
<223> n is a, c, g, or t

<400> 83
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cggctccaat ggcggcgaag gaaccgatgc gcgtgctcgt caccggcgcc gcaggacaaa 120

ttggatatgc tcttgttccg atgattgcta ggggaattat gcttggtgcg gaccagcctg 180

ttattctgca tatgctggat attccaccag ctgctgaagc tcttaatggt gttaagatgg 240

agttggttga tgccgcattt ccacttctca agggagttgt tgcaacaact gatgttgttg 300

aggcttgcac tggtgtgaat gctgcggtta tggttggtgg attccccagg aaggagggaa 360

tggaaaggaa ggatgttatg tctaagaatg tttcaatcta caaatctcaa gcatctgccc 420

ttgaagccca tgcagccccg aattgcaagg ttctggttgt tgccaatcca gcaaacacca 480

atgctcttat cttaaaggag tttgctccat ctattcctga gaagaacatc agttgtttga 540

cccgnctaga ccataacagg gcactcggnc agatctctga gagacttgat gtccaagtta 600

gtgatg 606

<210> 84
<211> 686
<212> DNA
<213> Lolium perenne

<220>
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<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (33)..(33)
<223> n is a, c, g, or t

<400> 84
nttcatcccg ttgtcgtcgc ctcctcccga acnctctccc catccccgaa ctccagaacc 60

ggctccaatg gcggcgaagg aaccgatgcg cgtgctcgtc accggcgccg caggacaaat 120

tggatatgct cttgttccga tgattgctag gggaattatg ctcggtgcgg accagcctgt 180

tattctgcat atgctggata ttccaccagc tgctgaagct cttaatggtg ttaagatgga 240

gttggttgat gccgcatttc cacttctcaa gggagttgtt gcaacaactg atgttgttga 300

ggcttgcact ggtgtgaatg ttgcggttat ggttggtgga ttccccagga aggagggaat 360

ggaaaggaag gatgttatgt ctaagaatgt ttcaatctac aaatctcaag catctgccct 420

tgaagccatg cagccccgaa ttgcaaggtt ctggttgttg ccaatccagc aaacaccaat 480

gctcttatct taaaggagtt tgctccatct attcctgaga agaacatcag ttgtttgacc 540

cgcctagacc ataacagggc acttggtcag atctctgaga gacttgatgt ccaagttagt 600

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cacgccaccg tgaagacttt cagtgg 686

<210> 85
<211> 341
<212> DNA
<213> Lolium perenne

<220>
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<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
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<222> (22)..(22)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (98)..(98)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (150)..(150)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (175)..(175)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (276)..(276)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (279)..(279)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (297)..(297)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (305)..(305)
<223> n is a, c, g, or t

<400> 85
ttcatcccnt tgtcgtngcc tnctcccgaa ccactctccc cttccccgaa ctccagaacc 60

ggctccaatg gcggcgaagg aaccgatgcg cgtgctcntc accggcgccg caggacaaat 120

tggatatgct cttgttccga tgattgctan gggaattatg cttggtgcgg accancctgt 180
tattctgcat atgctggata ttccaccagc tgctgaagct cttaatggtg ttaagatgga 240
gttggttgat gccgcatttc cacttctcaa gggagntgnt gcaacaactg atgttgntga 300
ggctngcact ggtgtgaatg ttgcggttat ggatggtgga t 341

<210> 86
<211> 349
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (245)..(245)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (265)..(265)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (278)..(278)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (294)..(294)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (300)..(300)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (312)..(312)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (326)..(328)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (331)..(331)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (333)..(334)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (340)..(340)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (345)..(345)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (348)..(349)
<223> n is a, c, g, or t

<400> 86
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gctccaatgg cggcgaagga accgatgcgc gtgctcgtca ccggcgccgc aggacaaatt 120

ggatatgctc ttgttccgat gattgctagg ggaattatgc ttggtgcgga ccagcctgtt 180

attctgcata tgcaggatat tccaccagct gctgaagctc ttaatggtgt taagatggag 240

ttggntgatg ccgcatttcc acttntcaag ggagttgntg caacaactga tgtngttgan 300

gcttgcactg gngtgaatgt tgcggnnntg ncnngcccan gtaanatnn 349

<210> 87
<211> 605
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (32)..(32)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (499)..(499)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (522)..(522)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (531)..(531)
<223> n is a, c, g, or t

<220>
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<222> (559)..(559)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<221> misc_feature
<222> (584)..(584)
<223> n is a, c, g, or t

<220>
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<222> (596)..(596)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (598)..(598)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (600)..(600)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (602)..(602)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (605)..(605)
<223> n is a, c, g, or t

<400> 87
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gctccaatgg cggcgaagga accgatgcgc gtgctcgtca ccggcgccgc aggacaaatt 120

ggatatgctc ttgttccgat gattgctagg ggaattatgc ttggtgcgga ccagcccgtt 180

attctgcata tgctggatat tccaccagct gctgaagctc ttaatggtgt taagatggag 240

ttggttgatg ccgcatttcc acttctcaag ggagttgttg caacaactga tgttgttgag 300

gcttgcactg gtgtgaatgt tgcggttatg gttggtggat tccccaggaa ggagggaatg 360

gaaaggaagg atgttatgtc taagaatgtt tcaatctaca aatctcaagc atctgccctt 420

gaagcccatg cagccccgaa ttgcaaggtt ctggttgttg ccaatccagc aaacaccaat 480

gctcttatct taaaggagnt tgctccatct attcctgaga anaacatcag ntgtttgacc 540

cgcctagacc ataacaggnc actcggncag anctctgaga gacntgatgc ccaagntngn 600

gntgn 605

<210> 88
<211> 685
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<400> 88
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gatatgctct tgttccgatg attgctaggg gaattatgct tggtgcggac cagcctgtta 180
ttctgcatat gctggatatt ccaccagctg ctgaagctct taatggtgtt aagatggagt 240
tggttgatgc cgcatttcca cttctcaagg gagttgttgc aacaactgat gttgttgagg 300
cttgcactgg tgtgaatgtt gcggttatgg ttggtggatt ccccaggaag gagggaatgg 360
aaaggaagga tgttatgtct aagaatgttt caatctacaa atctcaagca tctgcccttg 420
aagcccatgc agccccgaat tgcaaggttc tggttgttgc caatccagca aacaccaatg 480
ctcttatctt aaaggagttt gctccatcta ttcctgagaa gaacatcagt tgtttgaccc 540
gcctagacca taacagggca cttggtcaga tctctgagag acttgatgtc caagttagtg 600
atgtgaagaa tgttatcatc tgggcaaatc actcttccag tcagtaccct gatgtgaacc 660
acgccaccgt gaagacttcc agtgg 685

<210> 89
<211> 763
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (4)..(4)
<223> n is a, c, g, or t

<400> 89
ctcntcccgt tgtcgtcgcc tcctcccgac cactctcccc atccccgaac tccagaaccg 60
gctccaatgg cggcgaagga accgatgcgc gtgctcgtca ccggcgccgc aggacaaatt 120
ggatatgctc ttgttccgat gattgctagg ggaattatgc ttggtgcgga ccagcctgtt 180
attctgcata tgctggatat tccaccagct gctgaagctc ttaatggtgt taagatggag 240
ttggttgatg ccgcatttcc acttctcaag ggagttgttg caacaactga tgttgttgag 300
gcttgcactg gtgtgaatgt tgcggttatg gttggtggat tccccaggaa ggagggaatg 360
gaaaggaagg atgttatgtc taagaatgtt tcaatctaca aatctcaagc atctgccctt 420
gaagcccatg cagccccgaa ttgcaaggtt ctggttgttg ccaatccagc aaacaccaat 480
gctcttatct taaaggagtt tgctccatct attcctgaga agaacatcag ttgtttgacc 540
cgcctagacc ataacagggc acttggtcag atctctgaga gacttgatgt ccaagttagt 600
gatgtgaaga atgttatcat ctgggcaaat cactcttcca gtcagtaccc tgatgtgaac 660
cacgccaccg tgaagacttc cagtggcgag aagcctgttc gcgaacttgt taaagacgat 720
gaatggctaa atgcagggtt cattgccact gtccagcagc gtg 763

<210> 90
<211> 790
<212> DNA
<213> Lolium perenne

<220>

<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<400> 90
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ctccaatggc ggcgaaggaa ccgatgcgcg tgctcgtcac cggcgccgca ggacaaattg 120

gatatgctct tgttccgatg attgctaggg gaattatgct tggtgcggac cagcctgtta 180

ttctgcatat gctggatatt ccaccagctg ctgaagctct taatggtgtt aagatggagt 240

tggttgatgc cgcatttcca cttctcaagg gagttgttgc aacaactgat gttgttgagg 300

cttgcactgg tgtgaatgtt gcggttatgg ttggtggatt ccccaggaag gagggaatgg 360

aaaggaagga tgttatgtct aagaatgttt caatctacaa atctcaagca tctgcccttg 420

aagcccatgc agccccgaat tgcaaggttc tggttgttgc caatccagca aacaccaatg 480

ctcttatctt aaaggagttt gctccatcta ttcctgagaa gaacatcagt tgtttgaccc 540

gcctagacca taacagggca cttggtcaga tctctgagag acttgatgtc caagttagtg 600

atgtgaagaa tgttatcatc tggggcaatc actcttccag tcagtaccct gatgtgaacc 660

acgccaccgt gaagacttcc agtggcgaga agcctgttcg cgaacttgtt aaagacgatg 720

aatggctaaa tgcagggttc attgccactg tccagcagcg tggtgctgca atcatcaaag 780

cgaggaagct 790

<210> 91
<211> 690
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (678)..(678)
<223> n is a, c, g, or t

<400> 91
ttctcccgtt gtcgtcgcct cctcccgacc actctcccct ccccgaactc cagaaccggc 60

tccaatggcg gcgaaggaac cgatgcgcgt gctcgtcacc ggcgccgcag gacaaattgg 120

atatgctctt gttccgatga ttgctagggg aattatgctt ggtgcggacc agcctgttat 180

tctgcatatg ctggatattc caccagctgc tgaagctctt aatggtgtta agatggagtt 240

ggttgatgcc gcatttccac ttctcaaggg agttgttgca acaactgatg ttgttgaggc 300

ttgcactggt gtgaatgttg cggttatggt tggtggattc cccaggaagg agggaatgga 360

aaggaaggat gttatgtcta agaatgtttc aatctacaaa tctcaagcat ctgcccttga 420

agcccatgca gccccgaatt gcaaggttct ggttgttgcc aatccagcaa acaccaatgc 480

tcttatctta aaggagtttg ctccatctat tcctgagaag aacatcagtt gtttgacccg 540

cctagaccat aacagggcac tcggtcagat ctctgagaga cttgatgtcc aagttagtga 600

tgtgaagaat gttatcatct ggggtaatca ctcttccagt caatacccctg atgtgaacca 660

cgccaccgtg aagacttnca gtggcgagaa 690

<210> 92
<211> 700
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (679)..(679)
<223> n is a, c, g, or t

<400> 92
ttctcccgtt gtcgtcgcct cctcccgaac cactctcccc tccccgaact ccagaaccgg 60

ctccaatggc ggcgaaggaa ccgatgcgcg tgctcgtcac cggcgccgca ggacaaattg 120

gatatgctct tgttccgatg attgctaggg gaattatgct tggtgcggac cagcctgtta 180

ttctgcatat gctggatatt ccaccagctg ctgaagctct taatggtgtt aagatggagt 240

tggttgatgc cgcatttcca cttctcaagg gagttgttgc aacaactgat gttgttgagg 300

cttgcactgg tgtgaatgtt gcggttatgg ttggtggatt ccccaggaag gagggaatgg 360

aaaggaagga tgttatgtct aagaatgttt caatctacaa atctcaagca tctgcccttg 420

aagcccatgc agccccgaat tgcaaggttc tggttgttgc caatccagca aacaccaatg 480

ctcttatctt aaaggagttt gctccatcta ttcctgagaa gaacatcagt tgtttgaccc 540

gcctagacca taacagggca ctcggtcaga tctctgagag acttgatgtc caagttagtg 600

atgtgaagaa tgttatcatc tggggtaatc actcttccag tcaataccct gatgtgaacc 660

acgccaccgt gaagacttnc agtggcgaga agcctgttcg 700

<210> 93
<211> 679
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (515)..(515)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (524)..(524)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (526)..(526)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (571)..(571)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (575)..(575)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (596)..(596)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (617)..(617)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (627)..(627)
<223> n is a, c, g, or t

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<222> (631)..(631)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (643)..(643)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (660)..(660)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (671)..(671)
<223> n is a, c, g, or t

<400> 93
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caatggcggc gaaggaaccg atgcgcgtgc tcgtcaccgg cgccgcagga caaattggat 120

atgctcttgt tccgatgatt gctaggggaa ttatgcttgg tgcggaccag cctgttattc 180

tgcatatgct ggatattcca ccagctgctg aagctcttaa tggtgttaag atggagttgg 240

ttgatgccgc atttccactt ctcaagggag ttgttgcaac aactgatgtt gttgaggctt 300

gcactggtgt gaatgttgcg gttatggttg gtggattccc caggaaggag ggaatggaaa 360

ggaaggatgt tatgtctaaa aatgtttcaa tctacaaatc tcaagcatct gcccttgaag 420

cccatgcagc cccgaattgc aaggttctgg ttgttgccaa tccagcaaac accaatgctt 480

ttatcttaaa ggagtttgct ccatctattc ctganaagaa catnanttgt ttgacccgcc 540

taaaccataa cagggcactt ggtcagatct ntganagact tgatggccaa gttagngatg 600

tgaaaaatgt tatcatntgg ggcaatnact nttccagtca gtnccctgat gtgaaccacn 660

cccccggaaa nacttccag 679

<210> 94
<211> 676
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (27)..(27)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (676)..(676)
<223> n is a, c, g, or t

<400> 94
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ggcggcgaag gaaccgatgc gcgtgctcgt caccggcgcc gcaggacaaa ttggatatgc 120

tcttgttccg atgattgcta ggggaattat gcttggtgcg gaccagcctg ttattctgca 180

tatgctggat attccaccag ctgctgaagc tcttaatggt gttaagatgg agttggttga 240

tgccgcattt ccacttctca agggagttgt tgcaacaact gatgttgttg aggcttgcac 300

tggtgtgaat gttgcggtta tggttggtgg attccccagg aaggagggaa tggaaaggaa 360

ggatgttatg tctaagaatg tttcaatcta caaatctcaa gtatctgccc ttgaagccca 420

tgcagccccg aattgcaagg ttctggttgt tgccaatcca gcaaacacca atgctcttat 480

cttaaaggag tttgctccat ctattcctga gaagaacatc agttgtttga cccgcctaga 540

ccataacagg gcacttggtc agatctctga gagacttgat gtccaagtta gtgatgtgaa 600

gaatgttatc atctggggca atcactcttc cagtcagtac cctgatgtga accacgccac 660

cgtgaagact tccagn 676

<210> 95
<211> 786
<212> DNA
<213> Lolium perenne

<400> 95
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aatggcggcg aaggaaccga tgcgcgtgct cgtcaccggc gccgcaggac aaattggata 120

tgctcttgtt ccgatgattg ctaggggaat tatgcttggt gcggaccagc ctgttattct 180

gcatatgctg gatattccac cagctgctga agctcttaat ggtgttaaga tggagttggt 240

tgatgccgca tttccacttc tcaagggagt tgttgcaaca actgatgttg ttgaggcttg 300

cactggtgtg aatgttgcgg ttatggttgg tggattcccc aggaaggagg gaatggaaag 360

gaaggatgtt atgtctaaga atgtttcaat ctacaaatct caagcatctg cccttgaagc 420

ccatgcagcc ccgaattgca aggttctggt tgttgccaat ccagcaaaca ccaatgctct 480

tatcttaaag gagtttgctc catctattcc tgagaagaac atcagttatt tgacccgcct 540

agaccataac agggcacttg gtcagatctc tgagagactt gatgtccaag ttagtgatgt 600

gaagaatgtt atcatctggg gcaatcactc ttccagtcag taccctgatg tgaaccacgc 660

caccgtgaag acttccagtg gcgagaagcc tgttcgcgaa cttgttaaag acgatgaatg 720

gctaaatgca gggttcattg ccactgtcca gcagcgtggt gctgcaatca tcaaagcgag 780

gaagct 786

<210> 96
<211> 772
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (29)..(29)
<223> n is a, c, g, or t

<400> 96
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cgcgtgctcg tcaccggcgc cgcaggacaa attggatatg ctcttgttcc gatgattgct 120

aggggaatta tgcttggtgc ggaccagcct gttattctgc atatgctgga tattccacca 180

gctgctgaag ctcttaatgg tgttaagatg gagttggttg atgccgcatt tccacttctc 240

aagggagttg ttgcaacaac tgatgttgtt gaggcttgca ctggtgtgaa tgttgcggtt 300

atggttggtg gatcccccag gaaggaggga atggaaagga aggatgttat gtctaagaat 360

gtttcaatct acaaatctca agcatctgcc cttgaagccc atgcagcccc gaattgcaag 420

gttctggttg ttgccaatcc agcaaacacc aatgctctta tcttaaagga gtttgctcca 480

tctattcctg agaagaacat cagttgtttg acccgcctag accataacag ggcacttggt 540

cagatctctg agagacttga tgtccaagtt agtgatgtga agaatgttat catctggggc 600

aatcactctt ccagtcagta ccctgatgtg aaccacgcca ccgtgaggac ttccagtggc 660

gagaagcctg ttcgcgaact tgttaaagac gatgaatggc taaatgcagg gttcattgcc 720

actgtccagc agcgtggtgc tgcaatcatc aaagcgagga agctctccag tg 772

<210> 97
<211> 676
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (36)..(36)
<223> n is a, c, g, or t

<400> 97
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cgccgcagga caaattggat atgctcttgt tccgatgatt gctaggggaa ttatgcttgg 120

tgcggaccag cctgttattc tgcatatgct ggatattcca ccagctgctg aagctcttaa 180

tggtgttaag atggagttgg ttgatgccgc atttccactt ctcaagggag ttgttgcaac 240

aactgatgtt gttgaggctt gcactggtgt gaatgttgcg gttatggttg gtggattccc 300

caggaaggag ggaatggaaa ggaaggatgt tatgtctaag aatgtttcaa tctacaaatc 360

tcaagcatct gcccttgaag cccatgcagc cccgaattgt aaggttctgg ttgttgccaa 420

tccagcaaac accaatgctc ttatcttaaa ggagtttgct ccatctattc ctgagaagaa 480

catcagttgt ttgacccgcc tagaccataa cagggcactc ggtcagatct ctgagagact 540

tgatgtccaa gttagtgatg tgaagaatgt tatcatctgg ggtaatcact cttccagtca 600

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acttgttaaa gacgat 676

<210> 98
<211> 763
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (36)..(36)
<223> n is a, c, g, or t

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atgattgcta ggggaattat gcttggtgcg gaccagcctg ttattctgca tatgctggat 120

attccaccag ctgctgaagc tcttaatggt gttaagatgg agttggttga tgccgcattt 180

ccacttctca agggagttgt tgcaacaact gatgttgttg aggcttgcac tggtgtgaat 240

gttgcggtta tggttggtgg attccccagg aaggagggaa tggaaaggaa ggatgttatg 300

tctaagaatg tttcaatcta caaatctcaa gcatctgccc ttgaagccca tgcagccccg 360

aattgcaagg ttctggttgt tgccaatcca gcaaacacca atgctcttat cttaaaggag 420

tttgctccat ctattcctga gaagaacatc agttgtttga cccgcctaga ccataacagg 480

gcacttggtc agatctctga gagacttgat gtccaagtta gtgatgtgaa gaatgttatc 540

atctggggca atcactcttc cagtcagtac cctgatgtga accacgccac cgtgaagact 600

tccagtggcg agaagcctgt tcgcgaactt gttaaagacg atgaatggct aaatgcaggg 660

ttcattgcca ctgtccagca gcgtggtgct gcaatcatca aagcgaggaa gctctccagt 720

gctctctctg ctgccagctc tgcttgtgac cacatccgtg att 763

<210> 99
<211> 513
<212> DNA
<213> Lolium perenne

<220>
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<222> (435)..(435)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (453)..(453)
<223> n is a, c, g, or t

<220>
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<222> (458)..(458)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (469)..(469)
<223> n is a, c, g, or t

<220>
<221> misc_feature
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<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (485)..(486)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (488)..(488)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (491)..(491)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (500)..(501)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (503)..(503)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (506)..(506)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (511)..(511)
<223> n is a, c, g, or t

<400> 99
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gctcttaatg gtgttaagat ggagttggtt gatgccgcat ttccacttct caagggagtt 120

gttgcaacaa ctgatgttgt tgaggcttgc actggtgtga atgttgcggt tatggttggt 180

ggattcccca ggaaggaggg agtggaaagg aaggatgtta tgtctaagaa tgtttcaatc 240

tacaaatctc aagcatctgc ccttgaagcc catgcagccc cgaattgcaa ggttctggtt 300

gttgccaatc cagcaaacac caatgctctt atcttaaagg agtttgctcc atctattcct 360

gagaagaaca tcagttgttt gacccgccta gaccataaca gggcacttgg tcagatctct 420

gagagacttg atgtncaagt tagtgatgtg aanaatgnta tcatctggnc anctcactct 480

tncanncntt nccctgatgn nanccncgcc ncg 513

<210> 100
<211> 664
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (83)..(83)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (85)..(86)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (241)..(241)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (534)..(534)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (570)..(570)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (576)..(576)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (605)..(605)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (610)..(610)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (620)..(620)
<223> n is a, c, g, or t

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<222> (640)..(640)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (650)..(650)
<223> n is a, c, g, or t

<220>
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<222> (653)..(653)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (657)..(657)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (660)..(660)
<223> n is a, c, g, or t

<400> 100
tnggttggtg gattccccag gaaggaggga atggaaagga aggatgttat gtctaagaat 60

gtttcaatct acaaatctca agngnntgcc cttgaagccc atgcagcccc gaattgcaag 120

gttctggttg ttgccaatcc agcaaacacc aatgctctta tcttaaagga gtttgctcca 180

tctattcctg agaagaacat cagttgtttg acccgcctag accataacag ggcacttggt 240

nagatctctg agagacttga tgtccaagtt agtgatgtga agaatgttat catctggggc 300

aatcactctt ccagtcagta ccctgatgtg aaccacgcca ccgtgaagac ttccagtggc 360

gagaagcctg ttcgcgaact tgttaaagac gatgaatggc taaatgcagg gttcattgcc 420

actgtccagc agcgtggtgc tgcaatcatc aaagcgagga agctttccag tgctcttttt 480

gctgccagct ctgcttgtga ccacatccgg gattgggttc tcggaacccc tganggaaca 540

tttgtttcca tgggtgtgta ttctgatggn tatacngggt gcctggtggg cttatctact 600

ccttnccagn aacttgctgn ggggggaat ggacaattgn tcaaaggctn ccnatcnacn 660

agtt 664

<210> 101
<211> 734

<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (722)..(722)
<223> n is a, c, g, or t

<400> 101
taagcatctg cccttgaagc ccatgcagcc ccgaattgca aggttctggt tgttgccaat 60

ccagcaaaca ccaatgctct tatcttaaag gagtttgctc catctattcc tgagaagaac 120

atcagttgtt tgacccgcct agaccataac agggcactcg gtcagatctc tgagagactt 180

gatgtccaag ttagtgatgt gaagaatgtt atcatctggg gtaatcactc ttccagtcaa 240

taccctgatg tgaaccacgc caccgtgaag acttccagtg gcgagaagcc tgttcgcgaa 300

cttgttaaag acgatgaatg gctaaatgca gggttcattg ccactgtcca gcagcgtggt 360

gctgcaatca tcaaagcgag gaagctctcc agtgctctct ctgctgccag ctctgcttgt 420

gaccacatcc gtgattgggt tcttggaacc cctgagggaa catttgtttc catgggtgtg 480

tattctgatg gttcatacgg tgtgcctgct gggcttatct actccttccc agtaacttgc 540

tgcggtggtg aatggacaat tgttcaaggg ctcccgatcg acgagttctc aagaaagaag 600

atggatgcca cagcccagga gctctcggag gagaaggctc tcgcctactc gtgcctcgag 660

taactgcata ccagggagca gctgccgctc tgatgttttg aataaaagga acattttggc 720

tncatgaaac tcat 734

<210> 102
<211> 705
<212> DNA
<213> Lolium perenne

<220>
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<222> (14)..(14)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<220>
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<222> (456)..(456)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (608)..(608)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (689)..(689)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (698)..(698)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (701)..(701)
<223> n is a, c, g, or t

<400> 102
ccatgcaacc ccgnantgca aggttctggt tgttgccaat ccagcaaaca ccaatgctct 60

tatcttaaag gagtttgctc catctattcc tgagaagaac atcagttgtt tgacccgcct 120

agaccataac agggcacttg gtcagatctc tgagagactt gatgtccaag ttagtgatgt 180

gaagaatgtt atcatctggg gcaatcactc ttccagtcag taccctgatg tgaaccacgc 240

caccgtgaag acttccagtg gcgagaagcc tgttcgcgaa cttgttaaag acgatgaatg 300

gctaaatgca gggttcattg ccactgtcca gcagcgtggt gctgcaatca tcaaagcgag 360

gaagctctcc agtgctctct ctgctgccag ctctgcttgt gaccacatcc gtgattgggt 420

tctcggaacc cctgagggaa catttgtttc catggntgtg tattctgatg gttcatacgg 480

tgtgcctgct gggcttatct actccttccc agtaacttgc tgcggtggtg aatggacaat 540

tgttcaaggg ctcccgatcg acgagttctc aagaaagaag atggatgcca cagcccagga 600

gctctcgnag gagaaggctc tcgcctactc gtgcctcgag taactgcata ccagggagca 660

gctgtcgctc tgatgttttg aataaaagna cattttgnct ncatg 705

<210> 103
<211> 667
<212> DNA
<213> Lolium perenne

<400> 103
tgcagccccg attgcaaggt tctggttgtt gccaatccag caaacaccaa tgctcttatc 60

ttaaaggagt ttgctccatc tattcctgag aagaacatca gttgtttgac ccgcctagac 120

cataacaggg cacttggtca gatctctgag agacttgatg tccaagttag tgatgtgaag 180

aatgttatca tctggggcaa tcactcttcc agtcagtacc ctgatgtgaa ccacgccacc 240

gtgaagactt ccagtggcga gaagcctgtt cgcgaacttg ttaaagacga tgaatggcta 300

aatgcagggt tcattgccac tgtccagcag cgtggtgctg caatcatcaa agcgaggaag 360

ctctccagtg ctctctctgc tgccagctct gcttgtgacc acatccgtga ttgggttctc 420

ggaacccctg agggaacatt tgtttccatg ggtgtgtatt ctgatggttc atacggtgtg 480

cctgctgggc ttatctactc cttcccagta acttgctgcg gtggtgaatg gacaattgtt 540

caagggctcc cgatcgacga gttctcaaga aagaagatgg atgccacagc ccaggagctc 600

tcggaggaga aggctctcgc ctactcgtgc ctcgagtaac tgcataccag ggagcagctg 660

ccgctct 667

<210> 104

<211> 748
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (28)..(28)
<223> n is a, c, g, or t

<400> 104
gcaatcactc ttccagtcag taccctgngt gaaccacgcc accgtgaaga cttccagtgg 60

cgagaagcct gttcgcgaac ttgttaaaga cgatgaatgg ctaaatgcag ggttcattgc 120

cactgtccag cagcgtggtg ctgcaatcat caaagcgagg aagctctcca gtgctctctc 180

tgctgccagc tctgcttgtg accacatccg tgattgggtt ctcggaaccc ctgagggaac 240

atttgtttcc atgggtgtgt attctgatgg ttcatacggt gtgcctgctg ggcttatcta 300

ctccttccca gtaacttgct gcggtggtga atggacaatt gttcaagggc tcccgatcga 360

cgagttctca agaaagaaga tggatgccac agcccaggag ctctcggagg agaaggctct 420

cgcctactcg tgcctcgagt aactgcatac cagggagcag ctgccgctct gatgttttga 480

ataaaaggaa cattttggct ccatgaaact catctccact cagaacagtt gcacatcgcg 540

gtgcctttag ctggtttttc cagtgtgtat gaatgaggct tttgtagctc tattttcgcc 600

tgatgattta caggacagga tattggcagg aagattggaa caatttgacg tctgattaaa 660

accaacctct tattattccc gtgtgtatga atgaggcttt tgtagctcta ttttcgcctg 720

atgatttaca ggccatgata ttggcagg 748

<210> 105
<211> 646
<212> DNA
<213> Lolium perenne

<400> 105
gtaccctgat gtgaaccacg ccaccgtgaa gacttccagt ggcgagaagc ctgttcgcga 60

acttgttaaa gacgatgaat ggctaaatgc agggttcatt gccactgtcc agcagcgtgg 120

tgctgcaatc atcaaagcga ggaagctctc cagtgctctc tctgctgcca gctctgcttg 180

tgaccacatc cgtgattggg ttctcggaac ccctgaggga acatttgttt ccatgggtgt 240

gtattctgat ggttcatacg gtgtgcctgc tgggcttatc tactccttcc cagtaacttg 300

ctgcggtggt gaatggacaa ttgttcaagg gctcccggtc gacgagttct caagaaagaa 360

gatggatgcc acagcccagg agctctcgga ggagaaggct cttgcctact cgtgcctcga 420

gtaactgcat accagggagc agctgccgct ctgatgtttt gaataaaagg aacattttgg 480

ctccatgaaa ctcatctcca ctcagaacag ttgcacatcg cggtgccttt agctggtttt 540

tccagtgtgt atgaatgagg cttttgtagc tctattttcg cctgatgatt tacaggacag 600

gatattggca ggaagattgg aacaatttga cgtctgatta aaacca 646

<210> 106

<211> 750
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (4)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (82)..(82)
<223> n is a, c, g, or t

<400> 106
ttcngtggca agagcctgtt cgcgacttgt taaagacgat gaatggctaa atgcagggtt 60

cattgccact gtccagcagc gnggtgctgc aatcatcaaa gcgaggaagc tctccagtgc 120

tctctctgct gccagctctg cttgtgacca catccgtgat tgggttctcg gaacccctga 180

gggaacattt gtttccatgg gtgtgtattc tgatggttca tacggtgtgc ctgctgggct 240

tatctactcc ttcccagtaa cttgctgcgg tggtgaatgg acaattgttc aagggctccc 300

gatcgacgag ttctcaagaa agaagatgga tgccacagcc caggagctct cggaggagaa 360

ggctctcgcc tactcgtgcc tcgagtaact gcataccagg gagcagctgc cgctctgatg 420

ttttgaataa aaggaacatt ttggctccat gaaactcatc tccactcaga acagttgcac 480

atcgcggtgc cttcagctgg tttttccagt gtgtatgaat gaggcttttg tagctctatt 540

ttcgcctgat gatttacagg acaggatatt ggcaggaaga ttggaacaat ttgacgtctg 600

attaaaacca acctcttatt attcctgtgt gtatgaatga ggcttttgta gctctatttt 660

cgcctgatga tttacaggcc atgatattgg caggaggatt ggaacaattt gacgcctgat 720

taaaaccaac ctcttattac taaaaaaaaa 750

<210> 107
<211> 616
<212> DNA
<213> Lolium perenne

<400> 107
gcgagaagcc tgttcgcgaa cttgttaaag acgatgaatg gctaaatgca gggttcattg 60

ccactgtcca gcagcgtggt gctgcaatca tcaaagcgag gaagctctcc agtgctctct 120

ctgctgccag ctctgcttgt gaccacatcc gtgattgggt tctcggaacc cctgagggaa 180

catttgtttc catgggtgtg tattctgatg gttcatacgg tgtgcctgct gggcttatct 240

actccttccc agtaacttgc tgcggtggtg aatggacaat tgttcaaggg ctcccgatcg 300

acgagttctc aagaaagaag atggatgcca cagcccagga gctctcggag gagaaggctc 360

tcgcctactc gtgcctcgag taactgcata ccagggagca gctgccgctc tgatgttttg 420

aataaaagga acattttggc tccatgaaac tcatctccac tcagaacagt tgcacatcgc 480

ggtgccttta gctggttttt ccagtgtgta tgaatgaggc ttttgtagcg ctattttcgc 540

ctgatgattt acaggacagg atattggcag gaagattgga acaatttgac gtctgattaa 600

aaccaacctc ttatta 616

<210> 108
<211> 418
<212> DNA
<213> Lolium perenne

<220>
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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (223)..(223)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (412)..(413)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (415)..(415)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (417)..(418)
<223> n is a, c, g, or t

<400> 108
ccttcccgaa acccgagttc tcttttagag aggacgccac agcccaggag ctctcggagg 60

agaaggttnt cgcctactcg ggcctcgagt aactgcatac cagggagcag ctgccgctct 120

gatgttttga ataaaaggaa cattttggct ccatgaaact catctccact cagaacagtt 180

gcacatcgcg gtgcctttag ctggtttttc cagtgtgtat gantgaggct tttgtagctc 240

tattttcgcc tgatgattta caggacagga tattggcagg aagattggaa caatttgacg 300

tctgattaaa accaacctct tattattcct gtgtgtatga atgaggcttt tgtagctcta 360

ttttcgcctg atgatttaca ggacatgata ttggcaggag gattggaaca annanann 418

<210> 109
<211> 265
<212> DNA
<213> Lolium perenne

<400> 109
cctcggagga gaaggctctc gcctactcgt gcctcgagta actgcatacc agggagcagc 60

tgccgctctg atgttttgaa taaaaggaac attttggctc catgaaactc atctccactc 120

agaacagttg cacatcgcgg tgcctttagc tggtttttcc agtgtgtatg aatgaggctt 180

ttgtagctct attttcgcct gatgatttac aggacaggat attggcagga agattggaac 240

aatttgacgt ctgacaaaaa aaaaa 265

<210> 110
<211> 236
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (33)..(33)
<223> n is a, c, g, or t

<400> 110
gnaagnagct tttgtagctc tattttcgcc tgnagattta caggacagga tattggcagg 60

aagattggaa caatttgacg tctgattaaa accaacctct tatattcctg tgtgtatgaa 120

tgaggctttt gtagctctat tttcgcctga tgatttacag gccacgatat tggcaggagg 180

attggaacaa tttgacgcct gattaaaacc aacctcttat tattctaaaa aaaaaa 236

<210> 111
<211> 177
<212> DNA
<213> Lolium perenne

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<222> (3)..(3)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (25)..(25)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (30)..(30)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (106)..(106)
<223> n is a, c, g, or t

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<222> (133)..(133)
<223> n is a, c, g, or t

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<222> (137)..(137)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (142)..(143)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (145)..(145)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (155)..(155)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (163)..(163)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (165)..(166)
<223> n is a, c, g, or t

<220>
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<222> (168)..(168)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (175)..(175)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (177)..(177)
<223> n is a, c, g, or t

<400> 111
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gtaccaattg ctgctgaagt atttaaaaaa gctgggacat acaatnctaa gagattgttg 120

ggggttgaca acngttngat gnnantgaca gaccntgctc ttngnngncg aggtncn 177

<210> 112
<211> 58
<212> PRT
<213> Lolium perenne

<220>
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<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (9)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (36)..(36)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (45)..(46)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (48)..(49)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (52)..(52)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (55)..(56)
<223> Xaa can be any naturally occurring amino acid

<400> 112

Xaa His Lys Ala Ala Gln Ser Asn Xaa Xaa Asn Ile Ile Ser Asn Pro
1 5 10 15

Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val Phe Lys Lys Ala Gly
20 25 30

Thr Tyr Asn Xaa Lys Arg Leu Leu Gly Val Asp Asn Xaa Xaa Met Xaa
35 40 45

Xaa Thr Asp Xaa Ala Leu Xaa Xaa Arg Gly
50 55

<210> 113
<211> 664
<212> DNA
<213> Lolium perenne

<220>
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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (40)..(40)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (568)..(568)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (582)..(582)
<223> n is a, c, g, or t

<400> 113
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ggacatggcg tcagctgtta caatcagttc agtcagcgcg caggccgctt tggtttcaaa 120

accaaggaac catggcagca cgagctacag tggcctaaag gcatcatcgt cgtcgatcag 180

cttcgaatca ggaacatcat tcctgggcaa gaccgcctcc ctccgggcaa ctgttaccac 240

aagggttgtg ccaaaggcga agtctgggtc gcagatatcg cctcaggcat cttacaaggt 300

ggcggtgctt ggtgctgctg gtggcatcgg tcaaccactg ggcctgctga tcaagatgtc 360

tcctctggtc tcggagctgc gcctgtatga tatcgcgaat gtcaagggcg tcgctgcaga 420

tctcagccac tgcaacacgc ctgctcaggt catggacttc actggccccg cagagctagc 480

agagtgcttg aaaggtgtgg atgttgtcgt catccctgcg ggtgtcccaa ggaagccagg 540

catgacccgt gatgaccttt ttaacatnaa tgcgggaatc gncaagtcgc ttattgaggc 600

tgttgcagac aattgccctg agggccttat tcatatcatc aacaaccccg gtcaaactcc 660

ccct 664

<210> 114
<211> 221
<212> PRT
<213> Lolium perenne

<220>
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<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (13)..(13)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (189)..(189)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (194)..(194)
<223> Xaa can be any naturally occurring amino acid

<400> 114

Xaa Arg Ser Arg Arg Arg Gly Ala Glu Phe His Leu Xaa Thr Leu Pro
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Pro Pro Lys Leu Asp Met Ala Ser Ala Val Thr Ile Ser Ser Val Ser
            20   25   30

Ala Gln Ala Ala Leu Val Ser Lys Pro Arg Asn His Gly Ser Thr Ser
        35   40   45

Tyr Ser Gly Leu Lys Ala Ser Ser Ser Ser Ile Ser Phe Glu Ser Gly
    50   55   60

Thr Ser Phe Leu Gly Lys Thr Ala Ser Leu Arg Ala Thr Val Thr Thr
65   70   75   80

Arg Val Val Pro Lys Ala Lys Ser Gly Ser Gln Ile Ser Pro Gln Ala
85 90 95

Ser Tyr Lys Val Ala Val Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro
100 105 110

Leu Gly Leu Leu Ile Lys Met Ser Pro Leu Val Ser Glu Leu Arg Leu
115 120 125

Tyr Asp Ile Ala Asn Val Lys Gly Val Ala Ala Asp Leu Ser His Cys
130 135 140

Asn Thr Pro Ala Gln Val Met Asp Phe Thr Gly Pro Ala Glu Leu Ala
145 150 155 160

Glu Cys Leu Lys Gly Val Asp Val Val Val Ile Pro Ala Gly Val Pro
165 170 175

Arg Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Asn Xaa Asn Ala Gly
180 185 190

Ile Xaa Lys Ser Leu Ile Glu Ala Val Ala Asp Asn Cys Pro Glu Gly
195 200 205

Leu Ile His Ile Ile Asn Asn Pro Gly Gln Thr Pro Pro
210 215 220

<210> 115
<211> 1263
<212> DNA
<213> Lolium perenne

<220>
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<223> n is a, c, g, or t

<220>
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<222> (7)..(7)
<223> n is a, c, g, or t

<220>
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<222> (11)..(11)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<220>
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<222> (59)..(60)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (67)..(67)
<223> n is a, c, g, or t

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<222> (1179)..(1179)
<223> n is a, c, g, or t

<220>
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<222> (1242)..(1242)
<223> n is a, c, g, or t

<400> 115
tntttanccc nccaantatc cagnanccac ctggccctac acanaanaaa aacaaaaann 60

aaccagnacg caaggggcga gccggggcgc acgcagcaat tcccatctgc tcaccaaccc 120

aagttggaga tggcatcagc tgttaccatc agctcagtca gcgcgcaggc cgctttggtc 180

tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc taaaggcatc atcatcgtcg 240

atcagcttcg aatcagggac atcattcctg ggcaagaccg cctctcttcg ggcgactatc 300

acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga tatcacctca ggcctcgtac 360

aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac cactgggcct gctgatcaag 420

atgtctcctc tggtctcaga gctgcgcctg tatgatattg ccaatgtcaa gggagtcgct 480

gcagatctca gccactgcaa cacgccttct caggtcatgg acttcactgg cccagcagaa 540

ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc ctgcgggtgt cccaaggaag 600

ccaggcatga cccgtgatga cctttttaac atcaatgcgg gcatcgtcaa gtcgcttatt 660

gaggctgttg cagacaactg ccctgaggcc ttcatccata tcatcagcaa cccggtcaac 720

tccactgtgc cgattgctgc tgagattctg aaacagaagg gcgtctacaa ccccaagaag 780

ctcttcgggg tttccaccct ggatgttgtc agagctaaca catttgtagc tcagaagaag 840

aacctcagcc tcatcgatgt tgatgtccca gttgtcggtg gccatgctgg gatcacgatt 900

ctgcctctgt tgtccaagac taggccttct gtcagcttca cggacgagga aactgaacag 960

ctgacaaaga ggatacagaa cgctgggaca gaggcggtgg aggcgaaggc tggtgctggc 1020

tctgctactc tgtccatggc ttatgccgct gccagatttg ttgagtcatc gctccgcgca 1080

atggctggtg atccagatgt ttacgagtgc acgtatgttc agtctgagtt aacagagctt 1140

ccattcttcg cgtccagagt taagcttggg aaggacggng ttgagtccat catttcctcc 1200

gacctggagg gagtgacgga gtacgaggcc aaggcgcttg angcattgaa ggctgagctg 1260

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<400> 116

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Lys Thr Lys Xaa Asn Gln Xaa Ala Arg Gly Glu Pro Gly Arg Thr Gln
20 25 30

Gln Phe Pro Ser Ala His Gln Pro Lys Leu Glu Met Ala Ser Ala Val
35 40 45

Thr Ile Ser Ser Val Ser Ala Gln Ala Ala Leu Val Ser Lys Pro Arg
50 55 60

Asn His Gly Ser Thr Ser Tyr Ser Gly Leu Lys Ala Ser Ser Ser Ser
65 70 75 80

Ile Ser Phe Glu Ser Gly Thr Ser Phe Leu Gly Lys Thr Ala Ser Leu
85 90 95

Arg Ala Thr Ile Thr Ser Arg Ile Val Pro Lys Ala Lys Ser Gly Ser
100 105 110

Gln Ile Ser Pro Gln Ala Ser Tyr Lys Val Ala Val Leu Gly Ala Ala
115 120 125

Gly Gly Ile Gly Gln Pro Leu Gly Leu Leu Ile Lys Met Ser Pro Leu
130 135 140

Val Ser Glu Leu Arg Leu Tyr Asp Ile Ala Asn Val Lys Gly Val Ala
145 150 155 160

Ala Asp Leu Ser His Cys Asn Thr Pro Ser Gln Val Met Asp Phe Thr
165 170 175

Gly Pro Ala Glu Leu Ala Asp Cys Leu Lys Gly Val Asp Val Val Val
180 185 190

Ile Pro Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg Asp Asp Leu
195 200 205

Phe Asn Ile Asn Ala Gly Ile Val Lys Ser Leu Ile Glu Ala Val Ala
210 215 220

Asp Asn Cys Pro Glu Ala Phe Ile His Ile Ile Ser Asn Pro Val Asn
225 230 235 240

Ser Thr Val Pro Ile Ala Ala Glu Ile Leu Lys Gln Lys Gly Val Tyr
245 250 255

Asn Pro Lys Lys Leu Phe Gly Val Ser Thr Leu Asp Val Val Arg Ala
260 265 270

Asn Thr Phe Val Ala Gln Lys Lys Asn Leu Ser Leu Ile Asp Val Asp

275 280 285

Val Pro Val Val Gly Gly His Ala Gly Ile Thr Ile Leu Pro Leu Leu
290 295 300

Ser Lys Thr Arg Pro Ser Val Ser Phe Thr Asp Glu Glu Thr Glu Gln
305 310 315 320

Leu Thr Lys Arg Ile Gln Asn Ala Gly Thr Glu Ala Val Glu Ala Lys
325 330 335

Ala Gly Ala Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Ala Ala Arg
340 345 350

Phe Val Glu Ser Ser Leu Arg Ala Met Ala Gly Asp Pro Asp Val Tyr
355 360 365

Glu Cys Thr Tyr Val Gln Ser Glu Leu Thr Glu Leu Pro Phe Phe Ala
370 375 380

Ser Arg Val Lys Leu Gly Lys Asp Xaa Val Glu Ser Ile Ile Ser Ser
385 390 395 400

Asp Leu Glu Gly Val Thr Glu Tyr Glu Ala Lys Ala Leu Xaa Ala Leu
405 410 415

Lys Ala Glu Leu Lys
420

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ccagnacgca aggggcgagc cggggcgcac gcagcaattc ccatctgctc accaacccaa 120

gttggagatg gcatcagctg ttaccatcag ctcagtcagc gcgcaggccg ctttggtctc 180

gaaaccaagg aatcatggca gcacaagcta cagtggccta aaggcatcat catcgtcgat 240
cagcttcgaa tcagggacat cattcctggg caagaccacc tctcttcggg cgactatcac 300
ctcaaggatt gtgccaaagg caaagtctgg gtctcagata tcacctcagg cctcgtacaa 360
ggtggcggtg cttggtgctg acggtggcat cggtcaacca ctgggcctgc tgatcaagat 420
gtctcctctg gtctcagagc tgcgcctgta tgatattgac aatgtcaagg gagtcgctgc 480
agatctcagn cactgcaaca cgccttctca ggtcatggac ttcactggcc cagcagaact 540
agctgactgc ttgaaaggtg ttgatgttgt cgncatccct gcgggtgtnc caaggaagcc 600
agncatgacc cgtgatgacc tttttaacat caatgcgggc atcgnnaagt cgcttattga 660
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<210> 118
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gcaattccca tctgctcacc aacccaagtt ggagatggca tcagctgtta ccatcagctc 120
agtcagcgcg caggccgctt tggtctcgaa accaaggaat catggcagca caagctacag 180
tggcctaaag gcatcatcat cgtcgatcag cttcgaatca gggacatcat tcctgggcaa 240
gaccgcctct cttcgggcga ctatcacctc aaggattgtg ccaaaggcaa agtctgggtc 300
tcagatatca cctcaggcct cgtacaaggt ggcggtgctt ggtgctgccg gtggcatcgg 360
tcaaccactg ggcctgctga tcaagatgtc tcctctggtc tcagagctgc gcctgtatga 420
tattgccaat gtcaagggag tcgctgcaga tctcagccac tgcaacacgc cttctcaggt 480

catggacttc actggcccag cagaactagc tgactgcttg aaaggtgttg atgttgtcgt 540

catccctgcg ggtgtcccaa ggaagccagg catgacccgt gatgaccttt ttaacatcaa 600

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cggtcagcgc gcagtccgct ctggtttcga aaccaaggaa tcatggcagc acgagcttcg 180

gtggcctaaa ggcatcatcg gcgtcgatca gctttgaatc agggacatcg ttcctgggca 240

agactgcctc cctccgggcg actgttaccc caaggattgt gccaaaggca aagtctgggt 300

ctcagatatc gcctcaggca tcttacaagg tggcggtgct tggtgctgct ggtggcatcg 360

gccaaccact gggcctgctg atcaagatgt ctcctctagt ctcagagctg cgcctgtatg 420

atattgccaa tgtcaagggc gtcgctgcag atcttagcca ctgcaacacg ccttctcagg 480

tcatggactt cactggcccc gcggaactag ccgactgctt gaaaggtgtg gatgttgtcg 540

tcatccctgc gggtgtccca aggaagcctg gcatgactcg tgatgacctt tttaacatca 600

atgcgggcat cgtcaagtcg cttatcgagg ctgttgcaga caactgccct gaggccttca 660

tccatatcat cagcaacccg gtcaactcca cggtgccgat tgctgctgag attctgaaac 720

agaagggcgt ctacaacccc aagaagctct tcggggtttn caccctggat gttgtcagag 780

ctaacacatt tgtagctcan a 801

<210> 120
<211> 692
<212> DNA
<213> Lolium perenne

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<223> n is a, c, g, or t

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caattcccat ctgctcacca acccaagttg gagatggcat cagctgttac catcagctca 120
gtcagcgcgc aggccgcttt ggtctcgaaa ccaaggaatc atggcagcac aagctacagt 180
ggcctaaagg catcatcatc gtcgatcagc ttcgaatcag ggacatcatt cctgggcaag 240
accgcctctc ttcgggcgac tatcacctca aggattgtgc caaaggcaaa gtctgggtct 300
cagatatcac ctcaggcctc gtacaaggtg gcggtgcttg gtgctgccgg tggcatcggt 360
caaccactgg gcctgctgat caagatgtct cctctggtct cagagctgcg cctgtatgat 420
attgccaatg tcaagggagt cgctgcagat ctcagccact gcaacacgcc ttctcaggtc 480
atggacttca ctggcccagc agaactagct gactgcttga aaggtgttga tgttgtcgtc 540
atccctgcgg gtgtctcaag gaagccaggc atgacccgtg atgacctttt taacatcaat 600
gcgggcatcg tcaagtcgct tattgaggct gntgcagaca actgccctga ggccttcatc 660
catatcatca gcaacccggt caactncact gt 692

<210> 121

<211> 695
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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gcaattccca tctgctcacc aacccaagtt ggagatggca tcagctgtta ccatcagctc 120

agtcagcgcg caggccgctt tggtctcgaa accaaggaat catggcagca caagctacag 180

tggcctaaag gcatcatcat cgtcgatcag cttcgaatca gggacatcat tcctgggcaa 240

gaccgcctct cttcgggcga ctatcacctc aaggattgtg ccaaaggcaa agtctgggtc 300

tcagatatca cctcaggcct cgtacaaggt ggcggtgctt ggtgctgccg gtggcatcgg 360

tcaaccactg ggcctgctga tcaagatgtc tcctctggtc tcagagctgc gcctgtatga 420

tattgccaat gtcaagggag tcgctgcaga tctcagccac tgcaacacgc cttctcaggt 480

catggacttc actggcccag cagaactagc tgactgcttg aaaggtgttg atgttgtcgt 540

catccctgcg ggtgtcccaa ggaagccagg cacgacccgt gatgaccttt ttaacatcaa 600

tgcgggcatc gtcaagtcgc ttattgaggc tgttgcagac aactgccctg aggccttcat 660

ccatatcatc agcaacccgg tcaactncac tgtga 695

<210> 122
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caattcccat ctgctcacca acccaagttg gacatggcat cagctgttac catcagttcg 120

gtcagcgcgc agtccgctct ggtttcgaaa ccaaggaatc atggcagcac gagcttcggt 180

ggcctaaagg catcatcggc gtcgatcagc tttgaatcag ggacatcgtt cctgggcaag 240

actgcctccc tccgggcgac tgttacccca aggattgngc caaaggcaaa gtctgggtct 300

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<210> 123
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<223> n is a, c, g, or t

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attcccatct gctcaccaac ccaagttgga gatggcatca gctgttacca tcagctcagt 120

cagcgcgcag gccgctttgg tctcgaaacc aaggaatcat ggcagcacaa gctacagtgg 180

cctaaaggca tcatcatcgt cgatcagctt cgaatcaggg acatcattcc tgggcaagac 240

cgcctctctt cgggcgacta tcacctcaag gattgtgcca aaggcaaagt ctgggtctca 300

gatatcacct caggcctcgt acaaggtggc ggtgcttggt gctgccggtg gcatcggtca 360

accactgggc ctgctgatca agatgtctcc tctggtctca gagctgcgcc tgtatgatat 420

tgccaatgtc aagggagtcg ctgcagatct cagccactgg aacacgcctt ctcaggtcat 480

ggacttgact ggcccagcag aactagctga ctgcttgaaa ggtgctgatg ttgncngcat 540

ccctgcggnn gtcncaagga a 561

<210> 124
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aattcccatc tgctcaccaa cccaagttgg agatggcatc agctgttacc atcagctcag 120

tcagcgcgca ggccgctttg gtctcgaaac caaggaatca tggcagcaca agctacagtg 180

gcctaaaggc atcatcatcg tcgatcagct tcgaatcagg gacatcattc ctgggcaaga 240

ccgcctctct tcgggcgact atcacctcaa ggattgtgcc aaaggcaaag cctgggtctc 300

agatatcacc tcaggcctcg tacaaggtgg cggtgcttgg tgctgccggt ggcatcggtc 360

aaccactggg cctgctgatc aagatgtctc ctctggtctc agagctgcgc ctgtatgata 420

ttgccaatgt caagggagtc gctgcagatc tcagccactg caacacgcct tctcaggtca 480

tggacttcac tggcccagca gaactagctg actgcttgaa aggtgttgat gttgtcgtca 540

tccctgcggg tgtcccaagg aagccaggca tgacccgtga tgaccttttt aacatcaatg 600

cgggcatcgt caagtcgctt attgaggctg ttgcagacaa ctcccctgag gccttcatc 659

<210> 125
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<220>
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<223> n is a, c, g, or t

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aattcccatc tgctcaccaa cccaagttgg agatggcatc agctgttacc atcagctcag 120

tcagcgcgca ggccgctttg gtctcgaaac caaggaatca tggcagcaca agctacagtg 180

gcctaaaggc atcatcatcg tcgatcagct tcgaatcagg gacatcattc ctgggcaaga 240

ccgcctctct tcgggcgact atcacctcaa ggattgtgcc aaaggcaaag tctgggtctc 300

agatatcacc tcaggcctcg tacaaggtgg cggtgcttgg tgctgccggt ggcatcggtc 360

aaccactggg cctgctgatc aagatgtctc ctctggtctc agagctgcgc ctgtatgata 420

ttgccaatgt caagggagtc gctgcagatc tcagccactg caacacgcct tctcaggtca 480

tggacttcac tggcccagca gaactagctg gctgcttgaa aggtgttgat gttgtcgtca 540

tccctgcggg tgtcccaagg aagccaggca tgacccgtga tgaccttttt aacatcaatg 600

cgggcatcgt caagtcgctt attgaggctg ttgcagacaa ctgccctgag gccttcatcc 660

atatcatcag caacccggtc aactncactg tgccgattgc tgctga 706

<210> 126
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<212> DNA
<213> Lolium perenne

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<223> n is a, c, g, or t

<220>
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<222> (11)..(12)
<223> n is a, c, g, or t

<220>
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<222> (24)..(25)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (31)..(31)
<223> n is a, c, g, or t

<400> 126
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attcccatct gctcaccaac ccaagttgga gatggcatca gctgttacca tcagctcagt 120
cagcgcgcag gccgctttgg tctcgaaacc aaggaatcat ggcagcacaa gctacagtgg 180
cctaaaggca tcatcatcgt cgatcagctt cgaatcaggg acatcattcc tgggcaagac 240
cgcctctctt cgggcgacta tcacctcaag gattgtgcca aaggcaaagt ctgggtctca 300
gatatcacct caggcctcgt acaaggtggc ggtgcttggt gctgccggtg gcatcggtca 360
accactgggc ctgctgatca agatgtctcc tctggtctca gagctgcgcc tgtatgatat 420
tgccaatgtc aagggagtcg ctgcagatct cagccactgc aacacgcctt ctcaggtcat 480
ggacttcact ggcccagcag aactagctga ctgcttgaaa ggtgttgatg ttgtcgtcat 540
ccctgcgggt gtcccaagga agccaggcat gacccgtgat gacctttttta acatcaatgc 600
gggcatcgtc aagtcgctta ttgaggctgt tgcagacaac tgccctgagg ccttcatcca 660
tatcatcagc aacccggtca actccactgt gccgattgct gctgaa 706

<210> 127
<211> 802
<212> DNA
<213> Lolium perenne

<220>
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<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (30)..(30)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (89)..(89)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (242)..(242)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (726)..(726)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (798)..(798)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (801)..(801)
<223> n is a, c, g, or t

<400> 127
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ttcccatctg ctcaccaacc caagttggnc atggcatcag ctgttaccat cagttcggtc 120

agcgcgcagt ccgctctggt ttcgaaacca aggaatcatg gcagcacgag cttcggtggc 180

ctaaaggcat catcggcgtc gatcagcttt gaatcaggga catcgttcct gggcaagact 240

gnctccctcc gggcgactgt taccccaagg attgtgccaa aggcaaagtc tgggtctcag 300

atatcgcctc aggcatctta caaggtggcg gtgcttggtg ctgctggtgg catcggtcaa 360

ccactgggcc tgctgatcaa gatgtctcct ctggtctcag agctgcgcct gtatgatatt 420

gccaatgtca agggcgtcgc tgcagatctt agccactgca acacgccttc tcaggtcatg 480

gacttcactg gccccgcgga actagccgac tgcttgaaag gtgtggatgt tgtcgtcatc 540

cctgcgggtg tcccaaggaa gcctggcatg actcgtgatg acctttttaa catcaatgcg 600

ggcatcgtca agtcgcttat cgaggctgtt gcagacaact gccctgaggc cttcatccat 660

atcatcagca acccggtcaa ctccacggtg ccgattgctg ctgagattct gaaacagaag 720

ggcgtntaca accccaagaa gctcttcggg gtttccaccc tggatgttgt cagagctaac 780

acatttgtag ctcaaaanaa na 802

<210> 128
<211> 691
<212> DNA
<213> Lolium perenne

<220>
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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(19)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (24)..(25)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (31)..(32)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (658)..(658)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (684)..(684)
<223> n is a, c, g, or t

<400> 128
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attcccatct gctcaccaac ccaagttggg catggcatca gctgttacca tcagctcagt 120

cagcgcgcag gccgctttgg tctcgaaacc aaggaatcat ggcagcacaa gctacagtgg 180

cctaaaggca tcatcatcgt cgatcagctt cgaatcaggg acatcattcc tgggcaagac 240

cgcctctctt cgggcgacta tcacctcaag gattgtgcca aaggcaaagt ctgggtctca 300

gatatcacct caggcctcgt acaaggtggc ggtgcttggt gctgccggtg gcatcggtca 360

accactgggc ctgctgatca agatgtctcc tctggtctca gagctgcgcc tgtatgatat 420

tgccaatgtc aagggagtcg ctgcagatct cagccactgc aacacgcctt ctcaggtcat 480

ggacttcact ggcccagcag aactagctga ctgcttgaaa ggtgttgatg ttgtcgtcat 540

ccctgcgggt gtcccaagga agccaggcat gacccgtgat gaccttttta acatcaatgc 600

gggcatcgtc aagtcgctta ttgaggctgt tgcagacaac tgccctgagg ccttcatnca 660

tatcatcagc aacccggtca actncactgt g 691

<210> 129
<211> 705
<212> DNA
<213> Lolium perenne

<220>
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<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (24)..(24)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (30)..(30)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (36)..(36)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (217)..(217)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (629)..(629)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (683)..(683)
<223> n is a, c, g, or t

<400> 129
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ttcccatctg ctcaccaacc caagttggag atggcatcag ctgttaccat cagctcagtc 120

agcgcgcagg ccgctttggt ctcgaaacca aggaatcatg gcagcacaag ctacagtggc 180

ctaaaggcat catcatcgtc gatcagcttc gaatcangga catcattcct gggcaagacc 240

gcctctcttc gggcgactat cacctcaagg attgtgccaa aggcaaagtc tgggtctcag 300

atatcacctc aggcctcgta caaggtggcg gtgcttggtg ctgccggtgg catcggtcaa 360

ccactgggcc tgctgatcaa gatgtctcct ctggtctcag agctgcgcct gtatgatatt 420

gccaatgtca agggagtcgc tgcagatctc agccactgca acacgccttc tcaggtcatg 480

gacttcactg gcccagcaga actagctgac tgcttgaaag gtgttgatgt tgtcgtcatc 540

cctgcgggtg tctcaaggaa gccaggcatg acccgtgatg acctttttaa catcaatgcg 600

ggcatcgtca agtcgcttat tgaggctgnt gcagacaact gccctgaggc cttcatccat 660

atcatcagca acccggtcaa ctncactgtg ccgattgctg ctgag 705

<210> 130
<211> 680
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(22)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (28)..(28)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (656)..(656)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (680)..(680)
<223> n is a, c, g, or t

<400> 130
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tcccatctgc tcaccaaccc aagttggaga tggcatcagc tgttaccatc agttcagtca 120

gcgcgcaggc cgctttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc 180

taaaggcatc atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg 240

cctctcttcg ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga 300

tatcacctca ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac 360

cactgggcct gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg 420

ccaatgtcaa gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg 480

acttcactgg cccagcagaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc 540

ctgcgggtgt cccaaggaag ccaggcatga cccgtgatga cctttttaac atcaatgcgg 600

gcatcgtcaa gtcgcttatt gaggctgttg cagacaactg ccctgaggcc ttcatncata 660

tcatcagcaa cccggtcacn 680

<210> 131
<211> 705
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(22)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (28)..(28)
<223> n is a, c, g, or t

<400> 131
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cccgtctgct caccaaccca agttggagat ggcatcagct gttaccatca gctcagtcag 120

cgcgcaggcc gctttggtct cgaaaccaag gaatcatggc agcacaagct acagtggcct 180

aaaggcatca tcatcgtcga tcagcttcga atcagggaca tcattcctgg gcaagaccgc 240

ctctcttcgg gcgactatca cctcaaggat tgtgccaaag gcaaagtctg ggtctcagat 300

atcacctcag gcctcgtaca aggtggcggt gcttggtgct gccggtggca tcggtcaacc 360

actgggcctg ctgatcaaga tgtctcctct ggtctcagag ctgcgcctgt atgatattgc 420

caatgtcaag ggagtcgctg cagatctcag ccactgcaac acgccttctc aggtcatgga 480

cttcactggc ccagcagaac tagctgactg cttgaaaggt gttgatgttg tcgtcatccc 540

tgcgggtgtc ccaaggaagc caggcatgac ccgtgatgac ctttttaaca tcaatgcggg 600

catcgtcaag tcgcttattg aggctgttgc agacaactgc cctgaggcct tcatccatat 660

catcagcaac ccggtcaact ccactgtgcc gattgctgct gagat 705

<210> 132
<211> 706
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (6)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (27)..(27)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (627)..(627)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (681)..(681)
<223> n is a, c, g, or t

<400> 132
acacannnaa aancaaaaag naccagnagc aaggggcgag ccggggcgca cgcagcaatt 60

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cccatctgct caccaaccca agttggagat ggcatcagct gttaccatca gctcagtcag    120
cgcgcaggcc gctttggtct cgaaaccaag gaatcatggc agcacaagct acagtggcct    180
aaaggcatca tcatcgtcga tcagcttcga atcagggaca tcattcctgg gcaagaccgc    240
ctctcttcgg gcgactatca cctcaaggat tgtgccaaag gcaaagtctg ggtctcagat    300
atcacctcag gcctcgtaca aggtggcggt gcttggtgct gccggtggca tcggtcaacc    360
actgggcctg ctgatcaaga tgtctcctct ggtctcagag ctgcgcctgt atgatattgc    420
caatgtcaag ggagtcgctg cagatctcag ccactgcaac acgccttctc aggtcatgga    480
cttcactggc ccagcagaac tagctgactg cttgaaaggt gttgatgttg tcgtcatccc    540
tgcgggtgtc ccaaggaagc caggcatgac ccgtgatgac ctttttaaca tcaatgcggg    600
catcgtcaag tcgcttattg aggctgntgc agacaactgc cctgaggcct tcatccatat    660
catcagcaac ccggtcaact ncactgtgcc gattgctgct gagata                   706
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<210> 133
<211> 634
<212> DNA
<213> Lolium perenne

<220>
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<222> (3)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(21)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(27)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (87)..(87)
<223> n is a, c, g, or t

<400> 133

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ccatctgctc accaacccaa gttgggnatg gcatcagctg ttaccatcag ctcagtcagc    120
gcgcaggccg ctttggtctc gaaaccaagg aatcatggca gcacaagcta cagtggccta    180
aaggcatcat catcgtcgat cagcttcgaa tcagggacat cattcctggg caagaccgcc    240
tctcttcggg cgactatcac ctcaaggatt gtgccaaagg caaagtctgg gtctcagata    300
tcacctcagg cctcgtacaa ggtggcggtg cttggtgctg ccggtggcat cggtcaacca    360
ctgggcctgc tgatcaagat gtctcctctg gtctcagagc tgcgcctgta tgatattgcc    420
aatgtcaagg gagtcgctgc agatctcagc cactgcaaca cgccttctca ggtcatggac    480
ttcactggcc cagcagaact agctgactgc ttgaaaggtg ttgatgttgt cgtcatccct    540
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gcgggtgtcc caaggaagcc aggcatgacc cgtgatgacc ttttaacat caatgcgggc 600

atcgtcaagt cgcttattga ggctgttgca gaca 634

<210> 134
<211> 758
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (28)..(28)
<223> n is a, c, g, or t

<400> 134
gttccaagaa aangaaaaaa gagccagncg caaggggcga gccggggcgc acgcagcaat 60

tcccatctgc tcaccaaccc aagttggaga tggcatcagc tgttaccatc agctcagtca 120

gcgcgcaggc cgccttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc 180

taaaggcatc atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg 240

cctctcttcg ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga 300

tatcacctca ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac 360

cactgggcct gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg 420

ccaatgtcaa gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg 480

acttcactgg cccagcagaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc 540

ctgcgggtgt cccaaggaag ccaggcatga cccgtgatga cctttttaac atcaatgcgg 600

gcatcgtcaa gtcgcttatt gaggctgttg cagacaactg ccctgaggcc ttcatccata 660

tcatcagcaa cccggtcaac tccactgtgc cgattgctgc tgagattctg aaacagaagg 720

gcgtctacaa ccccaagaag ctcttcgggg tttccacc 758

<210> 135
<211> 761
<212> DNA
<213> Lolium perenne

<220>
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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (27)..(27)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (607)..(607)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (628)..(628)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (676)..(676)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (688)..(688)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (704)..(704)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (716)..(716)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (724)..(725)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (737)..(737)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (746)..(746)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (751)..(751)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (754)..(754)
<223> n is a, c, g, or t

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tcccatctgc tcaccaaccc aagttggaga tggcatcagc tgttaccatc agctcagtca 120

gcgcgcaggc cgctttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc 180

taaaggcatc atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg 240

cctctcttcg ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga 300

tatcacctca ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac 360

cactgggcct gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg 420

ccaatgtcaa gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg 480

acttcactgg cccagctgaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc 540

ctgcgggtgt cccaaggaag ccaggcatga cccgtgatga cctttttaac atcaatgcgg 600

gcatcgncaa gtcgcttatt gaggctgntg cagacaactg ccctgaggcc ttcatccata 660

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gcgnntacaa ccccaanaag ctcttngggg nttncaccct g 761

<210> 136
<211> 772
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (27)..(28)
<223> n is a, c, g, or t

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gcgcgcaggc cgctttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc 180

taaaggcatc atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg 240

cctctcttcg ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga 300

tatcacctca ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac 360

cactgggcct gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg 420

ccaatgtcaa gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg 480

acttcactgg cccagcagaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc 540

ctgcgggtgt cccaaggaag ccaggcatga cccgtgatga cctttttaac atcaatgcgg 600

gcatcgtcaa gtcgcttatt gaggctgttg cagacaactg ccctgaggcc ttcatccata 660

tcatcagcaa cccggtcaac tccactgtgc cgattgctgc tgagattctg aaacagaagg 720

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<210> 137
<211> 772
<212> DNA
<213> Lolium perenne

<220>
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<222> (2)..(2)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (27)..(28)
<223> n is a, c, g, or t

<220>
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<222> (772)..(772)
<223> n is a, c, g, or t

<400> 137
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tcccatctgc tcaccaaccc aagttggaga tggcatcagc tgttaccatc agctcagtca 120

gcgcgcaggc cgctttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc 180

taaaggcatc atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg 240

cctctcttcg ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga 300

tatcacctca ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac 360

cactgggcct gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg 420

ccaatgtcaa gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg 480

acttcactgg cccagcagaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc 540

ctgcgggtgt cccaaggaag ccaggcatga cccgtgatga cctttttaac atcaatgcgg 600

gcatcgtcaa gtcgcttatt gaggctgttg cagacaactg ccctgaggcc ttcatccata 660

tcatcagcaa cccggtcaac tccactgtgc cgattgctgc tgagattctg aaacagaagg 720

gcgtctacaa ccccaagaag ctcttcgggg tttccaccct ggatgttgtc an 772

<210> 138
<211> 807
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (27)..(28)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (794)..(794)
<223> n is a, c, g, or t

<400> 138
gnaccagaaa aagaaaaaag agccagnncg caaggggcga gccggggcgc acgcagcaat 60

tcccatctgc tcaccaaccc aagttggaga tggcatcagc tgttaccatc agctcagtca 120

gcgcgcaggc cgccttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc 180

taaaggcatc atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg 240

cctctcttcg ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga 300

tatcacctca ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac 360

cactgggcct gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg 420

ccaatgtcaa gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg 480

acttcactgg cccagcagaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc 540

ctgcgggtgt cccaaggaag ccaggcatga cccgtgatga cctttttaac atcaatgcgg 600

gcatcgtcaa gtcgcttatt gaggctgttg cagacaactg ccctgaggcc ttcatccata 660

tcatcagcaa cccggtcaac tccactgtgc cgattgctgc tgagattctg aaacagaagg 720

gcgtctacaa ccccaagaag ctcttcgggg tttccaccct ggatgttgtc agagctaaca 780

catttgtagc tcanaagaag aacctca 807

<210> 139
<211> 628
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(19)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(27)
<223> n is a, c, g, or t

<400> 139
canannaaaa anaaaaanna cccagnngca ggggcgagcc ggggcgcacg cagcaattcc 60

catctgctca ccaacccaag ttggagatgg catcagctgt taccatcagc tcagtcagcg 120

cgcaggccgc tttggtctcg aaaccaagga atcatggcag cacaagctac agtggcctaa 180

aggcaccatc atcgtcgatc agcttcgaat cagggacatc attcctgggc aagaccgcct 240

ctcttcgggc gactatcacc tcaaggattg tgccaaaggc aaagtctggg tctcagatat 300

cacctcaggc ctcgtacaag gtggcggtgc ttggtgctgc cggtggcatc ggtcaaccac 360

tgggcctgct gatcaagatg tctcctctgg tctcagagct gcgcctgtat gatattgcca 420

atgtcaaggg agtcgctgca gatctcagcc actgcaacac gccttctcag gtcatggact 480

tcactggccc agcagaacta gctgactgct tgaaaggtgt tgatgttgtc gtcatccctg 540

cgggtgtccc aaggaagcca ggcatgaccc atgatgacct ttttaacatc aatgcgggca 600

tcgtcaagtc gcttattgag gctgttgc 628

<210> 140
<211> 640
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(19)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(27)
<223> n is a, c, g, or t

<400> 140
canannaaaa anaaaaanna cccagnngca ggggcgagcc ggggcgcacg cagcaattcc 60

catctgctca ccaacccaag ttggagatgg catcagctgt taccatcagc tcagtcagcg 120

cgcaggccgc tttggtctcg aaaccaagga atcatggcag cacaagctac agtggcctaa 180

aggcatcatc atcgtcgatc agcttcgaat cagggacatc attcctgggc aagaccgcct 240

ctcttcgggc gactatcacc tcaaggattg tgccaaaggc aaagtctggg tctcagatat 300

cacctcaggc ctcgtacaag gtggcggtgc ttggtgctgc cggtggcatc ggtcaaccac 360

tgggcctgct gatcaagatg tctcctctgg tctcagagct gcgcctgtat gatattgcca 420

atgtcaaggg agtcgctgca gatctcagcc gctgcaacac gccttctcag gtcatggact 480

tcactggccc agcagaacta gctgactgct tgagaggtgt tgatgttgtc gtcatccctg 540

cgggtgtccc aaggaagcca ggcatgaccc gtgatgacct ttttaacatc aatgcgggca 600

tcgtcaagtc gcttattgag gctgttgcag acaactgccc 640

<210> 141
<211> 698
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(19)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (25)..(25)
<223> n is a, c, g, or t

<400> 141
canannaaaa acaaaaanna ccagnagcaa ggggcgagcc ggggcgcacg cagcaattcc 60
catctgctca ccaacccaag ttggagatgg catcagctgt taccatcagc tcagtcagcg 120
cgcaggccgc tttggtctcg aaaccaagga atcatggcag cacaagctac agtggcctaa 180
aggcatcatc atcgtcgatc agcttcgaat cagggacatc attcctgggc aagaccgcct 240
ctcttcgggc gactatcacc tcaaggattg tgccaaaggc aaagtctggg tctcagatat 300
cacctcaggc ctcgtacaag gtggcggtgt ttggtgctgc cggtggcatc ggtcaaccac 360
tgggcctgct gatcaagatg tctcctctgg tctcagagct gcgcctgtat gatattgcca 420
atgtcaaggg agtcgctgca gatctcagcc actgcaacac gccttctcag gtcatggact 480
tcactggccc agcagaacta gctgactgct tgaaaggtgt tgatgttgtc gtcatccctg 540
cgggtgtccc aaggaagcca ggcatgaccc gtgatgacct ttttaacatc aatgcgggca 600
tcgtcaagtc gcttattgag gctgttgcag acaactgccc tgaggccttc atccatatca 660
tcagcaaccc ggtcaactcc actgtgccga ttgctgct 698

<210> 142
<211> 713
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(19)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (627)..(627)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (655)..(655)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (681)..(681)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (713)..(713)
<223> n is a, c, g, or t

<400> 142
canannaaaa acaaaaanna nccagnacgc aaggggcgag ccggggcgca cgcagcaatt 60

cccatctgct caccaaccca agttggagat ggcatcagct gttaccatca gctcagtcag 120

cgcgcaggcc gctttgatct cgaaaccaag gaatcctggc agcacaagct acagtggcct 180

aaaggcatca tcatcgtcga tcagcttcga atcagggaca tcattcctgg gcaagaccgc 240

ctctcttcgg gcgactatca cctcaaggat tgtgccaaag gcaaagtctg ggtctcagat 300

atcacctcag gcctcgtaca aggtggcggt gcttggtgct gccggtggca tcggtcaacc 360

actgggcctg ctgatcaaga tgtctcctct ggtctcagag ctgcgcctgt atgatattgc 420

caatgtcaag ggagtcgctg cagatctcag ccactgcaac acgccttctc aggtcatgga 480

cttcactggc ccagcagaac tagctgactg cttgaaaggt gttgatgttg tcgtcatccc 540

tgcgggtgtc ccaaggaagc caggcatgac ccgtgatgac ctttttaaca tcaatgcggg 600

catcgtcaag tcgcttattg aggctgntgc agacaactgc cctgaggcct tcatncatat 660

catcagcaac ccggtcaact ncactgtgcc gattgctgct gagattctga aan 713

<210> 143
<211> 771
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

<400> 143
gaccagaaaa agaaaaaaga gccagncgca aggggcgagc cggggcgcac gcagcaattc 60

ccatctgctc accaacccaa gttggagatg gcatcagctg ttaccatcag ctcagtcagc 120
gcgcaggccg ctttggtctc gaaaccaagg aatcatggca gcacaagcta cagtggccta 180
aaggcatcat catcgtcgat cagcttcgaa tcagggacat cattcctggg caagaccgcc 240
tctcttcggg cgactatcac ctcaaggatt gtgccaaagg caaagtctgg gtctcagata 300
tcacctcagg cctcgtacaa ggtggcggtg cttggtgctg ccggtggcat cggtcaacca 360
ctgggcctgc tgaccaagat gtctcctctg gtctcagagc tgcgcctgta tgatattgcc 420
aatgtcaagg gagtcgctgc aggtctcagc cactgcaaca cgccttctca ggtcatggac 480
ttcactggtc cagcagaact agctgactgc ttgaaaggtg ttgatgttgt cgtcatccct 540
gcgggtgtcc caaggaagcc aggcatgacc cgtgatgacc tttttaacat caatgcgggc 600
atcgtcaagt cgcttattga ggctgttgca gacaactgcc ctgaggcctt catccatatc 660
atcagcaacc cggtcaactc cactgtgccg attgctgctg agattctgaa acagaagggc 720
gtctacaacc ccaagaagct cttcggggtt tccaccctgg atgttgtcag a 771

<210> 144
<211> 773
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (26)..(27)
<223> n is a, c, g, or t

<400> 144
gtccagaaaa agaaaaaaga gccagnncgc aaggggcgag ccggggcgca cgcagcaatt 60
cccatctgct caccaaccca agttggagat ggcatcagct gttaccatca gctcagtcag 120
cgcgcaggcc gctttggtct cgaaaccaag gaatcatggc agcacaagct acagtggcct 180
aaaggcatca tcatcgtcga tcagcttcga atcagggaca tcattcctgg gcaagaccgc 240
ctctcttcgg gcgactatca cctcaaggat tgtgccaaag gcaaagtctg ggtctcagat 300
atcacctcag gcctcgtaca aggtggcggt gcttggtgct gccggtggca tcggtcaacc 360
actgggcctg ctgatcaaga tgtctcctct ggtctcagag ctgcgcctgt atgatattgc 420
caatgtcaag ggagtcgctg cagatctcag ccactgcaac acgccttctc aggtcatgga 480
cttcactggc ccagcagaac tagctgactg cttgaaaggt gttgatgttg tcgtcatccc 540
tgcgggtgtc ccaaggaagc caggcatgac ccgtgatgac ctttttaaca tcaatgcggg 600
catcgtcaag tcgcttattg aggctgttgc agacaactgc cctgaggcct tcatccatat 660
catcagcaac ccggtcaact ccactgtgcc gattgctgct gagattctga aacagaaggg 720
cgtctacaac cccaagaagc tcttcggggt ttccaccctg gatgttgtca gag 773

<210> 145
<211> 684
<212> DNA

<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (545)..(545)
<223> n is a, c, g, or t

<400> 145
annaaaagna aaaagnnccc gncgcaaggg gcgagccggg gcgcacgcag caattcccat 60

ctgctcacca acccaagttg gggatggcat cagctgttac catcagctca gtcagcgcgc 120

aggccgcttt ggtctcgaaa ccaaggaatc atggcagcac aagctacagt ggcctaaagg 180

catcatcatc gtcgatcagc ttcgaatcag ggacatcatt cctgggcaag accgcctctc 240

ttcgggcgac tatcacctca aggattgtgc caaaggcaaa gtctgggtct cagatatcac 300

ctcaggcctc gtacaaggtg gcggtgcttg gtgctgccgg tggcatcggt caaccactgg 360

gcctgctgat caagatgtct cctctggtct cagaactgcg cctgtatgat attgccaatg 420

tcaagggagt cgctgcagat ctcagccact gcaacacgcc ttctcaggtc atggacttcg 480

ctggcccagc agaactagct gactgcttga aaggtgttga tgttgtcgtc atccctgcgg 540

gtgtnccaag gaagccaggc atgacccgtg atgacctttt taacatcaat gcgggcatcg 600

tcaagtcgct tattgaggct gttgcagaca actgccctga ggccttcatc catatcatca 660

gcaacccggt caacttcact gtgc 684

<210> 146
<211> 695
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4)..(5)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(18)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (25)..(25)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (680)..(680)
<223> n is a, c, g, or t

<400> 146
anannaaaan caaaaannan ccagnacgca aggggcgagc cggggcgcac gcagcaattc 60

ccatctgctc accaacccaa gttggagatg gcatcagctg ttaccatcag ctcagtcagc 120

gcgcaggccg ctttggtctc gaaaccaagg aatcatggca gcacaagcta cagtggccta 180

aaggcatcat catcgtcgat cagcttcgaa tcagggacat cattcctggg caagaccgcc 240

tctcttcggg cgactatcac ctcaaggatt gtgccaaagg caaagtctgg gtctcagata 300

tcacctcagg cctcgtacaa ggtggcggtg cttggtgctg ccggtggcat cggtcaacca 360

ctgggcctgc tgatcaagat gtctcctctg gtctcagagc tgcgcctgta tgatattgcc 420

aatgtcaagg gagtcgctgc agatctcagc cactgcaaca cgccttctca ggtcatggac 480

ttcactggcc cagcagaact agctgactgc ttgaaaggtg ttgatgttgt cgtcatccct 540

gcgggtgtcc caaggaagcc aggcatgacc cgtgatgacc tttttaacat caatgcgggc 600

atcgtcaagt cgcttattga ggctgttgca gacaactgcc ctgaggcctt catccatatc 660

atcagcaacc cggtcaactn cactgtgccg attgt 695

<210> 147
<211> 695
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (624)..(624)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (678)..(678)
<223> n is a, c, g, or t

<400> 147
aannaaaann aaaaannacc agnacgcaag gggcgagccg gggcgcacgc agcaattccc 60

atctgctcac caacccaagt tggagatggc atcagctgtt accatcagct cagtcagcgc 120

gcaggccgct ttggtctcga aaccaaggaa tcatggcagc acaagctaca gtggcctaaa 180

ggcatcatca tcgtcgatca gcttcgaatc agggacatca ttcctgggca agaccgcctc 240

tcttcgggcg actatcacct caaggattgt gccaaaggca aagtctgggt ctcagatatc 300

acctcaggcc tcgtacaagg tggcggtgct tggtgctgcc ggtggcatcg gtcaaccact 360

gggcctgctg atcaagatgt ctcctctggt ctcagagctg cgcctgtatg atattgccaa 420

tgtcaaggga gtcgctgcag atctcagcca ctgcaacacg ccttctcagg tcatggactt 480

cactggcccca gcagaactag ctgactgctt gaaaggtgtt gatgttgtcg tcatccctgc 540

gggtgtccca aggaagccag gcatgacccg tgatgacctt tttaacatca atgcgggcat 600

cgtcaagtcg cttattgagg ctgntgcaga caactgccct gaggccttca tccatatcat 660

cagcaacccg gtcaactnca ctgtgccgat tgctg 695

<210> 148
<211> 637
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (1)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(16)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<400> 148
nnnaaaaana aaaannancc agnagcaagg ggcgagccgg ggcgcacgca gcaattccca 60

tctgctcacc aacccaagtt ggagatggca tcagctgtta ccatcagctc agtcagcgcg 120

caggccgctt tggtctcgaa accaaggaat catggcagca caagctacag tggcctaaag 180

gcatcatcat cgtcgatcag cttcgaatca gggacatcat tcctgggcaa gaccgcctct 240

cttcgggcga ctatcacctc aaggattgtg ccaaaggcaa agtctgggtc tcagatatca 300

cctcaggcct cgtacaaggt ggcggtgctt ggtgctgccg gtggcatcgg tcaaccactg 360

ggcctgctga tcaagatgtc tcctctggtc tcagagctgc gcctgtatga tattgccaat 420

gtcaagggag tcgctgcaga tctcagccac tgcaacacgc cttctcaggt catggacttc 480

actggcccag cagaactagc tgactgcttg aaaggtgttg atgttgtcgt catccctgcg 540

ggtgtcccaa ggaagccagg catgacccgt gatgaccttt ttaacatcaa tgcgggcatc 600

gtcaagtcgc ttattgaggc tgttgcagac aactgcc 637

<210> 149
<211> 675
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(16)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (623)..(623)
<223> n is a, c, g, or t

<400> 149
annaaaanca aaaannacca gnacgcaagg ggcgagccgg ggcgcacgca gcaattccca 60

tctgctcacc aacccaagtt ggagatggca tcagctgtta ccatcagctc aatcagcgcg 120
caggccgctt tggtctcgaa accaaggaat catggcagca caagctacag tggcctaaag 180
gcatcatcat cgtcgatcag cttcgaatca gggacatcat tcctgggcaa gaccgcctct 240
cttcgggcga ctatcacctc aaggattgtg ccaaaggcaa agtctgggtc tcagatatca 300
cctcaggcct cgtacaaggt ggcggtgctt ggtgctgccg gtggcatcgg tcaaccactg 360
ggcctgctga tcaagatgtc tcctctggtc tcagagctgc gcctgtatga tattgccaat 420
gtcaagggag tcgctgcaga tctcagccac tgcaacacgc cttctcaggt catggacttc 480
actggcccag cagaactagc tgactgcttg aaaggtgttg atgttgtcgt catccctgcg 540
ggtgtcccaa ggaagccagg catgacccgt gatgaccttt ttaacatcaa tgcgggcatc 600
gtcaagtcgc ttattgaggc tgntgcagac aactgccctg aggccttcat ccatatcatc 660
agcaacccgg tcaac 675

<210> 150
<211> 764
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (720)..(720)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (741)..(741)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (745)..(745)
<223> n is a, c, g, or t

<400> 150
nagaaaaaca aaaaagagcc agacgcaagg ggcgagccgg ggcgcacgca gcaattccca 60
tctgctcacc aacccaagtt ggagatggca tcagctgtta ccatcagctc agtcagcgcg 120
caggccgctt tggtctcgaa accaaggaat catggcagca caagctacag tggcctaaag 180
gcatcatcat cgtcgatcag cttcgaatca gggacatcat tcctgggcaa gaccgcctct 240
cttcgggcga ctatcacctc aaggattgtg ccaaaggcaa agtctgggtc tcagatatca 300
cctcaggcct cgtacaaggt ggcggtgctt ggtgctgccg gtggcatcgg tcaaccactg 360
ggcctgctga tcaagatgtc tcctctggtc tcagagctgc gcctgtatga tattgccaat 420
gtcaagggag tcgctgcaga tctcagccac tgcaacacgc cttctcaggt catggacttc 480
actggcccag cagaactagc tgactgcttg aaaggtgttg atgttgtcgt catccctgcg 540

ggtgtcccaa ggaagccagg catgacccgt gatgaccttt ttaacatcaa tgcgggcatc 600
gtcaagtcgc ttattgaggc tgttgcagac aactgccctg aggccttcat ccatatcatc 660
agcaacccgg tcaactccac tgtgccgatt gctgctgaga ttctgaaaca gaacggcgtn 720
tccaccccaa gaagcttttc ngggnttaca ccctggatgt tgcc 764

<210> 151
<211> 785
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (393)..(393)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (745)..(745)
<223> n is a, c, g, or t

<400> 151
cagaaaaaag aaaagcagcc agacgcaagg ggcgagcccg ggcgcacgag caattcccat 60
ctgctcacca acccaagttg gacatggcat cagctgttac catcagttcg gtcagcgcgc 120
agtccgctct ggtttcgaaa ccaaggaatc atggcagcac gagcttcggt ggcctaaagg 180
catcatcggc gtcgatcagc tttgaatcag ggacatcgtt cctgggcaag actgcctccc 240
tccgggcgac tgttacccca aggattgtgc caaaggcaaa gtctgggtct cagatatcgc 300
ctcaggcatc ttacaaggtg gcggtgcttg gtgctgctgg tggcatcggt caaccactgg 360
gcctgctgat caagatgtct cctctggtct canagctgcg cctgtatgat attgccaatg 420
tcaagggcgt cgctgcagat cttagccact gcaacacgcc ttctcaggtc atggacttca 480
ctggccccgc ggaactagcc gactgcttga aaggtgtgga tgttgtcgtc atccctgcgg 540
gtgtcccaag gaagcctggc atgactcgtg atgacctttt taacatcaat gcgggcatcg 600
tcaagtcgct tatcgaggct gttgcagaca actgccctga ggccttcatc catatcatca 660
gcaacccggt caactccacg gtgccgattg ctgctgagat tctgaaacag aagggcgtct 720
acaaccccaa gaagctcttc ggggnttcca ccctggatgt tgtcagagct aacacatttg 780
tagct 785

<210> 152
<211> 706
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(15)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (676)..(676)
<223> n is a, c, g, or t

<400> 152
anaaaancaa aaannaccag nacgcaaggg gcgagccggg gcgcacgcag caattcccat 60

ctgctcacca acccaagttg gagatggcat cagctgttac catcagctca gtcagcgcgc 120

aggccgcttt ggtctcgaaa ccaaggaatc atggcagcac aagctacagt ggcctaaagg 180

catcatcatc gtcgatcagc ttcgaatcag ggacatcatt cctgggcaag accgcctctc 240

ttcgggcgac tatcacctca aggattgtgc caaaggcaaa gtctgggtct cagatatcac 300

ctcaggcctc gtacaaggtg gcggtgcttg gtgctgccgg tggcatcggt caaccactgg 360

gcctgctgat caagatgtct cctctggtct cagagctgcg cctgtatgat attgccaatg 420

tcaagggagt cgctgcagat ctcagccact gcaacacgcc ttctcaggtc atggacttca 480

ctggcccagc agaactagct gactgcttga aaggtgttga tgttgtcgtc atccctgcgg 540

gtgtcccaag gaagccaggc atgacccgtg atgacctttt taacatcaat gcgggcatcg 600

tcaagtcgct tattgaggct gttgcagaca actgccctga ggccttcatc catatcatca 660

gcaacccggt caactncact gtgccgattg ctgctgagat tctgaa 706

<210> 153
<211> 682
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (538)..(538)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (597)..(598)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (649)..(650)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (679)..(679)
<223> n is a, c, g, or t

<400> 153
naacannnaa aaacaaaaaa ngggcgagcc ggggcgcacg cagcaattcc catctgccca 60

ccaacccaag ttggacatgg catcagctgt caccatcagt tcagtcagcg cccaggccgc 120

tctggtgtca aaaccaagga gtcatggcag cacgagcttc agtggcctga aggcatcatc 180

atcgtcgatc agcttcgaat ctggaacatc attcctgggc aagactgcct ctcttcgggc 240

gtcagtcacc ccgaggattg tgccaaaggc aaagtctggg tctcagatat cgcctcaggc 300

atcttacaag gtggcggtgc ttggtgctgc cggtggcatc ggtcaaccac tgggcctgct 360

gatcaagatg tcgcctctgg tctcggagct gcgcctgtat gatattgcga atgtcaaggg 420

cgtcgctgcc gatctcagcc accgcaacac gcctgctcag gtcatggact tcactggccc 480

cgcggaacta gcagagtgct tgaaaggcgt ggatgttgtc gtcatccctg cgggtgtncc 540

aaggaagcca ggcatgaccc gtgatgacct ttttaacatc aatgcggcat cgtcagnngc 600

ttatcgaggc tgttgcagac actgcctgag gccttatcca tattatcann acccgggact 660

gcacggtgcc gattgctgna at 682

<210> 154
<211> 712
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (525)..(525)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (575)..(575)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (596)..(596)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (601)..(601)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (638)..(638)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (665)..(665)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (686)..(686)
<223> n is a, c, g, or t

<400> 154
gnacacanan naaaancaaa aaaggggcga gccggggcgc acacagcaat tcccatctgc 60

ccaccaaccc aagttggaca tggcatcagc tgtcaccatc agttcagtca gcgcccaggc 120

cgctctggtg tcaaaaccaa ggagtcatgg cagcacgagc ttcagtggcc tgaaggcatc 180

atcatcgtcg atcagcttcg aatctggaac atcattcctg ggcaagactg cctctcttcg 240

ggcgtcagtc accccgagga ttgtgccaaa ggcaaagtct gggtctcaga tatcgcctca 300

ggcatcttac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac cactgggcct 360

gctgatcaag atgtcgcctc tggcctcgga gctgcgcctg tatgatattg cgaatgtcaa 420

gggcgtcgct gccgatctca gccactgcaa cacgcctgct caggtcatgg acttcactgg 480

ccccgcggaa ctagcagagt gcttgaaagg cgtggatgtt gtcgnatccc tgcgggtgtt 540

ccaaggaagc caggcatgac ccgtgatgac ctttntaaca tcaatgcggg catcgncaag 600

ncgcttatcg aggctgttgc agacaactgc cctgaggnct tgatccatat tatgagaacc 660

ccggncaact ccacggcgcc gattgntgca gagattctga aacagaaggc gt 712

<210> 155
<211> 644
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (11)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(19)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (619)..(619)
<223> n is a, c, g, or t

<400> 155
aaaccaaaaa nnacccagna gccaaggggc gagccggggc gcacgcagca attcccatct 60

gctcaccaac ccaagttgga gatggcatca gctgttacca tcagctcagt cagcgcgcag 120

gccgctttgg tctcgaaacc aaggaatcat ggcagcacaa gctacagtgg cctaaaggca 180

tcatcatcgt cgatcagctt cgaatcaggg acatcattcc tgggcaagac cgcctctctt 240

cgggcgacta tcacctcaag gattgtgcca aaggcaaagt ctgggtctca gatatcacct 300

caggcctcgt acaaggtggc ggtgcttggt gctgccggtg gcatcggtca accactgggc 360

ctgctgatca agatgtctcc tctggtctca gagctgcgcc tgtatgatat tgccaatgtc 420

aagggagtcg ctgcagatct cagccactgc aacacgcctt ctcaggtcat ggacttcact 480

ggcccagcag aactagctga ctgcttgaaa gggttgatgt tgtcgtcatc cctgcgggtg 540

tcccaaggaa gccaggcatg acccgtgatg accttttttaa catcaatgcg ggcatcgtca 600

agtcgcttat tgaggctgnt gcagacaact gccctgaggc cttt 644

<210> 156
<211> 683
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (671)..(671)

<223> n is a, c, g, or t

<400> 156
gncacanann aaaaacaaaa aangggcgag ccggggcgca cgcagcaatt cccatctgcc 60

caccaaccca agttggacat ggcatcagct gtcaccatca gttcagtcag cgcccaggcc 120

gctctggtgt caaaaccaag gagtcatggc agcacgagct tcagtggcct gaaggcatca 180

tcatcgtcga tcagcttcga atctggaaca tcattcctgg gcaagactgc ctctcttcgg 240

gcgtcagtca ccccgaggat tgtgccaaag gcaaagtctg ggtctcagat atcgcctcag 300

gcatcttaca aggtggcggt gcttggtgct gccggtggca tcggtcaacc actgggcctg 360

ctgatcaaga tgtcgcctct ggtctcggag ctgcgcctgt atgatattgc gaatgtcaag 420

ggcgtcgctg ccgatctcag ccactgcaac acgcctgctc aggtcatgga cttcactggc 480

cccgcggaac tagcagagtg cttgaaaggc gtggatgttg tcgtcatccc tgcgggtgtc 540

ccaaggaagc caggcatgac ccgtgatgac ctttttaaca tcaatgcggg catcgtcaag 600

tcgcttatcg aggctgttgc agacaactgc cctgaggcct tcatccatat tatcagcaac 660

ccggtcaact ncacggtgcc gat 683

<210> 157
<211> 695
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (24)..(24)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (550)..(550)
<223> n is a, c, g, or t

<400> 157
gancccanan naaaaanaaa aaangggcga gccggggcgc acgcagcaat tcccatctgc 60

ccaccaaccc aagttggaca tggcatcagc tgtcaccatc agttcagtca gcgcccaggc 120

cgctctggtg tcaaaaccaa ggagtcatgg cagcacgagc ttcagtggcc tgaaggcatc 180
atcatcgtcg atcagcttcg aatctggaac atcattcctg ggcaagactg cctctcttcg 240
ggcgtcagtc accccgagga ttgtgccaaa ggcaaagtct gggtctcaga tatcgcctca 300
ggcatcttac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac cactgggcct 360
gctgatcaag atgtcgcctc tggtctcgga gctgcgcctg tatgatattg cgaatgtcaa 420
gggcgtcgct gccgatctca gccactgcaa cacgcctgct ctggtcatgg acttcactgg 480
ccccgcggaa ctagcagagt gcttgaaagg cgtggatgtt gtcgtcatcc ctgcgggtgt 540
cccaaggaan ccaggcatga cccgtgatga cctttttaac atcaatgcgg gcatcgtcaa 600
gtcgcttatc gaggctgttg cagacaactg ccctgaggcc ttcatccata ttatcagcaa 660
cccggtcaac tccacggtgc cgattgctgc agaga 695

<210> 158
<211> 802
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (89)..(89)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (740)..(740)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (773)..(773)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (780)..(780)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (783)..(783)
<223> n is a, c, g, or t

<400> 158
gaccagaaaa angaaaaaag gggcgagccg gggcgcacgc agcaattccc atctgcccac 60
caacccaagt tggacatggc atcagctgnc accatcagtt cagtcagcgc ccaggccgct 120
ctggtgtcaa aaccaaggag tcatggcagc acgagcttca gtggcctgaa ggcatcatca 180
tcgtcgatca gcttcgaatc tggaacatca ttcctgggca agactgcctc tcttcgggcg 240
tcagtcaccc cgaggattgt gccaaaggca aagtctgggt ctcagatatc gcctcaggca 300

tcttacaagg tggtggtgct tggtgctgct ggtggcatcg gtcaaccact gggcctgctg 360
atcaagatgt ctcctctggt ctcagagctg cgcctgtatg atattgccaa tgtcaagggc 420
gtcgctgcag atcttagcca ctgcaacacg ccttctcagg tcatggactt cactggcccc 480
gcggaactag ccgactgctt gaaaggtgtg gatgttgtcg tcatccctgc gggtgtccca 540
aggaagcctg gcatgactcg tgatgacctt tttaacatca atgcgggcat cgtcaagtcg 600
cttatcgagg ctgttgcaga caactgccct gaggccttca tccatatcat cagcaacccg 660
gtcaactcca cggtgccgat tgctgctgag attctgaaac agaagggcgt ctacaacccc 720
aagaagctct tcggggtttn caccctggat gttgtcagag ctaacacatt tgnagctcan 780
aanaagaacc tcagtcttat cg 802

<210> 159
<211> 637
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (4)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(19)
<223> n is a, c, g, or t

<400> 159
aaanaaaaan nacccagnng caaggggcga gccggggcgc acgcagcaat tcccatctgc 60
tcaccaaccc aagttggaga tggcatcagc tgttaccatc agctcagtca gcgcgcaggc 120
cgctttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc taaaggcatc 180
atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg cctctcttcg 240
ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga tatcacctca 300
ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac cactgggcct 360
gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg ccaatgtcaa 420
gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg acttcactgg 480
cccagcagaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc ctgcgggtgt 540
cccaaggaag ccagacaact gccctgaggc cttcatccat atcatcagca acccggtcaa 600
ctccactgtg ccgattgctg ctgagatcta aacagaa 637

<210> 160
<211> 686
<212> DNA

<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (673)..(673)
<223> n is a, c, g, or t

<400> 160
aanccaaaaa nnaccagnac gcagggggcg agccggggcg cacgcagcaa ttcccatctg 60

ctcaccaacc caagttggag atggcatcag ctgttaccat cagctcagtc agcgcgcagg 120

ccgctttggt ctcgaaacca aggaatcatg gcagcacaag ctacagtggc ctaaaggcat 180

catcatcgtc gatcagcttc gaatcaggga catcattcct gggcaagacc gcctctcttc 240

gggcgactat cacctcaagg attgtgccaa aggcaaagtc tgggtctcag atatcacctc 300

aggcctcgta caaggtggcg gtgcttggtg ctgccggtgg catcggtcaa ccactgggcc 360

tgctgatcaa gatgtctcct ctggtctcag agctgcgcct gtatgatatt gccaatgtca 420

agggagtcgc tgcagatctc agccactgca acacgccttc tcaggtcatg gacttcactg 480

gcccagcaga actagctgac tgcttgaaag gtgttgatgt tgtcgtcatc cctgcgggtg 540

tcccaaggaa gccaggcatg acccgtgatg acctttttaa catcaatgcg ggcatcgtca 600

agtcgcttat tgaggctgtt gcagacaact gccctgaggc cttcatccat atcatcagca 660

acccggtcaa ctncactgtg ccgatt 686

<210> 161
<211> 693
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (672)..(672)

<223> n is a, c, g, or t

<400> 161
aaacaaaaaa naccagnacg caaggggcga gccggggcgc acgcagcaat tcccatctgc 60

tcaccaaccc aagttggaga tggcatcagc tgttaccatc agctcagtca gcgcgcaggc 120

cgctttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc taaaggcatc 180

atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg cctctcttcg 240

ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga tatcacctca 300

ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac cactgggcct 360

gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg ccaatgtcaa 420

gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg gcttcactgg 480

cccagcagaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc ctgcgggtgt 540

cccaaggaag ccaggcatga cccgtgatga cctttttaac atcaatgcgg gcatcgtcaa 600

gtcgcttatt gaggctgttg cagacaactg ccctgaggcc ttcatccata tcatcagcaa 660

cccggtcaac tncactgtgc cgattgctgc tgc 693

<210> 162
<211> 647
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<400> 162
cacaananna aaaananaaa aggggcgagc cggggcgcac gcagcaattc ccatctgccc 60

accaacccaa gttggacatg gcatcagctg tcaccatcag ttcagtcagc gcccaggccg 120

ctctggtgtc aaaaccaagg agtcatggca gcacgagctt cagtggcctg aaggcatcat 180

catcgtcgat cagcttcgaa tctggaacat cattcctggg caagactgcc tctcttcggg 240

cgtcagtcac cccgaggatt gtgccaaagg caaagtctgg gtctcagata tcgcctcagg 300

catcttacaa ggtggcggtg cttggtgctg ccggtggcat cggtcaacca ctgggcctgc 360

tgatcaagat gtcgcctctg gtctcggagc tgcgcctgta tgatattgcg aatgtcaagg 420

gcgtcgctgc cgatctcagc cactgcaaca cgcctgctca ggtcatggac ttcactggcc 480

ccgcggaact agcagagtgc ttgaaaggcg tggatgttgt cgtcatccct gcgggtgtcc 540

caaggaagcc aggcatgacc cgtgatgacc tttttaacat caatgcgggc atcgtcaagt 600

cgcttatcga ggctgttgca gacaactgcc ctgaggcctt catccat 647

<210> 163
<211> 661
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<400> 163
aannaaaaan naccagnacg cagggggcga gccggggcgc acgcagcaat tcccatctgc 60

tcaccaaccc aagttggaga tggcatcagc tgttaccatc agctcagtca gcgcgcaggc 120

cgctttggtc tcgaaaccaa ggaatcatgg cagcacaagc tacagtggcc taaaggcatc 180

atcatcgtcg atcagcttcg aatcagggac atcattcctg ggcaagaccg cctctcttcg 240

ggcgactatc acctcaagga ttgtgccaaa ggcaaagtct gggtctcaga tatcacctca 300

ggcctcgtac aaggtggcgg tgcttggtgc tgccggtggc atcggtcaac cactgggcct 360

gctgatcaag atgtctcctc tggtctcaga gctgcgcctg tatgatattg ccaatgtcaa 420

gggagtcgct gcagatctca gccactgcaa cacgccttct caggtcatgg acttcactgg 480

cccagcagaa ctagctgact gcttgaaagg tgttgatgtt gtcgtcatcc ctgcgggtgt 540

cccaaggaag ccaggcatga cccgtgatga cctttttaac atcaatgcgg gcatcgtcaa 600

gtcgcttatt gaggctgttg cagacaactg ccctgaggcc ttcatccata tcatcagcaa 660

c 661

<210> 164
<211> 640
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<400> 164
gnnnaanaaa aanaaaanan gggcgagccg gggcgcacgc agcaattccc atctgcccac 60
caacccaagt tggacatggc atcagctgtc accatcagtt cagtcagcgc ccaggccgct 120
ctggtgtcaa aaccaaggag tcatggcagc acgagcttca gtggcctgaa ggcatcatca 180
tcgtcgatca gcttcgaatc tggaacatca ttcctgggca agactgcctc tcttcgggcg 240
tcagtcaccc cgaggattgt gccaaaggca aagtctgggt ctcagatatc gcctcaggca 300
tcttacaagg tggcggtgct tggtgctgcc ggtggcatcg gtcaaccact gggcctgctg 360
atcaagatgt cgcctctggt ctcggagctg cgcctgtatg atattgcgaa tgtcaagggc 420
gtcgctgccg acctcagcca ctgcaacacg cctgctcagg tcatggactt cactggcccc 480
gcggaactag cagagtgctt gaaaggcgtg gatgttgtcg tcatccctgc gggtgtccca 540
aggaagccag gcatgacccg tgatgacctt tttaacatca atgcgggcat cgtcaagtcg 600
cttatcgagg ctgttgcaga caactgccct gaggccttca 640

<210> 165
<211> 681
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(19)
<223> n is a, c, g, or t

<400> 165
canannaaaa acaaaaaang ggcgagccgg ggcgcacgca gcaattccca tctgcccacc 60

aacccaagtt ggacatggca tcagctgtca ccatcagttc agtcagcgcc caggccgctc 120
tggtgtcaaa accaaggagt catggcagca cgagcttcag tggcctgaag gcatcatcat 180
cgtcgatcag cttcgaatct ggaacatcat tcctgggcaa gactgcctct cttcgggcgt 240
cagtcacccc gaggattgtg ccaaaggcaa agtctgggtc tcagatatcg cctcaggcat 300
cttacaaggt ggcggtgctt ggtgctgccg gtggcatcgg ttaaccactg ggcctgctga 360
tcaagatgtc gcctctggtc tcggagctgc gcctgtatga tattgcgaat gtcaagggcg 420
tcgctgccga tctcagccac tgcaacacgc ctgctcaggt catggacttc actggccccg 480
cggaactagc agagtgcttg aaaggcgtgg atgttgtcgt catccctgcg ggtgtcccaa 540
ggaagccagg catgacccgt gatgaccttt ttaacatcaa tgcgggcatc gtcaagtcgc 600
ttatcgaggc tgttgcagac aactgccctg aggccttcat ccatattatc agcaacccgg 660
tcaactccac ggtgccgatt g 681

<210> 166
<211> 741
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<400> 166
gnaccagaaa aagaaaaaaa ggggcgagcc ggggcgcacg cagcaattcc catctgccca 60
ccaacccaag ttggacatgg catctgctgt caccatcagt tcagtcagcg cccaggccgc 120
tctggtgtca aaaccaagga gtcatggcag cacgagcttc agtggcctga aggcatcatc 180
atcgtcgatc agcttcgaat ctggagcatc attcctgggc aagactgcct ctcttcgggc 240
gtcagtcacc ccgaggattg tgccaaaggc aaagtctggg tctcagatat cgcctcaggc 300
atctcacaag gtggcggtgc ttggtgctgc cggtggcatc ggtcaaccac tgggcctgct 360
gatcaagatg tcgcctctgg tctcggagct gcgcctgtat gatattgcga atgtcaaggg 420
cgtcgctgcc gatctcagcc actgcaacac gcctgctcag gtcatggact tcactggccc 480
cgcggaacta gcagagtgct tgaaaggcgt ggatgttgtc gtcatccctg cgggtgtccc 540
aaggaagcca ggcatgaccc gtgatgacct ttttaacatc aatgcgggca tcgtcaagtc 600
gcttatcgag gctgttgcag acaactgccc tgaggccttc atccatatta tcagcaaccc 660
ggtcaactcc acggtgccga ttgctgcaga gattctgaaa cagaagggcg tctacaaccc 720
caagaagctc ttcggggttt c 741

<210> 167
<211> 665
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (614)..(614)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (664)..(664)
<223> n is a, c, g, or t

<400> 167
cannnnaaaa ncaaaaaagg gnacgagccg gggcgcacgc agcaattccc atctgcccac 60

caacccaagt tggacatggc atcagctgtc accatcagtt cagtcagcgc ccaggccgct 120

ctggtgtcaa aaccaaggag tcatggcagc acgagcttca gtggcctgaa ggcatcatca 180

tcgtcgatca gcttcgaatc tggaacatca ttcctgggca agactgcctc tcttcgggcg 240

tcagtcaccc cgaggattgt gccaaaggca aagtctgggt ctcagatatc gcctcaggca 300

tcttacaagg tggcggtgct tggtgctgcc ggtggcatcg gtcaaccact gggcctgctg 360

atcaagatgt cgcctctggt ctcggagctg cgcctgtatg atattgcgaa tgtcaagggc 420

gtcgctgccg atctcagcca ctgcaacacg cctgctcagg tcatggactt cactggcccc 480

gcggaactag cagagtgctt gaaaggcgtg gatgttgtcg tcatccctgc gggtgtccca 540

aggaagccag gcatgacccg tgatgacctt tttaacatca atgcgggcat cgtcaagtcg 600

cttatcgagg ctgntgcaga caactgccct gaggccttca tccatattat cagcaacccg 660

gtcna 665

<210> 168
<211> 680
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(6)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(19)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (667)..(667)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (680)..(680)
<223> n is a, c, g, or t

<400> 168
canannaaaa ananaaaang ggcgagccgg ggcgcacgca gcaattccca tctgcccacc 60

aacccaagtt ggacatggca tcagctgtca ccatcagttc agtcagcgcc caggccgctc 120

tggtgtcaaa accaaggagt catggcagca cgagcttcag tggcctgaag gcatcatcat 180

cgtcgatcag cttcgaatct ggaacatcat tcctgggcaa gactgcctct cttcgggcgt 240

cagccacccc gaggattgtg ccaaaggcaa agtctgggtc tcagatatcg cctcaggcat 300

cttacaaggt ggcggtgctt ggtgctgccg gtggcatcgg tcaaccactg ggcctgctga 360

tcaagatgtc gcctctggtc tcggagctgc gcctgtatga tattgcgaat gtcaagggcg 420

tcgctgccga tctcagccac tgcaacacgc ctgctcaggt catggacttc actggccccg 480

cggaactagc agagtgcttg aaaggcgtgg atgttgtcgt catccctgcg ggtgtcccaa 540

ggaagccagg catgacccgt gatgaccttt ttaacatcaa tgcgggcatc gtcaagtcgc 600

ttatcgaggc tgttgcagac aactgccctg aggccttcat ccatattatc agcaacccgg 660

tcaactncac ggtgccgatn 680

<210> 169
<211> 770
<212> DNA
<213> Lolium perenne

<400> 169
gaccagaaaa agaaaaaaag gggcgagccg gggcgcacgc agcaattccc atctgcccac 60

caacccaagt tggacatggc atcagccgtc accatcagtt cagtcagcgc ccaggccgct 120

ctggtgtcaa aaccaaggag tcatggcagc acgagcttca gtggcctgaa ggcatcatca 180

tcgtcgatca gcttcgaatc tggaacatca ttcctgggca agactgcctc tcttcgggcg 240

tcagtcaccc cgaggattgt gccaaaggca aagtctgggt ctcagatatc gcctcaggca 300

tcttacaagg tggcggtgct tggtgctgcc ggtggcatcg gtcaaccact gggcctgctg 360

atcaagatgt cgcctctggt ctcggagctg cgcctgtatg atattgcgaa tgtcaagggc 420
gtcgctgccg atctcagcca ctgcaacacg cctgctcagg tcatggactt cactggcccc 480
gcggaactag cagagtgctt gaaaggcgtg gatgttgtcg tcatccctgc gggtgtccca 540
aggaagccag gcatgacccg tgatgacctt tttaacatca atgcgggcat cgtcaagtcg 600
cttatcgagg ctgttgcaga caactgccct gaggccttca tccatattat cagcaacccg 660
gtcaactcca cggtgccgat tgctgcagag attctgaaac agaagggcgt ctacaacccc 720
aagaagctct tcggggtttc caccctggat gttgtcaggg ctaacacatt 770

<210> 170
<211> 702
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4)..(5)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g, or t

<400> 170
anannaaaaa naaaaaangg gcgagccggg gcgcacgcag caattcccat ctgcccacca 60
acccaagttg gacatggcat cagctgtcac catcagttca gtcagcgccc aggccgctct 120
ggtgtcaaaa ccaaggagtc atggcagcac gagcttcagt ggcctgaagg catcatcatc 180
gtcgatcagc ttcgaatctg gaacatcatt cctgggcaag actgcctctc ttcgggcgtc 240
agtcaccccg aggattgtgc caaaggcaaa gtctgggtct cagatatcgc ctcaggcatc 300
ttacaaggtg gcggtgcttg gtgctgccgg tggcatcggt caaccactgg gcctgctgat 360
caagatgtcg cctctggtct cggagctgcg cctgtatgat attgcgaatg tcaagggcgt 420
cgctgccgat ctcagccact gcaacacgcc tgctcaggtc atggacttca ctggccccgc 480
ggaactagca gagtgcttga aaggcgtgga tgttgtcgtc atccctgcgg gtgtcccaag 540
gaagccaggc atgacccgtg atgacctttt taacatcaat gcgggcatcg tcaagtcgct 600
tatcgaggct gttgcagaca actgccctga ggccttcatc catattatca gcaacccggt 660
caactccacg gtgccgattg ctgcagagat tctgaaacag ag 702

<210> 171

<211> 777
<212> DNA
<213> Lolium perenne

<400> 171
cagaaaaaga aaaaaagggg cgagccgggg cgcacgcagc aattcccatc tgcccaccaa 60

cccaagttgg acatggcatc agctgtcacc atcagttcag tcagcgccca ggccgctctg 120

gtgtcaaaac caaggagtca tggcagcacg agcttcagtg gcctgaaggc atcatcatcg 180

tcgatcagct tcgaatctgg aacatcattc ctgggcaaga ctgcctctct tcgggcgtca 240

gtcaccccga ggattgtgcc aaaggcaaag tctgggtctc agatatcgcc tcaggcatct 300

tacaaggtgg cggtgcttgg tgctgccggt ggcatcggtc aaccactggg cctgctgatc 360

aagatgtcgc ctctggtctc ggagctgcgc ctgtatgata ttgcgaatgt caagggcgtc 420

gctgccgatc tcagccactg caacacgcct gctcaggtca tggacttcac tggccccgcg 480

gaactagcag agtgcttgaa aggcgtggat gttgtcgtca tccctgcggg tgtcccaagg 540

aagccaggca tgacccgtga tgaccttttt aacatcaatg cgggcatcgt caagtcgctt 600

atcgaggctg ttgcagacaa ctgccctgag gccttcatcc atattatcag caacccggtc 660

aactccacgg tgccgattgc tgcagagatt ctgaaacaga agggcgtcta caaccccaag 720

aagctcttcg gggtttcccc cctggatgtt gtcagggcta acacatttgt agctcaa 777

<210> 172
<211> 707
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (659)..(659)
<223> n is a, c, g, or t

<400> 172
aaaaaaanaa ngggcgagcc ggggcgcacg cagcaattcc catctgccca ccaacccaag 60

ttggacatgg catcagctgt caccatcagt tcagtcagcg cccaggccgc tctggtgtca 120

aaaccaagga gtcatggcag cacgagcttc agtggcctga aggcatcatc atcgtcgatc 180

agcttcgaat ctggaacatc attcctgggc aagactgcct ctcttcgggc gtcagtcacc 240

ccgaggattg tgccaaaggc aaagtctggg tctcagatat cgcctcaggc atcttacaag 300

gtggcggtgc ttggtgctgc cggtggcatc ggtcaaccac tgggcctgct gatcaagatg 360

tcgcctctgg tctcggagct gcgcctgtat gatattgcga atgtcaaggg cgtcgctgcc 420

gatctcagcc actgcaacac gcctgctcag gtcatggact tcactggccc cgcggaacta 480

gcagagtgct tgaaaggcgt ggatgttgtc gtcatccctg cgggtgtccc aaggaagcca 540

ggcatgaccc gtgatgacct ttttaacatc aatgcgggca tcgtcaagtc gcttatcgag 600

gctgttgcag acaactgccc tgaggccttc atccatatta tcagcaaccc ggtcaactnc 660

acggtgccga ttgctgcaga gattctgaaa caaaaggcgt ctacaac 707

<210> 173
<211> 687
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (571)..(571)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (605)..(605)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (655)..(655)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (665)..(665)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (674)..(674)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (680)..(680)
<223> n is a, c, g, or t

<400> 173
aannaaaaaa ngggcgagcc ggggcgcacg cagcaattcc catctgccca ccaacccaag 60

ttggacatgg catcagctgt caccatcagt tcagtcagcg cccaggccgc tctggtgtca 120

aaaccaagga gtcatggcag cacgagcttc agtggcctga aggcatcatc atcgtcgatc 180

agcttcgaat ctggaacatc attcctgggc aagactgcct ctcttcgggc gtcagtcacc 240

ccgaggattg tgccaaaggc aaagtctggg tctcagatat cgcctcaggc atcttacaag 300

gtggcggtgc ttggtgctgc cggtggcatc ggtcaaccac tgggcctgct gatcaagatg 360
tcgcctctgg tctcggagct gcgcccgtat gataatgcga atgtcaaggg cgtcgctgcc 420
gatctcagcc actgcaacac gcctgctcag gtcatggact tcactggccc cgcggaacta 480
gcagagtgct tgaaaggcgt ggatgctgtc gtcatccctg cgggtgtccc aaggaagcca 540
ggcatgaccc gtgatgacct ttttaacatc natgcgggca tcgtcaagtc gcttatcgag 600
gctgntgcag acaactgccc tgaggccttc atccatatta tcagcaaccc ggtcnactcc 660
acggngccga ttgntgcaan attttgc 687

<210> 174
<211> 473
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (211)..(211)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (258)..(258)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (354)..(355)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (369)..(369)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (397)..(397)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (421)..(422)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (441)..(441)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (445)..(445)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (461)..(461)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (465)..(465)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (468)..(468)
<223> n is a, c, g, or t

<400> 174
caaggggcga gccggggcgc acgcagcaat tcccatctgc tcaccaaccc aagttggaga 60

tggcatcagc tgttaccatc agctcagtca gcgcgcaggc cgctttggtc tcgaaaccaa 120

ggaatcatgg cagcacaagc tacagtggcc taaaggcatc atcatcgtcg atcagcttcg 180

aatcagggcc atcattcctg gacaagaccg nctctcttcg ggcgactatc acctcaagga 240

ttgtgccaaa ggcaaagnct gggtctcaga tatcacctca ggcctcgtac aaggtggcgg 300

tgcttggtgc tgccggtggc atcggtcaac cactgggcct gctgatcaag atgnntcctc 360

tggtctcana gctgcgcctg tatgatattg ccaatgncaa gggagtcgct gcaaatctca 420

nncactgcaa cacgccttct naggncatgg acttcactgg nccancanaa cta 473

<210> 175
<211> 642
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (38)..(38)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (478)..(478)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (641)..(641)
<223> n is a, c, g, or t

<400> 175
anaggggcnn gccggggcgc cgcgaattcc atctgccncc accaagttgg acatggcatc 60

agctgtacca tcagttagta gcgcccaggc cgctctggtg taaaaccaag gagtcatggc 120

agcacgagct tcagtggcct gaaggcatca tcatcgtcga tcagcttcga atctggaaca 180

tcattcctgg gcaagactgc ctctcttcgg gcgtcagtca ccccgaggat tgtgccaaag 240

gcaaagtctg ggtctcagat atcgcctcag gcatcttaca aggtggcggt gcttggtgct 300

gctggtggca tcggtcaacc actgggcctg ctgatcaaga tgtctcctct ggtctcagag 360

ctgcgcctgt atgatattgc caatgtcaag ggcgtcgctg cagatcttag ccactgcaac 420

acgccttctc aggtcatgga cttcactggc cccgcggaac tagccgactg cttgaaangt 480

gtggatgttg tcgtcatccc tgcgggtgtc ccaaggaagc ctggcatgac tcgtgatgac 540

ctttttaaca tcaatgcggg catcgccaag tcgcttatca aggctgttgc agacaactcc 600

cttgaggcct tcatccatat catcagcaac ccggtcaact nc 642

<210> 176
<211> 767
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<400> 176
ggagccgggg cnccgcagca attcccatct gctcaccaac ccaagttgga gatggcatca 60

gctgttacca tcagctcagt cagcgcgcag gccgctttgg tctcgaaacc aaggaatcat 120

ggcagcacaa gctacagtgg cctaaaggca tcatcatcgt cgatcagctt cgaatcaggg 180

acatcattcc tgggcaagac cgcctctctt cgggcgacta tcacctcaag gattgtgcca 240

aaggcaaagt ctgggtctca gatatcacct caggcctcgt acaaggtggc ggtgcttggt 300

gctgccggtg gcatcggtca accactgggc ctgctgatca agatgtctcc tctggtctca 360

gagctgcgcc tgtatgatat tgccaatgtc aagggagtcg ctgcagatct cagccactgc 420

aacacgcctt ctcaggtcat ggacttcact ggcccagcag aactagctga ctgcttgaaa 480

ggtgttgatg ttgtcgtcat ccctgcgggt gtcccaagga agccaggcat gacccgtgat 540

gaccttttta acatcaatgc gggcatcgtc aagtcgctta ttgaggctgt tgcagacaac 600

tgccctgagg ccttcatcca tatcatcagc aacccggtca actccactgt gccgattgct 660

gctgagattc tgaaacagaa gggcgtctac aaccccaaga agctcttcgg ggtttccacc 720

ctggatgttg tcagagctaa cacatttgta gctcagaaga agaacct 767

<210> 177
<211> 701
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (637)..(637)
<223> n is a, c, g, or t

<400> 177
gggggcgcac gcacaattcc catctgctca ccaacccatt ggagatggca tcagctgtta 60

ccatcagctc agtcagcgcg caggccgctt tggtctcgaa accaaggaat catggcagca 120

caagctacag tggcctaaag gcatcatcat cgtcgatcag cttcgaatca gggacatcat 180
tcctgggcaa gaccgcctct cttcgggcga ctatcacctc aaggattgtg ccaaaggcaa 240
agtctgggtc tcagatatca ccccaggcct cgtacaaggt ggcggtgctt ggtgctgccg 300
gtggcatcgg tcaaccactg ggcctgctga tcaagatgtc tcctctggtc tcagagctgc 360
gcctgtatga tattgccaat gtcaagggag tcgctgcaga tctcagccac tgcaacacgc 420
cttctcaggt catggacttc actggcccag cagaactagc tgactgcttg aaaggtgttg 480
atgttgtcgt catccctgcg ggtgtcccaa ggaagccagg catgacccgt gatgaccttt 540
ttaacatcaa tgcgggcatc gtcaagtcgc ttattgaggc tgttgcagac aactgccctg 600
aggccttcat ccatatcatc agcaacccgg tcaactncac tgtgccgatt gctgctgaga 660
ttctgaaaca gaagggcgtc tacagcccca agaagctctt a 701

<210> 178
<211> 333
<212> DNA
<213> Lolium perenne

<220>
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<222> (1)..(1)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (33)..(33)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (281)..(281)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (293)..(293)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (297)..(297)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (303)..(303)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (327)..(327)
<223> n is a, c, g, or t

<400> 178

ncagcagcaa ttccctnctg cccaccaacc canttggaca tggcatcagc tgtcaccatc 60
agttcagtca gcgcccaggc cgctctggtg tcaaaaccaa ggagtcatgg cagcacgagc 120
ttcagtggcc tgaaggcatc atcatcgtcg atcagcttcg aatctggaac atcattcctg 180
ggcaagactg cctctcttcg ggcgtcagtc accccgagga ttgtgccaaa ggcaaagtct 240
gggtctcaga tatcgcctca ggcatcttac aaggtggcgg ngcttggtgc tgncggnggc 300
atnggccaac cactgggcct gctgatnaag atg 333

<210> 179
<211> 630
<212> DNA
<213> Lolium perenne

<220>
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<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (33)..(33)
<223> n is a, c, g, or t

<400> 179
gncacnacat tccccnnctg cccaccaacc canttggaat ggcatcagct gtcaccatca 60
gttcagtcag cgcccaggcc gctctggtgt caaaaccaag gagtcatggc agcacgagct 120
tcagtggcct gaaggcatca tcatcgtcga tcagcttcga atctggaaca tcattcctgg 180
gcaagactgc ctctcttcgg gcgtcagtca ccccgaggat tgtgccaaag gcaaagtctg 240
ggtctcagat atcgcctcag gcatcttaca aggtggcggt gcttggtgct gccggtggca 300
tcggtcaacc actgggcctg ctgatcaaga tgtcgcctct ggtctcggag ctgcgcctgt 360
atgatattgc gaatgtcaag ggcgtcgctg ccgatctcag ccactgcaac acgcctgctc 420
aggtcatgga cttcactggc cccgcggaac tagcagagtg cttgaaaggc gtggatgttg 480
tcgtcatccc tgcgggtgtc ccaaggaagc caggcatgac ccgtgatgac ctttttaaca 540
tcaatgcggg catcgtcaag tcgcttatcg aggctgttgc agacaactgc cctgaggcct 600
tcatccatat tatcagcaac ccggtcaact 630

<210> 180
<211> 671
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (467)..(467)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (617)..(617)
<223> n is a, c, g, or t

<400> 180
tctgcccacc aacccaagtt ggacatggca tcagctgtca ccatcagttc agtcagcgcc 60
caggccgctc tggtgtcaaa accaaggagt catggcagca cgagcttcag tggcctgaag 120
gcatcatcat cgtcgatcag cttcgaatct ggaacatcat tcctgggcaa gactgcctct 180
cttcgggcgt cagtcacccc gaggattgtg ccaaaggcaa agtctgggtc tcagatatcg 240
cctcaggcat cttacaaggt ggcggtgctt ggtgctgccg gtggcatcgg tcaaccactg 300
ggcctgctga tcaagatgtc gcctctggtc tcggagctgc gcctgtatga tattgcgaat 360
gtcaagggcg tcgctgccga tctcagccac tgcaacacgc ctgctcaggt catggacttc 420
actggccccg cggaactagc agagtgcttg aaaggcgtgg atgttgncgt catccctgcg 480
ggtgtcccaa ggaagccagg catgacccgt gatgaccttt ttaacatcaa tgcgggcatc 540
gtcaagtcgc ttatcgaggc tgttgcagac aactgccctg aggccttcat ccatattatc 600
agcaacccgg tcaactncac ggtgccgatt gctgcagaga ttctgaaaca gaagggcgtc 660
tacaacccca a 671

<210> 181
<211> 634
<212> DNA
<213> Lolium perenne

<400> 181
ttggtgctgc tggtggcatc ggtcaaccac tgggcctgct gatcaagatg tctcctctcg 60
tctcggagct gcgcctgtat gatatcgcca atgtcaaggg agtcgctgca gatctcagcc 120
actgcaacac gcctgctcag gccatggact tcactggccc cgcggaacta gcagagtgct 180
tgaaaggtgt ggatgttgtc gtcatccctg cgggtgtccc aaggaagcct ggcatgactc 240
gtgatgacct ttttaacatc aatgcgggca tcgtcaagtc gcttattgag gctgttgcag 300
acaactgccc agaggccttc atccatatca tcagcaaccc ggtcaactcc actgtgccga 360
ttgctgctga gattctgaaa cagaagggtg tctacaaccc caagaagctc ttcggggttt 420
ccaccctgga tgttgtcaga gctaacacat ttgtagctca gaagaagaac ctcagcctca 480
tcgatgttga tgtcccagtt gtcggtggcc atgctgggat cacgattctg cctctgttgt 540
ccaagactag gccttctgtc agcttcacgg acgaggaaac tgaacagctg acaaagagga 600
tacagaacgc tgggacagag gtggtggagg cgaa 634

<210> 182
<211> 777

<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (693)..(693)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (756)..(756)
<223> n is a, c, g, or t

<400> 182
gatcagccct gcaacacgcc tgctcaggcc atggacttca ctggccccgc ggaactagca 60

gagtgcttga aaggtgtgga tgttgtcgtc atccctgcgg gtgtcccaag gaagcctggc 120

atgactcgtg atgacctttt taacatcaat gcgggcatcg tcaagtcgct tattgaggct 180

gttgcagaca actgcccaga ggccttcatc catatcatca gcaacccggt caactccact 240

gtgccgattg ctgctgagat tctgaaacag aagggtgtct acaaccccaa gaagctcttc 300

ggggtttcca ccctggatgt tgtcagagct aacacatttg tagctcagaa gaagaacctc 360

agcctcatcg atgttgatgt cccagttgtc ggtggccatg ctgggatcac gattctgcct 420

ctgttgtcca agactaggcc ttctgtcagc ttcacggacg aggaaactga acagctgaca 480

aagaggatac agaacgctgg gacagaggcg gtggaggcga aggctggtgc tggctctgct 540

actctgtcca tggcttatgc cgctgccaga tttgttgagt catcgctccg cgcaatggct 600

ggtgatccag atgtttacga gtgcacgtat gttcagtctg agttaacaga gcttccattc 660

ttcgcgtcca gagttaagct tgggaaggac ggngttgagt ccatcatttc ctccgacctg 720

gagggagtga cggagtacga ggccaaggcg cttgangcat tgaaggctga gctgaag 777

<210> 183
<211> 414
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (47)..(47)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (347)..(347)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (360)..(360)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (394)..(394)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (405)..(405)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (409)..(409)
<223> n is a, c, g, or t

<400> 183
gnaaacagnn gcgncttttc ctncantgtt gccgtgcaat cgctganaag tatccagaaa 60

tcatatacga ggaagtaatt attgataact gctgtatgac gctcgtgaag aaccctggta 120

cgtttgatgt attagtgatg ccaaatctat atggcgacat tattagtgat ctatgtgctg 180

gtttgatcgg aggcttgggc ctaactccca gctgcaacat tggtgaaggt ggcatttgtc 240

ttgcagaggc tgtccatggc tctgcacctg atatatctgg caagaacctg gcaaacccaa 300

ctgctcttat gctgagtgct gttatgatgt tgcgccactt gcaattnaac gaccaagcan 360

aacggatcca caatgctatc ctccagacta tcgncgaggg gaagnacana actg 414

<210> 184
<211> 137
<212> PRT
<213> Lolium perenne

<220>
<221> misc_feature
<222> (3)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (7)..(8)
<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature
<222> (15)..(15)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (115)..(115)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (120)..(120)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (131)..(131)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (135)..(136)
<223> Xaa can be any naturally occurring amino acid

<400> 184

Lys Gln Xaa Xaa Leu Phe Xaa Xaa Cys Cys Arg Ala Ile Ala Xaa Lys
1 5 10 15

Tyr Pro Glu Ile Ile Tyr Glu Glu Val Ile Ile Asp Asn Cys Cys Met
20 25 30

Thr Leu Val Lys Asn Pro Gly Thr Phe Asp Val Leu Val Met Pro Asn
35 40 45

Leu Tyr Gly Asp Ile Ile Ser Asp Leu Cys Ala Gly Leu Ile Gly Gly
50 55 60

Leu Gly Leu Thr Pro Ser Cys Asn Ile Gly Glu Gly Gly Ile Cys Leu
65 70 75 80

Ala Glu Ala Val His Gly Ser Ala Pro Asp Ile Ser Gly Lys Asn Leu
85 90 95

Ala Asn Pro Thr Ala Leu Met Leu Ser Ala Val Met Met Leu Arg His
100 105 110

Leu Gln Xaa Asn Asp Gln Ala Xaa Arg Ile His Asn Ala Ile Leu Gln
115 120 125

Thr Ile Xaa Glu Gly Lys Xaa Xaa Thr
130 135

<210> 185
<211> 652
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (646)..(646)
<223> n is a, c, g, or t

<400> 185
gncaccncca gnnacaactc tggtacctca attgctactc cacacctcac tacttctacc 60

aatccactac acagcttcga gctaccccgc ccccgcaatc caaactacct ctccctagca 120

aatctacaac atgaaggcag tcgtagctgg agccgccggt ggcattggac agccattgtc 180

cctcctcctt aagacctgcc cgctcgtcac tgagctcgcc ctatacgatg tcgtcaacgc 240

cgtcggtgtc gcgactgacc tctcccacat ctcctcgccc gcgaaagtaa ccggctacct 300

gccggcaaat gacggtatgc agcaggctct cactggcgcc gacatcgtgg tcatccccgc 360

tggtattccc cgcaagcccg gcatgacccg tgacgacctc ttcaagatca acgccggcat 420

tgtccagggt ctcatcgagg gtgtcgccaa gcactgcccc aaggcatacg ttctcgtcat 480

ctccaacccc gtcaactcga ctgtgcccat cgccgccgag gtgctgaaga aggccggtgt 540

cttcgacccc aagaagctct tcggtgtcac caccctcgat gtcgtccgcg ccgagacctt 600

cgttgccgag atcactggcg agaaggaccc agcgaagttg aacatncccg ta 652

<210> 186
<211> 216
<212> PRT
<213> Lolium perenne

<220>
<221> misc_feature
<222> (1)..(2)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (214)..(214)
<223> Xaa can be any naturally occurring amino acid

<400> 186

Xaa Xaa Pro Xaa Thr Thr Leu Val Pro Gln Leu Leu Leu His Thr Ser

1 5 10 15

Leu Leu Leu Pro Ile His Tyr Thr Ala Ser Ser Tyr Pro Ala Pro Ala
20 25 30

Ile Gln Thr Thr Ser Pro Gln Ile Tyr Asn Met Lys Ala Val Val Ala
35 40 45

Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ser Leu Leu Leu Lys Thr
50 55 60

Cys Pro Leu Val Thr Glu Leu Ala Leu Tyr Asp Val Val Asn Ala Val
65 70 75 80

Gly Val Ala Thr Asp Leu Ser His Ile Ser Ser Pro Ala Lys Val Thr
85 90 95

Gly Tyr Leu Pro Ala Asn Asp Gly Met Gln Gln Ala Leu Thr Gly Ala
100 105 110

Asp Ile Val Val Ile Pro Ala Gly Ile Pro Arg Lys Pro Gly Met Thr
115 120 125

Arg Asp Asp Leu Phe Lys Ile Asn Ala Gly Ile Val Gln Gly Leu Ile
130 135 140

Glu Gly Val Ala Lys His Cys Pro Lys Ala Tyr Val Leu Val Ile Ser
145 150 155 160

Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val Leu Lys Lys
165 170 175

Ala Gly Val Phe Asp Pro Lys Lys Leu Phe Gly Val Thr Thr Leu Asp
180 185 190

Val Val Arg Ala Glu Thr Phe Val Ala Glu Ile Thr Gly Glu Lys Asp
195 200 205

Pro Ala Lys Leu Asn Xaa Pro Val
210 215

<210> 187
<211> 769
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (31)..(31)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (149)..(149)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (624)..(624)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (669)..(669)
<223> n is a, c, g, or t

<400> 187
gngtacacga aatagaatca acggaaagca ngaagtgatg attgggtatc agcattctgg 60

gaaggatgct ggccgtttct ctgctggttg gcacttgtac aaagctcaag aggagcttat 120

taaggttgcg gagacgtttg gggttaagnt gactatgttt catggacgag ggggtactgt 180

tggaagaggt ggcggcccta cccatcttgc tatactgtca caacctccag atactgtcca 240

tggatcactt cgggtaactg ttcaaggtga agtcattgag cagtccttcg gagaggagca 300

tttgtgtttt agaacgcttc aacgttttac agctgctact cttgaacatg gtatgcatcc 360

accaatctca cctaaaccag aatggcgtgc tttgatggat gaaatggctg ttgttgccac 420

agaggaatac cgttccattg ttttccaaga accaagattt gttgagtatt tccgccttgc 480

aacaccagag ctcgagtatg gtaggatgaa tattggaagc aggccatcaa aacgtaagcc 540

aagcggagga atcgaatcat tgcgtgcaat tccttggata tttgcttgga cacagactag 600

attccacctg ccagtgtggc ttgnttttgg tgcggccttc aagcatgtcc tgcaaaagga 660

cattcgtant cttcaaatcc ttcagcagat gtacaacgag tggccgttta gggttaccat 720

aaacctggtt gagatggtgt ttgccaaggg cgatccaggt atagcagct 769

<210> 188
<211> 256
<212> PRT
<213> Lolium perenne

<220>
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<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (50)..(50)
<223> Xaa can be any naturally occurring amino acid

<220>

<221> misc_feature
<222> (208)..(208)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (223)..(223)
<223> Xaa can be any naturally occurring amino acid

<400> 188

Xaa Thr Arg Asn Arg Ile Asn Gly Lys Xaa Glu Val Met Ile Gly Tyr
1   5   10   15

Gln His Ser Gly Lys Asp Ala Gly Arg Phe Ser Ala Gly Trp His Leu
            20   25   30

Tyr Lys Ala Gln Glu Glu Leu Ile Lys Val Ala Glu Thr Phe Gly Val
        35   40   45

Lys Xaa Thr Met Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly
    50   55   60

Gly Pro Thr His Leu Ala Ile Leu Ser Gln Pro Pro Asp Thr Val His
65   70   75   80

Gly Ser Leu Arg Val Thr Val Gln Gly Glu Val Ile Glu Gln Ser Phe
                85   90   95

Gly Glu Glu His Leu Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala
            100   105   110

Thr Leu Glu His Gly Met His Pro Pro Ile Ser Pro Lys Pro Glu Trp
        115   120   125

Arg Ala Leu Met Asp Glu Met Ala Val Val Ala Thr Glu Glu Tyr Arg
    130   135   140

Ser Ile Val Phe Gln Glu Pro Arg Phe Val Glu Tyr Phe Arg Leu Ala
145   150   155   160

Thr Pro Glu Leu Glu Tyr Gly Arg Met Asn Ile Gly Ser Arg Pro Ser
                165   170   175

Lys Arg Lys Pro Ser Gly Gly Ile Glu Ser Leu Arg Ala Ile Pro Trp
            180   185   190

Ile Phe Ala Trp Thr Gln Thr Arg Phe His Leu Pro Val Trp Leu Xaa
        195   200   205

Phe Gly Ala Ala Phe Lys His Val Leu Gln Lys Asp Ile Arg Xaa Leu
    210   215   220

Gln Ile Leu Gln Gln Met Tyr Asn Glu Trp Pro Phe Arg Val Thr Ile

225 230 235 240

Asn Leu Val Glu Met Val Phe Ala Lys Gly Asp Pro Gly Ile Ala Ala
245 250 255

<210> 189
<211> 1640
<212> DNA
<213> Lolium perenne

<220>
<221> misc_feature
<222> (24)..(24)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (31)..(31)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (192)..(192)
<223> n is a, c, g, or t

<220>
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<222> (1194)..(1194)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1514)..(1514)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1530)..(1530)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1584)..(1584)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1616)..(1616)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1622)..(1622)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1633)..(1633)
<223> n is a, c, g, or t

<400> 189
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ttggtgctta catcatctca atggcaactg ccccatctga tgtgcttgct gttgagcttt 120

tgcagcggga gtgccatata aaaaagccat tgagagttgt tccactattt gaaaagcttg 180
cagatcttga ancagctcca gcatctgttg cacgactatt ttcaatagac tggtacatga 240
atagaatcaa tggcaagcag gaggtcatga ttggatactc agactctggg aaggacgctg 300
ggcgtctctc tgcagcgtgg caaatgtata aagcacaaga agatctcata aaggtggcaa 360
agcaatatgg agtaaagtta acaatgtttc atggaagagg tggaacggtt ggcagaggag 420
gtggtcccag tcatcttgct atattatctc aaccaccaga cacgatacaa ggatcacttc 480
gtgtaacagt tcaaggcgag gtcatagagc actcatttgg agaggaacac ttgtgcttca 540
gaactctgca acgtttcact gcagctactc ttgagcatgg aatgcatcct ccaatttcac 600
ccaagccaga atggcgtgct ataatggatg agatggctgt agtggcaaca aaagaatatc 660
gatcaattgt cttccaagaa ccacgttttg tcgaatactt ccgctcggca acacctgaga 720
ctgaatatgg tcggatgaat attggtagcc ggccatcaaa gagaaagcct agtggaggca 780
tagaatcgct ccgtgcaatt ccatggatct ttgcttggac acagacaagg tttcatcttc 840
ctgtatggct tggatttggt gcagcgttca aacatatcat gcagaaggac atcaggaata 900
tccatactct gaaagaaatg tacaatgagt ggccattctt tagggtcacc cttgacttgc 960
ttgagatggt ttttgccaag ggagatccag gaattgctgc tttatatgac aaattgcttg 1020
tgtctgaaga tctgcagccc tttggggagc agctgagaaa caactttgaa gagacgaaac 1080
agttactcct tcaggttgct ggccacaagg acgttcttga aggggatcct tacctgaagc 1140
agcgtctgcg gttgcgtgag tcatacatca caacattgaa tgtttgccaa gccnacaccc 1200
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Asp Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys His Ile Lys Lys
        35                  40                  45

Pro Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala Asp Leu Glu Xaa
    50                  55                  60

Ala Pro Ala Ser Val Ala Arg Leu Phe Ser Ile Asp Trp Tyr Met Asn
65                  70                  75                  80

Arg Ile Asn Gly Lys Gln Glu Val Met Ile Gly Tyr Ser Asp Ser Gly
                85                  90                  95

Lys Asp Ala Gly Arg Leu Ser Ala Ala Trp Gln Met Tyr Lys Ala Gln
            100                 105                 110

Glu Asp Leu Ile Lys Val Ala Lys Gln Tyr Gly Val Lys Leu Thr Met
        115                 120                 125

Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro Ser His
    130                 135                 140

Leu Ala Ile Leu Ser Gln Pro Pro Asp Thr Ile Gln Gly Ser Leu Arg
145                 150                 155                 160

Val Thr Val Gln Gly Glu Val Ile Glu His Ser Phe Gly Glu Glu His
                165                 170                 175

Leu Cys Phe Arg Thr Leu Gln Arg Phe Thr Ala Ala Thr Leu Glu His
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Gly Met His Pro Pro Ile Ser Pro Lys Pro Glu Trp Arg Ala Ile Met
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Asp Glu Met Ala Val Val Ala Thr Lys Glu Tyr Arg Ser Ile Val Phe
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Gln Glu Pro Arg Phe Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr
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Glu Tyr Gly Arg Met Asn Ile Gly Ser Arg Pro Ser Lys Arg Lys Pro
245 250 255

Ser Gly Gly Ile Glu Ser Leu Arg Ala Ile Pro Trp Ile Phe Ala Trp
260 265 270

Thr Gln Thr Arg Phe His Leu Pro Val Trp Leu Gly Phe Gly Ala Ala
275 280 285

Phe Lys His Ile Met Gln Lys Asp Ile Arg Asn Ile His Thr Leu Lys
290 295 300

Glu Met Tyr Asn Glu Trp Pro Phe Phe Arg Val Thr Leu Asp Leu Leu
305 310 315 320

Glu Met Val Phe Ala Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp
325 330 335

Lys Leu Leu Val Ser Glu Asp Leu Gln Pro Phe Gly Glu Gln Leu Arg
340 345 350

Asn Asn Phe Glu Glu Thr Lys Gln Leu Leu Leu Gln Val Ala Gly His
355 360 365

Lys Asp Val Leu Glu Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu
370 375 380

Arg Glu Ser Tyr Ile Thr Thr Leu Asn Val Cys Gln Ala Xaa Thr Leu
385 390 395 400

Lys Arg Ile Arg Asp Pro Ser Phe Glu Val Thr Pro Gln Gln Ala Pro
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Leu Ser Lys Glu Phe Ala Asp Glu Lys Glu Pro Ala Glu Leu Val Gln
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tgcagcggga gtgccatata aaaaagccat tgagagttgt tccactattt gaaaagcttg 180

cagatcttga ancagctcca gcatctgttg cacgactatt ttcaatagac tggtacatga 240

atagaatcaa tggcaagcag gaggtcatga ttggatactc agactctggg aaggacgctg 300
ggcgtctctc tgcagcgtgg caaatgtata aagcacaaga agatctcata aaggtggcaa 360
agcaatatgg agtaaagtta acaatgtttc atggaagagg tggaacggtt ggcagaggag 420
gtggtcccag tcatcttgct atattatctc aaccaccaga cacgatacaa ggatcacttc 480
gtgtaacagt tcaaggcgag gtcatagagc actcatttgg agaggaacac ttgtgcttca 540
naactctgca acgtttcact gcagctactc ttgagcatgg aatgcatcct ccaatttccc 600
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atctcaacca ccagacacga tacaaggatc acttcgtgta acagttcaag gcgaggtcat 180
agagcactca tttggagggg aacacttgtg cttcagaact ctgcaacgtt tcactgcagc 240
tactcttgag catggaatgc atcctccaat ttcacccaag ccagaatggc gtgctataat 300
ggatgagatg gctgtagtgg caacaaaaga atatcgatca attgtcttcc aagaaccacg 360
ttttgtcgaa tacttccgct cggcaacacc tgagactgaa tatggtcgga tgaatattgg 420
tagccggcca tcaaagagaa agcctagtgg aggcatagaa tcgctccgtg caattccatg 480
gatctttgct tggacacaga caaggtttca tcttcctgta tggcttggat ttggtgcagc 540
gttcaaacat atcatgcaga aggacatcag gaatatccat actctgaaag aaatgtacaa 600
tgagtggcca ttctttaggg tcacccttga cttgcttgag atggtttttg ccaagggaga 660
tccaggaatt gctgctttat atgacaaatt gcttgtgtct gaagatctgc agccctttgg 720
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atagagcact catttggaga ggaacacttg tgcttcagaa ctctgcaacg tttcactgca 180
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atggatgaga tggctgtagt ggcaacaaaa gaatatcgat caattgtctt ccaagaacca 300
cgttttgtcg aatacttccg ctcggcaaca cctgagactg aatatggtcg gatgaatatt 360
ggtagccggc catcaaagag aaagcctagt ggaggcatag aatcgctccg tgcaattcca 420
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gatccaggga ttgctgcttt atatgacaaa ttgcttgtgt ctgaagatct gcagcccttt 660
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tgtgcttcag aactctgcaa cgtttcactg cagctactct tgagcatgga atgcatcctc 180
caatttcacc caagccagaa tggcgtgcta taatggatga gatggctgta gtggcaacaa 240
aagaatatcg atcaattgtc ttccaagaac cacgttttgt cgaatacttc cgctcggcaa 300
cacctgagac tgaatatggt cggatgaata ttggtagccg gccatcaaag agaaagccta 360
gtggaggcat agaatcgctc cgtgcaattc catggatctt tgcttggaca cagacaaggt 420
ttcatcttcc tgtatggctt ggatttggtg cagcgttcaa acatatcatg cagaaggaca 480

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tcaggaatat ccatactctg aaagaaatgt acaatgagtg gccattcttt agggtcaccc    540
ttgacttgct tgagatggtt tttgccgagg gagatccagg aattgctgct ttatatgaca    600
aattgcttgt gtctgaagat ctgcagccct ttggggagca gctgagaaac aactttgaag    660
agacgaaaca gttactcctt caggttgctg gccacaagga cgttcttgag gggatccttt    720
acctgaagca gcgtctgcgg ttgcgtgagt catacatcac aaca                      764
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tctgcagccc tttggggagc ngctgagaaa caactttgaa gagacgaaac agttactcct    120
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tcaggttgct ggccacaagg acgttcttga aggggatcct tacctgaagc agcgtctgcg 180
gttgcgtgag tcatacatca caacattgaa tgtttgccaa gcctacaccc tgaagcggat 240
aagagacccct agcttcgagg tgacaccgca gcaggcacct ctgtcgaagg agttcgctga 300
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ggaggacacc ctcatcctta ccatgaaggg tattgctgtg gaatgcaaaa cacaggctag 420
gccagtttgc ctattggaat aactgtcatt ccgtcagatg gggcgtgaat atgtgtgttc 480
cccaaatgct agtgaaccct ggaggcattt tggccactta catgcctttt ggttatgnat 540
gnacttgatc ttaatgncaa gggttgttga agcctgatct aaataaaata tggaacaatg 600
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cacaacattg aatgtttgcc aagcgnncac cctgaagcgg ataagagacc ctagcttcga 120
ggtgacaccg cagcaggcac ctctgtcgaa ggagttcgct gatgagaagg agccagctga 180
gctggtgcaa ctgaaccgtg ggagcgagta cgccccaggc ctggaggaca ccctcatcct 240
taccatgaag ggtatttgct gtggaatgca aaacacaggc taggccagtt tgcctatttg 300
gaataactgt catcccgtca gatgggcgtg aatatgtgtg ttccccaaat gctagtgaac 360
cctggaggca tttggccact tacatgcctt ttggttatgg atgnactttg atcttaatgt 420
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gcacactgaa tatggtcggc atgaatattg gtagccggcc atcaaagaga aagcctagtg 120

gaggcataga atcgctccgt gcaattccat gcatctttgn ttggacacag acaaggnttn 180

atntttcctgt atgncttgna ttcgnctcca ccnccacccc cnta 224

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<400> 198

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            20   25   30

Pro Ser Lys Arg Lys Pro Ser Gly Gly Ile Glu Ser Leu Arg Ala Ile
        35   40   45

Pro Cys Ile Phe Xaa Trp Thr Gln Thr Arg Xaa Xaa Xaa Pro Val Xaa
    50   55   60

Leu Xaa Phe Xaa Ser Thr Xaa Thr Pro
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gacccagact accacgtcgc actgcggccc catctttcca aggaggttat ggacacaagc 180

aagccggctt ccgagcttgt gacgctgaac ccggccagcg agtacgcccc ggggctggag 240

gacaccctca tcttgaccat gaagggcgtt gctgccggtc tgcaaaacac cggttagggc 300

caggagagat gcctgatcac catctttttg tatcttcatg atgatgcgat gtttttcttt 360

agtcgtttgc ggtgggcctt atatctctcg gacgtagctg catctgtctc cctgctcagt 420

gaggaataat ggcgtttcgc ccaagtatat tgataaataa agggaaccga tgttaatttc 480

agatttgttt gttagtaatt gttctattta ttttgcgaaa aaaaaaa 527

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<400> 200

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Arg Leu Arg Leu Arg Asp Ala Tyr Ile Thr Thr Met Asn Val Cys Gln
20 25 30

Ala Tyr Thr Leu Lys Arg Ile Arg Asp Pro Asp Tyr His Val Ala Leu
35 40 45

Arg Pro His Leu Ser Lys Glu Val Met Asp Thr Ser Lys Pro Ala Ser
50 55 60

Glu Leu Val Thr Leu Asn Pro Ala Ser Glu Tyr Ala Pro Gly Leu Glu
65 70 75 80

Asp Thr Leu Ile Leu Thr Met Lys Gly Val Ala Ala Gly Leu Gln Asn
85 90 95

Thr Gly

<210> 201
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atagaagatc tgatgtttga gctctctatg tggcgctgca gtgatgaact tagggtccgt 120

gcagatgaag tacatctgtc ctcaaaaaaa aaatctgcaa agcattacat agagttctgg 180

aagcaagttc ctccaaatga accttatcgt gtcatacttg gcgatgtcag ggataaactg 240

tactatacgc gcgaacgttc tcgccacata ttgacaactg gaatttcaga cattccagaa 300

gngtcaactt ttactaatgt tgaactgttt ctggaacctc ttgagctgtg ctacagatcc 360

ttatcttnct gtggngacaa anctattgct ganggaagcc ttcttgattt ctngcgnncn 420

gnatcnactt tgtgggctta ctctngcgaa 450

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<400> 202

Val Thr Arg Ala Val Cys Leu Leu Ala Arg Xaa Met Ala Ala Asn Leu
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Tyr Phe Ser Gln Ile Glu Asp Leu Met Phe Glu Leu Ser Met Trp Arg
20 25 30

Cys Ser Asp Glu Leu Arg Val Arg Ala Asp Glu Val His Leu Ser Ser
35 40 45

Lys Lys Lys Ser Ala Lys His Tyr Ile Glu Phe Trp Lys Gln Val Pro
50 55 60

Pro Asn Glu Pro Tyr Arg Val Ile Leu Gly Asp Val Arg Asp Lys Leu
65 70 75 80

Tyr Tyr Thr Arg Glu Arg Ser Arg His Ile Leu Thr Thr Gly Ile Ser

85 90 95

Asp Ile Pro Glu Xaa Ser Thr Phe Thr Asn Val Glu Leu Phe Leu Glu
100 105 110

Pro Leu Glu Leu Cys Tyr Arg Ser Leu Ser Xaa Cys Xaa Asp Lys Xaa
115 120 125

Ile Ala Xaa Gly Ser Leu Leu Asp Phe Xaa Xaa Xaa Xaa Xaa Thr Leu
130 135 140

Trp Ala Tyr Ser Xaa Glu
145 150

<210> 203
<211> 644
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<213> Lolium perenne

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<223> n is a, c, g, or t

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cactccgggt gactgttcaa ggtgaagtta ttgagcagag ctttggggag gaacacttgt 120
gcttcaggac gctgcagcgt ttcacagctg ctactcttga gcatgggatg cgtccaccca 180
tttcaccaaa gccagagtgg cgagctcttc ttgatgagat ggctgtggtt gcaactgagg 240
aataccggtc aatcgtcttc caagaaccac gcttcgtcga gtatttccgc cttgcaacac 300
cagagacaga gtatggcagg atgaatatag gaagcaggcc atcaaagaga aaaccaagtg 360
gtggcattga atcactccgt gcaattccat ggatcttcgc atggacgcag acacggttcc 420
accttccagt ctggttgggc tttggtggtg cattcaagca tatcctcaag aaggacatca 480
gaaatttcca tatgctccag gagatgtaca acgagtggcc atttttcagg gtcacgatcg 540
atcttgttga gatggtgttc gccaagggta accctggcat tgctgccttg tatgacaggc 600
tcctggtttc agaggagcta cagccactgg gtgacaagct gagg 644

<210> 204
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<212> PRT
<213> Lolium perenne

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<400> 204

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Gly Gly Gly Pro Xaa His Leu Ala Xaa Leu Ser Xaa Pro Pro Xaa Thr
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Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly Glu Val Ile Glu Gln
            20                  25                  30

Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr Leu Gln Arg Phe Thr
        35                  40                  45

Ala Ala Thr Leu Glu His Gly Met Arg Pro Pro Ile Ser Pro Lys Pro
    50                  55                  60

Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val Val Ala Thr Glu Glu
65                  70                  75                  80

Tyr Arg Ser Ile Val Phe Gln Glu Pro Arg Phe Val Glu Tyr Phe Arg
                85                  90                  95

Leu Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met Asn Ile Gly Ser Arg
            100                 105                 110

Pro Ser Lys Arg Lys Pro Ser Gly Gly Ile Glu Ser Leu Arg Ala Ile
        115                 120                 125

Pro Trp Ile Phe Ala Trp Thr Gln Thr Arg Phe His Leu Pro Val Trp
    130                 135                 140

Leu Gly Phe Gly Gly Ala Phe Lys His Ile Leu Lys Lys Asp Ile Arg
145                 150                 155                 160
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Asn Phe His Met Leu Gln Glu Met Tyr Asn Glu Trp Pro Phe Phe Arg
165 170 175

Val Thr Ile Asp Leu Val Glu Met Val Phe Ala Lys Gly Asn Pro Gly
180 185 190

Ile Ala Ala Leu Tyr Asp Arg Leu Leu Val Ser Glu Glu Leu Gln Pro
195 200 205

Leu Gly Asp Lys Leu Arg
210

<210> 205
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<213> Trifolium repens

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atggccaaag acccagttcg tgttcttgtc actggtgctg caggacaaat tgggtatgct 120

cttgtcccta tgattgctag gggagtgatg ctcggccctg accagcctgt gatcctccac 180

atgcttgaca ttccacctgc agccgaatca ctcaacggtg ttaaaatgga gttggtggat 240

gctgcattcc ctcttcttaa aggagttgtt gctacaactg atgtggttga ggcatgcact 300

ggtgtcaata ttgccgttat ggttggtggg ttccctagaa aagaaggtat ggagaggaaa 360

gatgtgatga caaaaaatgt ctctatttac aagtctcagg cttctgccct tgaaaaacat 420

gctgctgcaa actgcaaggt tcttgttgtt gccaacccag caaacaccaa tgcattgatc 480

ttgaaggaat atgctccatc cattcctgag aaaaacattt ctgctttgac tagattggac 540

cataacaggg cactaggtca aatttctgaa agactaaacg ttgaagtttc tgatgtgaaa 600

aatgttataa tatgggggaa atnattcatc aactcaatac cctgntgtna accacncaac 660

cgttaaaatc tcct 674

<210> 206
<211> 201
<212> PRT
<213> Trifolium repens

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<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

<400> 206

Met Ala Lys Asp Pro Val Arg Val Leu Val Thr Gly Ala Ala Gly Gln
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Ile Gly Tyr Ala Leu Val Pro Met Ile Ala Arg Gly Val Met Leu Gly
            20   25   30

Pro Asp Gln Pro Val Ile Leu His Met Leu Asp Ile Pro Pro Ala Ala
        35   40   45

Glu Ser Leu Asn Gly Val Lys Met Glu Leu Val Asp Ala Ala Phe Pro
    50   55   60

Leu Leu Lys Gly Val Val Ala Thr Thr Asp Val Val Glu Ala Cys Thr
65   70   75   80

Gly Val Asn Ile Ala Val Met Val Gly Gly Phe Pro Arg Lys Glu Gly
                85   90   95

Met Glu Arg Lys Asp Val Met Thr Lys Asn Val Ser Ile Tyr Lys Ser
            100   105   110

Gln Ala Ser Ala Leu Glu Lys His Ala Ala Ala Asn Cys Lys Val Leu
        115   120   125

Val Val Ala Asn Pro Ala Asn Thr Asn Ala Leu Ile Leu Lys Glu Tyr
    130   135   140

Ala Pro Ser Ile Pro Glu Lys Asn Ile Ser Ala Leu Thr Arg Leu Asp
145 150 155 160

His Asn Arg Ala Leu Gly Gln Ile Ser Glu Arg Leu Asn Val Glu Val
165 170 175

Ser Asp Val Lys Asn Val Ile Ile Trp Gly Lys Xaa Phe Ile Asn Ser
180 185 190

Ile Pro Xaa Cys Xaa Pro Xaa Asn Arg
195 200

<210> 207
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atggccaaag acccagttcg tgttcttgtc nctggtgctg caggacaact tgggtatgct 120

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atgcttgaca ttncacctgg ag 202

<210> 208
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<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

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tggccaaaga cccagttcgt gttcttgtca ctggtgctgc aggacaaatt gggtatgctc 120

tcgtccctat gattgctagg ggagtgatgc tcggccctga ccagcctgtg atcctccaca 180

tgcttgacat cccacctgca gccgaatcac tgaacggtgt aaaaatggag ttggtggatg 240

ctgcattccc tcttcttaaa ggagttgttg ctaccactga tgtggttgag gcatgcactg 300

gggtcaatat tgccgttatg gttggcgggt tccctagaaa agaaggtatg gagaggaaag 360
atgtgatgac aaaaaatgtc tctatttaca agtctcaggc ttctgccctt gaaaaacatg 420
ctgctgcaaa ctgcaaggtt cttgttgttg ccaacccagc aaacaccaat gcattgatct 480
tgaaggaata tgctccatcc attcctgaga aaaacatttc tgctttgact agattggacc 540
ataacagggc acttggtca 559

<210> 209
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<212> DNA
<213> Trifolium repens

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gccaaagacc cagttcgtgt tcttgtcact ggtgctgcag gacaaattgg gtatgctctt 120
gtccctatga ttgctagggg agtgatgctc ggccctgacc agcctgtgat cctccacatg 180
cttgacattc cacctgcagc cgaatcactc aacggtgtta aaatggagtt ggtggatgct 240
gcattccctc ttcttaaagg agttgttgct acaactgatg tggttgaggc atgcactggt 300
gtcaatattg ccgttatggt tggtgggttc cctagaaaag aaggtatgga gaggaaagat 360
gtgatgacaa aaaatgtctc tatttacaag tctcaggctt ctgcccttga aaaacatgct 420
gctgcaaact gcaaggttct tgttgttgcc aacccagcaa acaccaatgc attgatcttg 480
aaggaatatg ctccatccat tcctgagaaa aacatttctg ctttgactag attggaccat 540
aacagggcac taggtcaaat ttctgaa 567

<210> 210
<211> 575
<212> DNA
<213> Trifolium repens

<400> 210
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gccaaagacc cagttcgtgt tcttgtcact ggtgctgcag gacaaattgg gtatgctctt 120
gtccctatga ttgctagggg agtgatgctc ggccctgacc agcctgtgat cctccacatg 180
cttgacattc cacctgcagc cgaatcactg aacggtgtta aaatggagtt ggtggatgct 240
gcattccctc ttcttaaagg agttgttgct acaactgatg tggttgaggc atgcactggt 300
gtcaatattg ccgttatggt tggtgggttc cctagaaaag aaggtatgga gaggaaagat 360
gtgatgacaa aaaatgtctc tatttacaag tctcaggctt ctgcccttga aaaacatgct 420
gctgcaaact gcaaggttct tgttgttgcc aacccagcaa acaccaatgc attgatcttg 480
aaggaatatg ctccatccat tcctgagaaa aacatttctg ctttgactag attggaccat 540

aacagggcac taggtcaaat ttctgaaaga ctaaa 575

<210> 211
<211> 606
<212> DNA
<213> Trifolium repens

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<400> 211
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caaagaccca gttcgtgttc ttgtcactgg tgctgcagga caacttgggt atgctcttgt 120
ccctatgatt gctaggggag tgatgctcgg ccctgaccag cctgtgatcc tccacatgct 180
tgacattcca cctgcagccg aatcactcaa cggtgttaaa atggagttgg tggatgctgc 240
attccctctt cttaaaggag ttgttgctac aactgatgtg gttgaggcat gcactggtgt 300
caatattgcc gttatggttg gtgggttccc tagaaaagaa ggtatggaga ggaaagatgt 360
gatgacaaaa aatgtctcta tttacaagtc tcaggcttct gcccttgaaa aacatgctgc 420
tgcaaactgc aaggttcttg ttgttgccaa cccagcaaac accaatgcat tgatcttgaa 480
ggaatatgct ccatccattc ctgagaaaaa catttctgct ttgactagat tggaccataa 540
cagggcacta ggtcaaattt ctgaaagact aaacgttgaa gtttctgatg tgaaaaatgt 600
tataat 606

<210> 212
<211> 344
<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<400> 212
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aaagacccag ttcgtgttct tgtcactggt gctgcaggac aacttgggta tgctcttgtc 120

cctatgattg ctaggggagt gatgctcggc cctgaccagc ctgtgatcct ccacatgctt 180

gacattccac ctgcagccga atcactcaac ggtgttaaaa tggagttggt ggatgctgca 240

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aatattgacg ntatggntgg ngggttncnt acnanacaac gtnt 344

<210> 213
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ttcgtgttct tgtcactggt gctgcaggac aaattgggta tgctcttgtc cctatgattg 120
ctaggggagt gatgctcggc cctgaccagc ctgtgatcct ccacatgctt gacattccac 180
ctgcagccga atcactcaac ggtgttaaaa tggagttggt ggatgctgca ttccctcttc 240
ttaaaggagt tgttgctaca actgatgtgg ttgaggcatg cactggtgtc aatattgccg 300
ttatggttgg tgggttccct agaaaagaag gtatggagag gaaagatgtg atgacaaaaa 360
atgtctctat ttacaagtct caggcttctg cccttgaaaa acatgctgct gcaaactgca 420
aggttcttgt tgttgccaac ccagcaaaca ccaatgcatt gatcttgaag gaatatgctc 480
catccattcc tgagaaaaac atttctgctt tgactagatt ggaccataac agggcactag 540
gtcaaatttc tgaaagac 558

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taggggagtg atgctcggcc ctgaccagcc tgtgatcctc cacatgcttg acattccacc 180
tgcagccgaa tcactcaacg gtgttaaaat ggagttggtg gatgctgcat tccctcttct 240
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tatggttggt gggttcccta gaaaagaagg tatggagagg aaagatgtga tgacaaaaaa 360
tgtctctatt tacaagtctc aggcttctgc ccttgaaaaa catgctgctg caaactgcaa 420
ggttcttgtt gttgccaacc cagcaaacac caatgcattg atcttgaagg aatatgctcc 480
atccattcct gagaaaaaca tttctgcttt gactagattg gaccataaca gggcactagg 540
tcaaatttct gaaagactaa acgttgaagt ttctgatgtg aaaaatgtta taatctggg 599

<210> 215
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<212> DNA
<213> Trifolium repens

<220>
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<223> n is a, c, g, or t

<400> 215
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tgttcttgta ctggtgctgc aggacaactt gggtatgctc ttgtccctat gattgctagg 120
ggagtgatgc tcggccctga ccagcctgtg atcctccaca tgcttgacat tccacctgca 180
gccgaatcac tcaacggtgt taaaatggag ttggtggatg ctgcattccc tcttcttaaa 240
ggagttgttg ctacaactga tgtggttgag gcatgcactg gtgtcaatat tgccgttatg 300
gttggtgggt tccctagaaa agaaggtatg gagaggaaag atgtgatgac aaaaaatgtc 360
tctatttaca agtctcaggc ttctgccctt gaaaaacatg ctgctgcaaa ctgcaaggtt 420
cttgttgttg ccaacccagc aaacaccaat gcattgatct tgaaggaata tgctccatcc 480
attcctgaga aaaacatttc tgctttgact agattggacc ataacagggc actaggtcaa 540
atttctgaaa gactaaacgt tgaagtttct gatgtgg 577

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tgttcttgtc actggtgctg caggacaaat tgggtatgct cttgtcccta tgattgctag 120
gggagtgatg ctcggccctg accagcctgt gatcctccac atgcttgaca ttccacctgc 180
agccgaatca ctcaacggtg ttaaaatgga gttggtggat gctgcattcc ctcttcttaa 240
aggagttgtt gctacaactg atgtggttga ggcatgcact ggtgtcaata ttgccgttat 300
ggttggtggg ttccctagaa aagaaggtat ggagaggaaa gatgtgatga caaaaaatgt 360
ctctatttac aagtctcagg cttctgccct tgaaaaacat gctgctgcaa actgcaaggt 420
tcttgttgtt gccaacccag caaacaccaa tgcattgatc ttgaaggaat atgctccatc 480
cattcctgag aaaaacattt ctgctttgac tagattggac cataacaggg cactaggtca 540
aatttctgaa agactaaacg ttgaagtttc tgatgtgaaa aatgttataa tctg 594

<210> 217
<211> 653
<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

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ggggagtgat gctcggccct gaccagcctg tgatcctcca catgcttgac attccacctg 180

cagccgaatc actcaacggt gttaaaatgg agttggtgga tgctgcattc cctcttctta 240

aaggagttgt tgctacaact gatgtggttg aggcatgcac tggtgtcaat attgccgtta 300

tggttggtgg gttccctana aaagaangta tggagaggaa agatgtgatg acaaaaatgt 360

ctctatttac aagtcttaag cttttgncct tgaaaaacat gctgctgcaa actgcaaggt 420

tcttgttgtt gncaacccac caaacaccaa tgcattgatc ttgaaggaat atgctccatn 480

cattcctgan aaaaacattt ntgctttgac tagattggac cataacaggg cactagggca 540

aatttntgaa anactaaacg ttgaagtttn tgatgtgaaa aatgttatat atgggggaaa 600

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<223> n is a, c, g, or t

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tcaaaaatgg ccaaagaccc agttcgtgtt ctcgtcactg gtgctgcagg gcaaattggt 180

tatgcacttg tccctatgat tgctagggga gtgatgcttg gtcctgatca acctgtgatc 240
cttcacatgc ttgatattcc tccagcagca gagtcattga atggagttaa gatggagttg 300
gtcgatgctg catttccact tcttaaaggt gttgttgcta caactgatgt tgttgaagca 360
tgcactggag tcaatattgc agtcatggtt ggtggattcc caagaaaaga aggtatggag 420
aggaaggatg tgatgtctaa gaacgtctct atttacaagt cccaggcttc tgcccttgaa 480
aagcatgctg ctgccaactg caaggttttg gttgttgcta acccagcaaa caccaatgca 540
ttgatcttga aggaatttgc tccatctatt ccagagaaaa acatttcttg tttgactaga 600
cttgatcaca acagggcatt gggccaaatt tctgaaagat tgaatgttca agtttctgat 660
gtaaagaatg tcattatctg ggtaatcat tcatcaactc agtatcctga tgtcaaccat 720
gcaactgtta acacccccgc tggggagaag cctgtccgtg agcttgtttc tgatgacgcc 780
tggttgaatg gagaattcat atctaccgtt caacaacgtg gtgctgcaat tattaaggct 840
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gttcttggaa ctccccaggg caccttcgtt tcaatgggag tgtattctga tggttcttac 960
aacgtaccag ctggactcat ctattcattc cctgtcacca ctgctaatgg ggaatggaaa 1020
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<210> 219
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<400> 219

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1 5 10 15

Ile Gly Tyr Ala Leu Val Pro Met Ile Ala Arg Gly Val Met Leu Gly
20 25 30

Pro Asp Gln Pro Val Ile Leu His Met Leu Asp Ile Pro Pro Ala Ala
35 40 45

Glu Ser Leu Asn Gly Val Lys Met Glu Leu Val Asp Ala Ala Phe Pro
50 55 60

Leu Leu Lys Gly Val Val Ala Thr Thr Asp Val Val Glu Ala Cys Thr
65 70 75 80

Gly Val Asn Ile Ala Val Met Val Gly Gly Phe Pro Arg Lys Glu Gly
85 90 95

Met Glu Arg Lys Asp Val Met Ser Lys Asn Val Ser Ile Tyr Lys Ser
100 105 110

Gln Ala Ser Ala Leu Glu Lys His Ala Ala Ala Asn Cys Lys Val Leu
115 120 125

Val Val Ala Asn Pro Ala Asn Thr Asn Ala Leu Ile Leu Lys Glu Phe
130 135 140

Ala Pro Ser Ile Pro Glu Lys Asn Ile Ser Cys Leu Thr Arg Leu Asp
145 150 155 160

His Asn Arg Ala Leu Gly Gln Ile Ser Glu Arg Leu Asn Val Gln Val
165 170 175

Ser Asp Val Lys Asn Val Ile Ile Trp Gly Asn His Ser Ser Thr Gln
180 185 190

Tyr Pro Asp Val Asn His Ala Thr Val Asn Thr Pro Ala Gly Glu Lys
195 200 205

Pro Val Arg Glu Leu Val Ser Asp Asp Ala Trp Leu Asn Gly Glu Phe
210 215 220

Ile Ser Thr Val Gln Gln Arg Gly Ala Ala Ile Ile Lys Ala Arg Lys
225 230 235 240

Leu Ser Ser Ala Leu Ser Ala Ala Ser Ala Ala Cys Asp His Ile Arg
245 250 255

Asp Trp Val Leu Gly Thr Pro Gln Gly Thr Phe Val Ser Met Gly Val
260 265 270

Tyr Ser Asp Gly Ser Tyr Asn Val Pro Ala Gly Leu Ile Tyr Ser Phe
275 280 285

Pro Val Thr Thr Ala Asn Gly Glu Trp Lys Ile Val Gln Gly Leu Ser
290 295 300

Ile Asp Glu Phe Ser Arg Lys Lys Leu Asp Leu Thr Ala Glu Glu Leu
305 310 315 320

Ser Glu Glu Lys Ser Leu Ala Tyr
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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acccagttcg tgttctcgtc actggtgctg cagggcaaat tggttatgca cttgtcccta 180

tgattgctag gggagtgatg cttggtcctg atcaacctgt gatcctacac atgcttgata 240

ttccacccgc agcagagtca ttgaatggag ttaagatgga gatggncgat gctgnattnn 300

cacttgttaa aggngangct gct 323

<210> 221
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<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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ccagttcgtg ttctcgtcac tggtgctgca gggcaaattg gttatgcact tgtccctatg 180

attgctaggg gagtgatgct tggtcctgat caacctgtga tcctacacat gcttgatatt 240

ccacccgcag cagagtcatt gaatggagtt aagatggagt tggtcgatgc tgcatttcca 300

cttgttaaag gtgntgatgn tacaactgat gatggngacg natnnnctgg 350

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tgttctcgtc actggtgctg caggccaaat tggttatgca cttgtcccta tgattgctag 180

gggagtgatg cttggtcctg atcaacctgt gatccttcac atgcttgata tccctccagc 240

agcagagtca ttgaatggag ttaaaatgga gttggtggat gctgcatttc cacttcttaa 300

aggtgttgtt gctacaactg atgttgttga agcatgcact ggagtcaata ttgcagtcat 360

ggttggtgga ttcccaagaa aagaaggtat ggagaggaag gatgtgatga ctaagaatgt 420

ctctatttac aagtcccagg cttctgccct tgaaaagcat gctgctgcca actgcaaggt 480

tttggttatt gctaacccag caaataccaa tgcattgatc ttgaaggagt ttgctccatc 540

tattccagag aaaaacattt cagctttgac tagacttgat cacaa 585

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<223> n is a, c, g, or t

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taatcttcgc ggttcgattc cttccgtttc ttcagcaatg gccaaagacc cagttcgtgt 120

cctcgttact ggtgctgcag gccaaattgg ttatgcactt gtccctatga ttgctagggg 180

agtgatgctt ggtcctgatc aacctgtgat ccttcacatg cttgatatcc ctccagcagc 240

agagtcattg aatggagtta aaatggagtt ggtggatgct gcatttccac ttcttaaagg 300

cgttgttgct acaactgatg ttgttgaagc atgcactgga gtcaatattg cagtcatggt 360

tggtggattc ccaagaaaag aaggtatgga gaggaaggat gtgatgacta agaatgtctc 420
tatttacaag tcccaggctt ctgcccttga aaagcatgct gctgccaact gcaaggtttt 480
ggttattgct aacccagcaa ataccaatgc attgatcttg aaggagtttg ctccatctat 540
tccagagaaa aacatttcag ctttgactag acttgatcac aacagggcat tgg 593

<210> 224
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<213> Trifolium repens

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<222> (497)..(497)
<223> n is a, c, g, or t

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<222> (520)..(520)
<223> n is a, c, g, or t

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<222> (528)..(528)
<223> n is a, c, g, or t

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ttaatcttcc ctgtttgatt ccttccgttc ttcaaaaatg gccaaagacc cagttcgtgt 120
tctcgtcact ggtgctgcag ggcaaattgg ttatgcactt gtccctatga ttgctagggg 180
agtgatgctt ggtcctgatc aacctgtgat ccttcacatg cttgatattc ctccagcagc 240
agagtcattg aatggagtta agatggagtt ggtcgatgct gcatttccac ttcttaaagg 300
tgttgttgct acaactgatg ttgttgaggc atgcactgga gtcaatattg cagtcatggt 360
tggtggattc ccaagaaaag aaggtatgga gaggaaggat gtgatgtcta agaacgtctc 420
tatttacaag tcccaggctt ctgcccttga aaagcatgct gctgccaact gcaaggnttt 480
ggttgntgct aacccancaa caccaatgca ttgatcttgn aggaatcngc t 531

<210> 225
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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cgcggttcga ttccttccgg gtcttcagca atggccaaag acccagttcg tgtcctcgtt 120
actggtgctg caggccaaat tggttatgca cttgtcccta tgattgctag gggagtgatg 180
cttggtcctg atcaacctgt gatccttcac atgcttgata tccctccagc agcagagnca 240
ttgaatggag ttaaaatgga gttggtggat gctgcatttc cacttcttaa aggcgttgtt 300
gctacaactg atgttgttga agcatgcact ggagtcaata ttgcagtcat ggttggtgga 360
ttcccaagaa aagaaggtat ggagaggaag gatgtgatga ctaagaatgt ctctatttac 420
aagtcccagg cttctgccct tgaaaagcat gctgctgcca actgcaaggt tttggttatt 480
gctaacccag caaataccaa tgcattgatc ttgaaggagt ttgctccatc tattccagag 540

aaaaacattt cagctttgac tagacttgat cac 573

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<222> (24)..(24)
<223> n is a, c, g, or t

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<222> (30)..(31)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (48)..(48)
<223> n is a, c, g, or t

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tcgcggttcg attccttccg tttcttcagc aatggccaaa gacccagttc gtgtcctcgt 120

tactggtgct gcaggccaaa ttggttatgc acttgtccct atgattgcta ggggagtgat 180

gcttggtcct gatcaacctg tgatccttca catgcttgat atccctccag cagcagagtc 240

attgaatgga gttaaaatgg agttggcgga tgctgcattt ccacttctta aaggcgttgt 300

tgctacaact gatgttgttg aagcatgcac tggagtcaat attgcagtca tggttggtgg 360

attcccaaga aaagaaggta tggagaggaa ggatgtgatg actaagaatg tctctattta 420

caagtcccag gcttcagccc ttgaaaagca tgctgctgcc aactgcaagg ttttggttat 480

tgctaaccca gcaaatacca atgcattgat cttgaaggag tttgctccat ctattccaga 540

gaaaaacatt tcagctttga ctagacttga tcacaacagg gcattgggcc aaatttctga 600

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cgcggttcga ttccttccgt ttcttcagca atggccaaag acccagttcg tgtcctcgtt 120

actggtgctg caggccaaat tggttatgca cttgtcccta tgattgctag gggagtgatg 180

cttggtcctg atcaacctgt gatccttcac atgcttgata tccctccagc agcagagtca 240

ttgaatggag ttaaaatgga gttggtggat gctgcatttc cacttcttaa aggcgttgtt 300

gctacaactg atgttgttga agcatgcact ggagtcaata ttgcagtcat ggttggtgga 360

ttcccaagaa aagaaggtat ggagaggaag gatgtgatga ctaagaatgt ctctatttac 420

aagtcccagg cttctgccct tgaaaagcat gctgctgcca actgcaaggt tttggttatt 480

gctaacccag caaataccaa tgcattgatc ttgaaggagt ttgctccatc tattccagag 540

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<223> n is a, c, g, or t

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ccttctattt cttcaaaaat ggccaaagac ccagttcgtg ttctcgtcac tggtgctgca 120

ggccaaattg gttatgcact tgtccctatg attgctaggg gagtgatgct tggtcctgat 180

caacctgtga tccttgacat gcttgatatt gctgcagnag nagagtnatt gaatggagct 240

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<212> DNA
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tcgattcctt ccacttcttc aaaaatggcc naagacccag ttcgtgttct cgtcactggt 120

gctgcngggc aaattggtta tgcacttgtc cctatgattg ctaggggagt gatgcttggt 180

cctgatcaac ctgtgatcct acacatgctt gatattccac ccgcagcaga gtcattgaat 240

ggagttaaga tggagttggt cgatgctgca tttccacttc ttaaaggtgt tgttgctaca 300

actgatgttg ttgaggcatg cactggagtc aatatcgcag tcatggttgg tggattccca 360

agaaaagaag gtatgganag gaaggatgtt atgtctaaga acgtctctat ttacaagtcc 420

caagcttctg cccttgaaaa gcatgctgct gccaactgca aggttttggt tgttgctaac 480

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atttcttgtt ngactagact tgatcac 567

<210> 230
<211> 569
<212> DNA
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<223> n is a, c, g, or t

<400> 230
caaacacacc taacctactn ctctctnaac aaaactgttc ttcctctctt aatcttccct 60

gtttgattcc ttccagttct tcaaaaatgg ccaaagaccc agttcgtgtt ctcgtcactg 120

gtgctgcagg gcaaattggt tatgcacttg tccctatgat tgctagggga gtgatgcttg 180

gtcctgatca acctgtgatc cttcacatgc ttgatattcc tccagcagca gagtcattga 240

atggagttaa gatggagttg gtcgatgctg catttccact tcttaaaggt gttgttgcta 300

caactgatgt tgttgaggca tgcactggag tcaatattgc agtcatggtt ggtggattcc 360

caagaaaaga aggtatggag aggaaggatg tgatgtctaa gaacgtctct atttacaagt 420

cccaggcttc tgcccttgaa aagcatgctg ctgccaactg caaggttttg gttgttgcta 480

acccagcaac accaatgcat tgatcttgaa ggaatttgct ccatctattc cagagaaaaa 540

catttcttgt ttgactagac ttgatcacc 569

<210> 231
<211> 592
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (28)..(28)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (52)..(52)
<223> n is a, c, g, or t

<400> 231
aacactaaac cctactnctc tctctctnaa caaaactgtt cttcctctct tnatcttccc 60

tgttcgattc cttccacttc ttcaaaaatg gccaaagacc cagttcgtgt tctcgtcact 120

ggtgctgcag ggcaaattgg ttatgcactt gtccctatga ttgctagggg agtgatgctt 180

ggtcctgatc aacctgtgat cctacacatg cttgatattc cacccgcagc agagtcattg 240

aatggagtta agatggagtt ggtcgatgct gcatttccac ttcttaaagg tgttgttgct 300

acaactgatg ttgttgaggc atgcactgga gtcaatatcg cagtcatggt tggtggattc 360

ccaagaaaag aaggtatgga gaggaaggat gttatgtcta agaacgtctc tatttacaag 420

tcccaagctt ctgcccttga aaagcatgct gctgccaact gcaaggtttt ggttgttgct 480

aacccagcaa acaccaatgc attgatcttg aaggaatttg ctccatctat tccagagaaa 540

aacatttctt gtttgactag acttgatcac aacagggcat tgggccaaat tt 592

<210> 232
<211> 585
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

<400> 232
cntaaccctn actcnctctc tnaaanaaaa ctattcttat ctcttaatct tcgcggttcg 60

attccttccg tttcttcagc aatggccaaa gacccagttc gtttcctcgt tactggtgct 120

gcaggccaaa ttggttatgc acttgtccct atgattgcta ggggagtgat gcttggtcct 180

gatcaacctg tgatccttca catgcttgat atccctccag cagcagagtc attgaatgga 240

gttaaaatgg agttggtgga tgctgcattt ccacttctta aaggcgttgt tgctacaact 300

gatgttgttg aagcatgcac tggagtcaat attgcagtca tggttggtgg attcccaaga 360

aaagaaggta tggagaggaa ggatgtgatg actaagaatg tctctattta caagtcccag 420

gcttctgccc ttgaaaagca tgctgctgcc aactgcaagg ttttggttat tgctaaccca 480

gcaaatacca atgcattgat cttgaaggag tttgctccat ctattccaga gaaaaacatt 540

tcagctttga ctagacttga tcacaacagg gcattgggcc aaatt 585

<210> 233
<211> 462
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (87)..(87)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (392)..(392)
<223> n is a, c, g, or t

<400> 233
gtcatcactn ctnctncaan aaaaactgtt cttccactct taatcttccc tgttcgattc 60
cttctatttc ttcaaaaatg gccaaanacc cagttcgtgt tctcgtcact ggtgctgcag 120
gccaaattgg ttatgcactt gtccctatga ttgctagggg agtgatgctt ggtcctgatc 180
aacctgtgat ccttcacatg cttgatattc ctccagcagc agagtcattg aatggagtta 240
aaatggagtt ggtggatgct gcatttccac ttcttaaagg tgttgttgct acaactgatg 300
ttgttgaagc atgcactgga gtcaatattg cagtcatggt tggtggattc ccaagaaaag 360
aaggtatgga gaggaaggat gtgatgacta anaatgtctc tatttacaag tcccaggctt 420
ctgcccttga aaagcatgct gctgccaact gcaaggtttt gg 462

<210> 234
<211> 573
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (11)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<400> 234
cactaaacct nnctnctctc tctctaaaca aaactgttct tcctctctta atcttccctg 60
ttcgattcct tccacttctt caaaaatggc caaagaccca gttcgtgttc tcgtcactgg 120
tgctgcaggg caaattggtt atgcacttgt ccctatgatt gctaggggag tgatgcttgg 180
tcctgatcaa cctgtgatcc tacacatgct tgatattcca cccgcagcag agtcattgaa 240
tggagttaag atggagttgg tcgatgctgc atttccactt cttaaaggtg ttgttgctac 300
aactgatgtt gttgaggcat gcactggagt caatatcgca gtcatggttg gtggattccc 360
aagaaaagaa ggtatggaga ggaaggatgt tatgtctaag aacgtctcta tttacaagtc 420
ccaagcttct gcccttgaaa agcatgctgc tgccaactgc aaggttttgg ttgttgctaa 480
cccagcaaac accaatgcat tgatcttgaa ggaatttgct ccatctattc cagagaaaaa 540
catttcttgt ttgactagac ttgatcacaa cag 573

<210> 235
<211> 603
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(19)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (50)..(50)
<223> n is a, c, g, or t

<400> 235
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tttgattcct tccgttcttc aaaaatggcc aaagacccag ttcgtgttct cgtcactggt 120

gctgcagggc aaattggtta tgcacttgtc cctatgattg ctaggggagt gatgcttggt 180

cctgatcaac ctgtgatcct acacatgctt gatattccac ccgcagcaga gtcattgaat 240

ggagttaaga tggagttggt cgatgctgca tttccacttc ttaaaggtgt tgttgctaca 300

actgatgttg ttgaggcatg cactggagtc aatatcgcag tcatggttgg tggattccca 360

agaaaagaag gtatggagag gaaggatgtt atgtctaaga acgtctctat ttacaagtcc 420

caagcttctg cccttgaaaa gcatgctgct gccaactgca aggttttggt tgttgctaac 480

ccagcaaaca ccaatgcatt gatcttgaag gaatttgctc catctattcc agagaaaaac 540

atttcttgtt tgactagact tgatcacaac agggcattgg gccaaatttc tgaaagattg 600

aat 603

<210> 236
<211> 550
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (462)..(462)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (482)..(482)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (532)..(532)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (545)..(545)
<223> n is a, c, g, or t

<400> 236
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gattccttct atttcttcaa aaatggccaa agacccagtt cgtgttctcg tcactggtgc 120

tgcaggccaa attggttatg cacttgtccc tatgattgct aggggagtga tgcttggtcc 180

tgatcaacct gtgatccttc acatgcttga tattcctcca gcagcagagt cattgaatgg 240

agttaaaatg gagttggtgg atgctgcatt tccacttctt aaaggtgttg ttgctacaac 300

tgatgttgtt gaagcatgca ctggagtcaa tattgcagtc atggttggtg gattcccaag 360

aaaagaaggt atggagagga aggatgtgat gactaagaat gtctctattt acaagtccca 420

ggcttctgcc cttgaaaagc atgctgctgc caactgcaag gntttgggta ttgctaaccc 480

ancaaatacc aatgcattga tcttgaagga gtttgctcca tctattccag anaaaaacat 540

ttcanctttg 550

<210> 237
<211> 591
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (5)..(5)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n is a, c, g, or t

<400> 237
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attccttccg ttcttcaaaa atggccaaag acccagttcg tgttctcgtc actggtgctg 120

cagggcaaat tggttatgca cttgtcccta tgattgctag gggagtgatg cttggtcctg 180

atcaacctgt gatccttcac atgcttgata ttcctccagc agcagagtca ttgaatggag 240

ttaagatgga gttggtcgat gctgcatttc cacttcttaa aggtgttgtt gctacaactg 300
atgttgttga ggcatgcact ggagtcaata ttgcagtcat ggttggtgga ttcccaagaa 360
aagaaggtat ggagaggaag gatgtgatgt ctaagaacgt ctctatttac aagtcccagg 420
cttctgccct tgaaaagcat gctgctgcca actgcaaggt tttggttgtt gctaacccag 480
caacaccaat gcattgatct tgaaggaatt tgctccatct attccagaga aaaacatttc 540
ttgtttgact agacttgatc acaacagggc attgggccaa atttctgaaa g 591

<210> 238
<211> 571
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (4)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(17)
<223> n is a, c, g, or t

<400> 238
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ttctatttct tcaaaaatgg ccaaagaccc agttcgtgtt ctcgtcactg gtgctgcagg 120
ccaaattggt tatgcacttg tccctatgat tgctagggga gtgatgcttg gtcctgatca 180
acctgtgatc cttcacatgc ttgatattcc tccagcagca gagtcattga atggagttaa 240
aatggagttg gtggatgctg catttccact tcttaaaggt gttgttgcta caactgatgt 300
tgttgaagca tgcactggag tcaatattgc agtcatggtt ggtggattcc caagaaaaga 360
aggtatggag aggaaggatg tgatgactaa gaatgtctct atttacaagt cccaggcttc 420
tgcccttgaa aagcatgctg ctgccaactg caaggttttg gttattgcta acccagcaaa 480
taccaatgca ttgatcttga aggagtttgc tccatctatt ccagagaaaa acatttcagc 540
tttgactaga cttgatcaca acagggcatt g 571

<210> 239
<211> 433
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (28)..(28)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (358)..(358)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (386)..(386)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (402)..(402)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (404)..(406)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (409)..(409)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (413)..(413)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (416)..(416)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (430)..(430)
<223> n is a, c, g, or t

<400> 239
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tcttcaaaaa tggccaaaga cccagttcgt gttctcgtca ctggtgctgc aggccaaatt 120

ggttatgcac ttgtccctat gattgctagg ggagtgatgc ttggtcctga tcaacctgtg 180

atccttcaca tgcttgatat tcctccagca gcagagtcat tgaatggagt taaaatggag 240

ttggtggatg ctgcatttcc acttcttaaa ggtgttgttg ctacaactga tgttgttgaa 300

gcatgcactg gagtcaatat tgcagtcatg gttggtggat tcccaagaaa agaaggtntg 360

gagaggaagg atgtgatgac taagantgtc tctatttaca anannnagnc ttntgncctt 420

gaaaaagatn ctg 433

<210> 240
<211> 585
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (35)..(35)
<223> n is a, c, g, or t

<400> 240
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tcttcaaaaa tggccaaaga cccagttcgt gttctcgtca ctggtgctgc agggcaaatt 120

ggttatgcac ttgtccctat gattgctagg ggagtgatgc ttggtcctga tcaacctgtg 180

atccttcaca tgcttgatat tcctccagca gcagagtcat tgaatggagt taagatggag 240

ttggtcgatg ctgcatttcc acttcttaaa ggtgttgttg ctacaactga tgttgttgag 300

gcatgcactg gagtcaatat tgcagtcatg gttggtggat tcccaagaaa agaaggtatg 360

gagaggaagg atgtgatgtc taagaacgtc tctatttaca agtcccaggc ttctgcccttt 420

gaaaagcatg ctgctgccaa ctgcaaggtt ttggttgttg ctaacccagc aaacaccaat 480

gcattgatct tgaaggaatt tgctccatct attccagaga aaaacatttc ttgtttgact 540

agacttgatc acaacagggc attgggccaa atttctgaaa gattg 585

<210> 241
<211> 610
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (30)..(30)
<223> n is a, c, g, or t

<400> 241
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caaaaatggc caaagaccca gttcgtgttc tcgtcactgg tgctgcaggc caaattggtt 120

atgcacttgt ccctatgatt gctaggggag tgatgcttgg tcctgatcaa cctgtgatcc 180

ttcacatgct tgatattcct ccagcagcag agtcattgaa tggagttaaa atggagttgg 240

tggatgctgc atttccactt cttaaaggtg ttgttgctac aactgatgtt gttgaagcat 300

gcactggagt caatattgca gtcatggttg gtggattccc aagaaaagaa ggtatggaga 360

ggaaggatgt gatgactaag aatgtctcta tttacaagtc ccaggcttct gcccttgaaa 420

agcatgctgc tgccaactgc aaggttttgg ttattgctaa cccagcaaat accaatgcat 480

tgatcttgaa ggagtttgct ccatctattc cagagaaaaa catttcagct ttgactagac 540

ttgatcacaa cagggcattg ggccaaattt ctgaaagatt gaatattcaa gtttctgatg 600

taaagaatgt 610

<210> 242
<211> 568
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (53)..(53)
<223> n is a, c, g, or t

<400> 242
caaaaactgc tcttcctctc ttnatcttcc ctgttcgatt ccttcccttc ttnaaaatgg 60

ccaaagaccc agttcgtgtt ctcgtcactg gtgctgcagg gcaaattggt tatgcacttg 120

tccctatgat tgctagggga gtgatgcttg gtcctgatca acctgtgatc ctacacatgc 180

ttgatattcc acccgcagca gagtcattga atggagttaa gatggagttg gtcgatgctg 240

catttccact tcttaaaggt gttgttgcta caactgatgt tgttgaggca tgcactggag 300

tcaatatcgc agtcatggtt ggtggattcc caagaaaaga aggtatggag aggaaggatg 360

ttatgtctaa gaacgtctct atttacaagt cccaagcttc tgcccttgaa aagcatgctg 420

ctgccaactg caaggttttg gttgttgcta acccagcaaa caccaatgca ttgatcttga 480

aggaatttgc tccatctatt ccagagaaaa acatttcttg tttgactaga cttgatcaca 540

acagggcatt gggccaaatt tctgaaag 568

<210> 243
<211> 558
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t

<400> 243
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caaagaccca gttcgtgttc tcgtcactgg tgctgcaggg caaattggtt atgcacttgt 120

ccctatgatt gctaggggag tgatgcttgg tcctgatcaa cctgtgatcc tacacatgct 180

tgatattcca cccgcagcag agtcattgaa tggagttaag atggagttgg tcgatgctgc 240

atttccactt cttaaaggtg ttgttgctac aactgatgtt gttgaggcat gcactggagt 300

caatatcgca gtcatggttg gtggattccc aagaaaagaa ggtatggaga ggaaggatgt 360

tatgtctaag aacgtctcta tttacaagtc ccaagcttct gcccttgaaa agcatgctgc 420

tgccaactgc aaggttttgg ttgttgctaa cccagcaaac accaatgcat tgatcttgaa 480

ggaatttgct ccatctattc cagagaaaaa catttcttgt ttgactagac ttgatcacaa 540

cagggcattg ggccaaat 558

<210> 244
<211> 752
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<400> 244
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agacccagtt cgtgttctcg tcactggtgc tgcagggcaa attggttatg cacttgtccc 120

tatgattgct aggggagtga tgcttggtcc tgatcaacct gtgatccttc acatgcttga 180

tattcctaca gcagcagagt cattgaatgg agttaagatg gagttggtcg atgctgcatt 240

tccacttctt aaaggtgttg ttgctacaac tgatgttgtt gaggcatgca ctggagtcaa 300

tattgcagtc atggttggtg gattcccaag aaaagaaggt atggagagga aggatgtgat 360

gtctaagaac gtctctattt acaagtccca ggcttctgcc cttgaaaagc atgctgctgc 420

caactgcaag gttttggttg ttgctaaccc agcaaacacc aatgcattga tcttgaagga 480

atttgctcca tctattccag agaaaaacat ttcttgtttg actagacctg atcacaacag 540

ggcattgggc caaatttctg aaagattgaa tgttcaagtt tctgatgtaa agaatgtcat 600

tatctggggt aatcattcat caactcagta tcctgatgtc aaccatgcaa ctgttaacac 660

ccccgctggg gagaagcctg tccgtgagct tgtttctgat gacgcctggt tgaatggaga 720

attcatatct accgttcaac aacgtggtgc tg 752

<210> 245
<211> 583
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (46)..(46)
<223> n is a, c, g, or t

<400> 245
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cccagttcgt gttctcgtca ctggtgctgc aggccaaatt ggttatacac ttgtccctat 120

gattgctagg ggagtgatgc ttggtcctga tcaacctgtg atccttcaca tgcttgatat 180

tcctccagca gcagagtcat tgaatggagt taaaatggag ttggtggatg ctgcatttcc 240

acttcttaaa ggtgttgttg ctacaactga tgttgttgaa gcatgcactg gagtcaatat 300

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tgcagtcatg gttggtggat tcccaagaaa agaaggtatg gagaggaagg atgtgatgac    360
taagaatgtc tctatttaca agtcccaggc ttctgccctt gaaaagcatg ctgctgccaa    420
ctgcaaggtt ttggttattg ctaacccagc aaataccaat gcattgatct tgaaggagtt    480
tgctccatct attccagaga aaaacatttc agctttgact agacttgatc acaacagggc    540
attgggccaa atttctgaaa gattgaatat tcaagtttct gat                      583
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<210> 246
<211> 573
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<400> 246

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ttcctctctt natcttccct gtttgattcc ttccgttctt caaaatggcc aagacccagt     60
tcgtgttctc gtcactggtg ctgcagggca aattggttat gcacttgtcc ctatgattgc    120
taggggagtg atgcttggtc ctgatcaacc tgtgatcctt cacatgcttg atattcttcc    180
agcagcagag tcattgaatg gagttaagat ggagttggtc gatgctgcat ttccacttct    240
taaaggtgtt gttgctacaa ctgatgttgt tgaggcatgc actggagtca atattgcagt    300
catggttggt ggattcccaa gaaaagaagg tatggagagg aaggatgtga tgtctaagaa    360
cgtctctatt tacaagtccc aggcttctgc ccttgaaaag catgctgctg ccaactgcaa    420
ggttttggtt gttgctaacc cagcaaacac caatgcattg atcttgaagg aatttgctcc    480
atctattcca gagaaaaaca tttcttgttt gactagactt gatcacaaca gggcattggg    540
ccaaatttct gaaagattga atgttcaagt ttc                                  573
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<210> 247
<211> 562
<212> DNA
<213> Trifolium repens

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<222> (24)..(24)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (38)..(38)
<223> n is a, c, g, or t

<400> 247

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ggggagtgat gcttggtcct gatnacctgt gatccttnca tgcttgatat ccctccagca     60
gcagagtcat tgaatggagt taaaatggag ttggtggatg ctgcatttcc acttcttaaa    120
ggcattgttg ctacaactga tgttgttgaa gcatgcactg gagtcaatat tgcagtcatg    180
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gttggtggat tcccaagaaa agaaggtatg gagaggaagg atgtgatgac taagaatgtc 240
tctatttaca agtcccaggc ttctgccctt gaaaagcaag ctgctgccaa ctgcaaggtt 300
ttggttattg ctaacccagc aaataccaat gcattgatct tgaaggagtt tgctccatct 360
attccagaga aaaacatttc agctttgact agacttgatc acaacagggc attgggccaa 420
atttctgaaa gattgaatat tcaagtttct gatgtaaaga atgtcattat ctggggtaat 480
cattcatcaa ctcagtatcc tgatgtcaac catgcaactg ttaacacccc cgccggggag 540
aagcctgtcc gtgaacttgt tt 562

<210> 248
<211> 515
<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
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<222> (11)..(11)
<223> n is a, c, g, or t

<220>
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<222> (17)..(17)
<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<220>
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<222> (482)..(482)
<223> n is a, c, g, or t

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<222> (488)..(489)
<223> n is a, c, g, or t

<220>
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<222> (500)..(500)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (510)..(510)
<223> n is a, c, g, or t

<400> 248
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ccacttctta aaggtgttgt tgctacaact gatgttgttg aggcatgcac tggagtcaat 120

attgcagtca tggttggtgg attcccaaga aaagaaggta tggagaggaa ggatgtgatg 180

tctaagaacg tctctattta caagtcccag gcttctgccc ttgaaaagca tgctgctgcc 240

aactgcaagg ttttggttgt tgctaaccca gcaaacacca atgcattgat cttgaaggaa 300

tttgctccat ctattccaga gaaaaacatt tcttgtttga ctagacttga tcacaacagg 360

gcattgngcc aaatttctga aagattgaat gtccaagttt ctgatgtaaa gaatgtcatt 420

atctggngta atcattcatc aactcagcat cctgatgtca accatgcaac tgttaacacc 480

cncgctgnng agaagcctgn ccgtgagctn gtttc 515

<210> 249
<211> 598
<212> DNA
<213> Trifolium repens

<220>
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<223> n is a, c, g, or t

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cttcttaaag gtgttgttgc tacaactgat gttgttgagg catgcactgg agtcaatatt 120

gcagtcatgg ttggtggatt cccaagaaaa gaaggtatgg agaggaagga tgtgatgtct 180

aagaacgtct ctatttacaa gtcccaggct tctgcccttg aaaagcatgc tgctgccaac 240

tgcaaggttt tggttgttgc taacccagca aacaccaatg cattgatctt gaaggaattt 300

gctccatcta ttccagagaa aaacatttct tgtttgacta gacttgatca caacagggca 360

ttgggccaaa tttctgaaag attgaatgtc caagtttctg atgtaaagaa tgtcattatc 420

tggggtaatc attcatcaac tcagtatcct gatgtcaacc atgcaactgt taacaccccc 480

gctggggaga agcctgtccg tgagcttgtt tctgatgacg cctggttgaa tggagaattc 540

atatctaccg ttcaacaacg tggtgctgca attattaagg ctagaaagct ttcaagtg 598

<210> 250
<211> 603
<212> DNA
<213> Trifolium repens

<400> 250
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tgaaaagcat gctgctgcca actgcaaggt tttggttgtt gctaacccag caaacaccaa 120

tgcattgatc ttgaaggaat ttgctccatc tattccagag aaaaacattt cttgtttgac 180

tagacttgat cacaacaggg cattgggcca aatttctgaa agattgaatg ttcaagtttc 240

tgatgtaaag aatgtcatta tctggggtaa tcattcatca actcagtatc ctgatgtcaa 300

ccatgcaact gttaacaccc ccgctgggga gaagcctgtc cgtgagcttg tttctgatga 360

cgcctggttg aatggagaat tcatatctac cgttcaacaa cgtggtgctg caattattaa 420

ggctagaaag ctttcaagcg cactatccgc tgctagcgct gcttgcgacc acattcgcga 480

ttgggttctt ggaactcccc agggcacctt cgtttcaatg ggagtgtatt ctgatggttc 540

ttacaacgta ccagctggac tcatctattc attccctgtc accactgcta atggggaatg 600

gaa 603

<210> 251
<211> 695
<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

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<222> (12)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (25)..(25)
<223> n is a, c, g, or t

<400> 251
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tgaaaagcat gctgctgcca actgcaaggt tttggttgtt gctaacccag caaacaccaa 120

tgcattgatc ttgaaggaat ttgctccatc tattccagag aaaaacattt cttgtttgac 180

tagacttgat cacaacaggg cattgggcca aatttctgaa agattgaatg ttcaagtttc 240

tgatgtaaag aatgtcatta tctggggtaa tcattcatca actcagtatc ctgatgtcaa 300

ccatgcaact gttaacaccc ccgctgggga gaagcctgtc cgtgagcttg tttctgatga 360

cgcctggttg aatggagaat tcatatctac cgttcaacaa cgtggtgctg caattattaa 420

ggctagaaag ctttcaagcg cactatccgc tgctagcgct gcttgcgacc acattcgcga 480
ttgggttctt ggaactcccc agggcacctt cgtttcaatg ggagtgtatt ctgatggttc 540
ttacaacgta ccagctggac tcatctattc attccctgtc accactgcta atggggaatg 600
gaaaattgtt caaggacttt caattgacga gttctcaagg aagaagttgg acttgacagc 660
tgaagagtta tccgaggaaa agagtttggc atact 695

<210> 252
<211> 1408
<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (46)..(46)
<223> n is a, c, g, or t

<220>
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<222> (767)..(767)
<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<222> (823)..(823)
<223> n is a, c, g, or t

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<221> misc_feature
<222> (851)..(851)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

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<222> (933)..(933)
<223> n is a, c, g, or t

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<222> (1360)..(1360)
<223> n is a, c, g, or t

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<222>  (1386)..(1386)
<223>  n is a, c, g, or t

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<223>  n is a, c, g, or t

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<223>  n is a, c, g, or t

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<223>  n is a, c, g, or t

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gctctctctc tctttattct cgaaaagctt tttcagccaa caacggagag aattatgagg     120

ccgtcgatgc tcagatccgt ccaatcagcc gtctcccgcg cctcttctca cctaacccgc     180

cgtggctatg ctaccgaacc agttccagaa cgcaaggtgg ccattctcgg cgctgccggc     240

gggatcggcc agcctctctc tcttctcatg aagctcaacc ctctcgtttc aaccctatct     300

ctttatgata ttgctggaac ccctggtgtc gccgctgatg tcagccacat caactccaga     360

tctgaggtaa ctgggtatgc aggtgaagaa gagcttggaa aagctttgga gggtgctgat     420

gttgttataa ttcctgctgg tgtgcccaga aagcctggaa tgactcgtga tgatcttttc     480

aatattaacg ctggcattgt caagtcactt gccactgcta tttctaagta ctgcccccat     540

gcccttgtta acatgataag caaccctgtg aactccaccg ttcccattgc tgcagaggtt     600

ttcaagaagg cagggacata tgacgagaag agattgtttg ggttacaac ccttgatgta      660

gtcagggcaa aaactttcta tgccgggaaa gctaaagttc cagttgccga ggtcaatgta     720

cctgttatag gaggccatgc aggagttact attcttccat tattttntca ggcaacacct     780

caagccaatc tgggtgatga tacccttaag gntttaacgg nanggacaca agatggagga     840

acagaagttg ngaccgccaa ggctggaaag ggttctgcaa ctttgtcaat ggcttatgct     900

ggagccatat ttgctgatgc tngcctcaaa ggnctgaatg gagttccaga tgttattgag     960

tgctcatatg tgcaatccaa tatcatctct gaccttcctt tctttgcttc caaggtgagg    1020

attgggaaga atggtgtgga agaaattctg ggcttaggtt ctctcacaga tttcgagcaa    1080

caaggccttg aaaacctcaa ggctgaactc aaatcatcta ttgaaaaggg aatcaaattt    1140

gcctcccagt aatcgaacat gtcatacatt actggatttt tccatttaga accagatcaa    1200

attttgcaaa ttcagaacaa ttgtttgtaa tgttgccggt aggtataccc ctagatttaa    1260

taagtaaatc tgcgagagca gtttattgct gcagggactg aaattaaaac cagttttagg    1320

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gggtgntggn cancgataca canccccc                                        1408
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<210> 253
<211> 345
<212> PRT
<213> Trifolium repens

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<222> (218)..(218)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (233)..(233)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (236)..(237)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (246)..(246)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (270)..(270)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (273)..(273)
<223> Xaa can be any naturally occurring amino acid

<400> 253

Met Arg Pro Ser Met Leu Arg Ser Val Gln Ser Ala Val Ser Arg Ala
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Ser Ser His Leu Thr Arg Arg Gly Tyr Ala Thr Glu Pro Val Pro Glu
20 25 30

Arg Lys Val Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu
35 40 45

Ser Leu Leu Met Lys Leu Asn Pro Leu Val Ser Thr Leu Ser Leu Tyr
50 55 60

Asp Ile Ala Gly Thr Pro Gly Val Ala Ala Asp Val Ser His Ile Asn
65 70 75 80

Ser Arg Ser Glu Val Thr Gly Tyr Ala Gly Glu Glu Glu Leu Gly Lys
85 90 95

Ala Leu Glu Gly Ala Asp Val Val Ile Ile Pro Ala Gly Val Pro Arg
100 105 110

Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile

115 120 125

Val Lys Ser Leu Ala Thr Ala Ile Ser Lys Tyr Cys Pro His Ala Leu
130 135 140

Val Asn Met Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala
145 150 155 160

Glu Val Phe Lys Lys Ala Gly Thr Tyr Asp Glu Lys Arg Leu Phe Gly
165 170 175

Val Thr Thr Leu Asp Val Val Arg Ala Lys Thr Phe Tyr Ala Gly Lys
180 185 190

Ala Lys Val Pro Val Ala Glu Val Asn Val Pro Val Ile Gly Gly His
195 200 205

Ala Gly Val Thr Ile Leu Pro Leu Phe Xaa Gln Ala Thr Pro Gln Ala
210 215 220

Asn Leu Gly Asp Asp Thr Leu Lys Xaa Leu Thr Xaa Xaa Thr Gln Asp
225 230 235 240

Gly Gly Thr Glu Val Xaa Thr Ala Lys Ala Gly Lys Gly Ser Ala Thr
245 250 255

Leu Ser Met Ala Tyr Ala Gly Ala Ile Phe Ala Asp Ala Xaa Leu Lys
260 265 270

Xaa Leu Asn Gly Val Pro Asp Val Ile Glu Cys Ser Tyr Val Gln Ser
275 280 285

Asn Ile Ile Ser Asp Leu Pro Phe Phe Ala Ser Lys Val Arg Ile Gly
290 295 300

Lys Asn Gly Val Glu Glu Ile Leu Gly Leu Gly Ser Leu Thr Asp Phe
305 310 315 320

Glu Gln Gln Gly Leu Glu Asn Leu Lys Ala Glu Leu Lys Ser Ser Ile
325 330 335

Glu Lys Gly Ile Lys Phe Ala Ser Gln
340 345

<210> 254
<211> 537
<212> DNA
<213> Trifolium repens

<220>
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<222> (5)..(5)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (31)..(31)
<223> n is a, c, g, or t

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ctctctctct ttattctcga aaagcttctt cagccaacaa cgagagaata atgaggccgt 120

cgatgctcag atccgtccaa tcagccgtat cccgcgcctc ctctcaccta acccgccgtg 180

gctatgctac cgaaccagtt ccagaacgca aggtggccat tctcggtgct gccggcggga 240

tcggacagcc tctctctctt ctcatgaagc tcaaccctct cgtttcaacc ctatctcttt 300

atgatattgc tggaacccct ggtgtcgccg ctgatgtcag ccacatcaac tccagatctg 360

aggtaactgg gtatgcaggt gaagaagagc ttggaaaagc tttggagggt gctgatgttg 420

ttataattcc tgctggtgtg cccagaaagc ctggaatgac tcgtgatgat cttttcaata 480

ttaacgctgg cattgtcaag tcacttgcca ctgctatttc taagtactgc ccccatg 537

<210> 255
<211> 608
<212> DNA
<213> Trifolium repens

<220>
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<222> (4)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

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tctctcttta ttctcgaaaa gctttttcag ccaacaacga gagaataatg aggccgtcga 120

tgctcagatc cgtccaatca gccgtatccc gcgcctcctc tcacctaacc cgccgtggct 180

atgctaccga accagttcca gaacgcaagg tggccattct cggtgctgcc ggcgggatcg 240

gacagcctct ctctcttctc atgaagctca accctctcgt ttcaacccta tctctttatg 300

atattgctgg aacccctggt gtcgccgctg atgtcagcca catcaactcc agatctgagg 360

taactgggta tgcaggtgaa gaagagcttg gaaaagcttt ggagggtgct gatgttgtta 420

taattcctgc tggtgtgccc agaaagcctg gaatgactcg tgatgatctt ttcaatatta 480

acgctggcat tgtcaagtca cttgccactg ctatttctaa gtactgcccc catgcccttg 540

ttaacatgat aagcaaccct gtgaactcca ccgttcccat tgctgcagag gttttcaaga 600

aggcaggg 608

<210> 256
<211> 575
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (33)..(33)
<223> n is a, c, g, or t

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gaaaagcttt ttcagccatc aacggagaga attatgagtc cgtcgatgct cagatccgtc 120

caatcagccg tctcccgcgc ctcttctcac ctaacccgcc gtggctatgc taccgaacca 180

gttccagaac gcaaggtggc cattctcggc gctgccggcg ggatcggcca gcctctctct 240

cttctcatga agctcaaccc tctcgtttca accctatctc tttatgatat tgctggaacc 300

cctggtgtcg ccgctgatgt cagccacatc aactccagat ctgaggtaac tgggtatgca 360

ggtgaagaag agcttggaaa agctttggag ggtgctgatg ttgttataat tcctgccggt 420

gtgcccagaa agcctggaat gactcgtgat gatcttttta atattaatgc tggcattgtc 480

aagtcacttg ccactgctat ttctaagtac tgcccccatg cccttgttaa catgataagc 540

aaccctgtga actccaccgt tcccattgct gcagg 575

<210> 257
<211> 563
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (24)..(24)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (27)..(27)
<223> n is a, c, g, or t

<400> 257
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cagccacaac gagagaataa tgaggccgtc gatgctcaga tctgtccaat cagccgtatc 120

ccgcgcctcc tctcacctaa cccgccgtgg ctatgctacc gaaccagttc cagaacgcaa 180

ggtggccatt ctcggtgctg ccggcgggat cggacagcct ctctctcttc tcatgaagct 240

caaccctctc gtttcaaccc tatctcttta tgatattgct ggaacccctg gtgtcgccgc 300

tgatgtcagc cacatcaact ccagatctga ggtaactggg tatgcaggtg aagaagagct 360

tggaaaagct ttggagggtg ctgatgttgt tataattcct gctggtgtgc ccagaaagcc 420

tggaatgact cgtgatgatc ttttcaatat taacgctggc attgtcaagt cacttgccac 480

tgctatttct aagtactgcc cccatgccct tgttaacatg ataagcaacc ctgtgaactc 540

caccgttccc attgctgcag agg 563

<210> 258
<211> 583
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

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aacaacggag agaattatga ggccgtcgat gttcagatcc gtccaatcag ccgtctcccg 120

cgcctcttct cacctaaccc gccgtggcta tgctaccgaa ccagttccag aacgcaaggt 180

ggccattctc ggcgctgccg gcgggatcgg ccagcctctc tctcttctca tgaagctcaa 240

ccctctcgtt tcaaccctat ctctttatga tattgctgga acccctggtg tcgccgctga 300

tgtcagccac atcaactcca gatctgaggt aactgggtat gcaggtgaag aagagcttgg 360

aaaagctttg gagggtgctg atgttgttat aattcctgcc ggtgtgccca gaaagcctgg 420

aatgactcgt gatgatcttt tcaatattaa cgctggcatt gtcaagtcac ttgccactgc 480

tatttctaag tactgccccc atgcccttgt taacatgata agcaaccctg tgaactccac 540

cgttcccatt gctgcagagg ttttcaagaa ggcagggaca tat 583

<210> 259
<211> 598
<212> DNA
<213> Trifolium repens

<220>
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<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

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<222> (18)..(18)
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<220>
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acaacggaga gaattatgag gccgtcgatg ttcagatccg tccaatcagc cgtctcccgc 120

gcctcttctc acctaacccg ccgtggctat gctaccgaac cagttccaga acgcaaggtg 180

gccattctcg gcgctgccgg cgggatcggc cagcctctct ctcttctcat gaagctcaac 240

cctctcgttt caaccctatc tctttatgat attgctggaa cccctggtgt cgccgctgat 300

gtcagccaca tcaactccag atctgaggta actgggtatg caggtgaaga agagcttgga 360

aaagctttgg agggtgctga tgttgttata attcctgccg gtgtgcccag aaagcctgga 420

atgactcgtg atgatctttt caatattaac gctggcattg tcaagtcact tgccactgct 480

atttctaagt actgccccca tgcccttgtt aacatgataa gcaaccctgt gaactccacc 540

gttcccattg ctgcagaggt tttcaagaag gcagggacat atgacgagaa gagattgt 598

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cgcgcctctt ctcacctaac ccgccgtggc tatgctaccg aaccagttcc agaacgcaag 180

gtggccattc tcggcgctgc cggcgggatc ggccagcctc tctctcttct catgaagctc 240

aaccctctcg tttcaaccct atctctttat gatattgctg gaacccctgg tgtcgccgct 300

gatgtcagcc acatcaactc cagatctgag gtaactgggt atgcaggtga agaagagctt 360

ggaaaagctt tggagggtgc tgatgttgtt ataattcctg ccggtgtgcc cagaaagcct 420

ggaatgactc gtgatgatct tttcaatatt aacgctggca ttgtcaagtc acttgccact 480
gctatttcta agtactgccc ccatgccctt gttaacatga taagcaaccc tgtgaactcc 540
accgttccca ttgctgcaga ggttttcaag aaggcaggga catatgacga gaagagattg 600
tttggggtta caacccttga tgtagtcagg gcgaaaactt tttatgccgg gaaagctaaa 660
gttccagttg ccgaggtcaa tgtacctgtt tttggaggcc atgcaggagt tactattntt 720
ccattatttt ntaaggaaca cctnaagcca atntggntga tgaaaccctt naggntttaa 780
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<212> DNA
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ccaacaacga gagaataatg aggccgtcga tgctcagatc cgtccaatca gccgtatccc 120
gcgcctcctc tcacctaacc cgccgtggct atgctaccga accagttcca gaacgcaggg 180
tggccattct cggtgctgct ggcgggatcg gacagcctct ctctcttctc atgaagctca 240
accctctcgt ttcaacccta tctctttatg atattgctgg aacccctggt gtcgccgctg 300
atgtcagcca catcaactcc agatctgagg taactgggta tgcaggtgaa gaagagcttg 360
gaaaagcttt ggagggtgct gatgttgtta taattcctgc tggtgtgccc agaaagcctg 420
gaatgactcg tgatgatctt ttcaatatta acgctggcat tgtcaagtca cttgccactg 480
ctatttctaa gtactgcccc catgcccttg ttaacatgat aagcaaccct gtgaactcca 540
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gcctcttctc acctaacccg ccgtggctat gctaccgaac cagttccaga acgcaaggtg 180
gccattctcg gcgctgccgg cgggatcggc cagcctctct ctcttctcat gaagctcaac 240
cctctcgttt caaccctatc tctttatgat attgctggaa cccctggtgt cgccgctgat 300
gtcagccaca tcaactccag atctgaggta actgggtatg caggtgaaga agagcttgga 360
aaagctttgg agggtgctga tgttgttata attcctgccg gtgtgcccag aaagcctgga 420
atgactcgtg atgatctttt caatattaac gctggcattg ttaagtcact tgccactgct 480
atttctaagt actgccccca tgcccttgtt aacatgataa gcaaccctgt gaactccacc 540
gttcccattg ctgcagaggt tttcaagaag gcagggacat atgacgagaa gagattgttt 600
ggggttacaa cccttgatgt agtcagggcg aaaactttct atgccgggaa agctaaagtt 660
ccagttgccg aggtcaatgt ac 682

<210> 263
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cctcttctca cctaacccgc cgtggctatg ctaccgaacc agttccagaa cgcaaggngg 180

ccattctcgg cgctgccggc gggatcggcc agcctctctc tcttctcatg aagctcaacc 240

ctctcgtttc aaccctatct ctttatgata ttgctggaac ccctggtgtc gccgctgatg 300

tcagccacat caactccaga tctgaggtaa ctgggtatgc aggtgaagaa gagcttggaa 360

aagctttgga gggtgctgat gttgttataa ttcctgccgg tgtgcccaga aagcctggaa 420

tgactcgtga tgatcttttc aatattaacg ctggcattgt caagtcactt gccactggta 480

tttctaagta ctgcccccat gcccttgtta acatgataag caaccctgtg aactccaccg 540

ttcccattgc tgnagaggtt ttcaagaagg cngggacata tgacnagaan aaattgtttg 600

gggttcaacc cttgatgtag tcagggggaa aacttttttt gccgggaaag ctaaagttcc 660

agttgccgng ggnaatgnnc ctgttnttgg aggcctgcng agtnctattn tcccttttttt 720

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aanggggaac aaaanttnga c 801

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ccagttccag aacgcaaggt ggccattctc ggcgctgccg gcgggatcgg ccagcctctc 180

tctcttctca tgaagctcaa ccctctcgtt tcaaccctat ctctttatga tattgctgga 240

acccctggtg tcgccgctga tgtcagccac atcaactcca gatctgaggt aactgggtat 300

gcaggtgaag aagagcttgg aaaagctttg gagggtgctg atgttgttat aattcctgcc 360

ggtgtgccca gaaagcctgg aatgactcgt gatgatcttt tcaatattaa cgctggcatt 420

gtcaagtcac ttgccactgc tatttctaag tactgccccc atgcccttgt taacatgata 480

agcaaccctg tgaactccac cgttcccatt gctgcagagg ttttcaagaa ggcagggaca 540

tatgacgaga agagattgtt tggggttaca acccttg 577

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<212> DNA
<213> Trifolium repens

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ccatcagccg tatcccgcgc ctcctctcac ctaacccgcc gtgggtatgc taccgaacca 120

gttccagaac gcaaggtggc cattctcggc gctgctggcg ggatcggcca gcctctctct 180

cttctcatga agctcaatcc tctcgtttca accctatctc tttatgatat tgctggaacc 240

cctggtgtcg ccgctgatgt cagccacatc aactccagat ctgaggtaac tgggtatgca 300

ggtgaagaag agcttggaaa agctttggag ggtgctgatg ttgttataat tcctgctggt 360

gtgcccagaa agcctggaat gactcgtgat gatcttttca atattaacgc tggcattgtc 420

aagtcacttg ccactgctat ttctaagtac tgcccccatg cccttgttaa catgataagc 480

aaccctgtga actccaccgt tcccattgct gcagaggttt tcaagaaggc agggacatat 540

gacgagaaga gattgtttgg ggttacaacc cttgatgtag tcagggcaaa aact 594

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gtccaatcag ccgtatcccg ggcctcctct cacctaaccc gccgtgggta tgctaccgaa 120

ccagttccag aacgcaaggn ggccattctc ggtgctgccg gcgggatcgg acagcctctc 180

tctcttctca tgaagctcaa ccctctcgtt tcaaccctat ctctttatga tattgctgga 240

acccctggtg tcgccgctga tgtcagccac atcaactcca gatctgaggt aactgggtat 300
gcaggtgaag aagagcttgg aaaagctttg gagggtgctg atgttgttat aattcctgct 360
ggtgtgccca gaaagcctgg aatgactcgt gatgatcttt tcaatattaa cgctggcatt 420
gtcaagtcac ttgccactgc tatttctaag tactgccccc atgcccttgt taacatgata 480
agcaaccctg tgaactccac cgttcccatt gctgcanagg ttttcaagaa ggcagggaca 540
tatgacnaga agagattgtt tggggttaca acccttgatg tagncagggc aaaaactttt 600
tatgctggga aagctaaagt tccagttgcc gaggncaatg gacctgttat aggaggccat 660
gcaggagtta ctattctncc attattttnt naggcaacac ctnaagccaa tntgggtgan 720
gatnccctta aggntttaac ggnanggacc caananggag gaacanaant tnngaccccc 780
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tcacttgcca ctgctatttc taagtactgc ccccatgccc ttgttaacat gataagcaac 240
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gagaagagat tgtttggggt tacaaccctt gatgtagtca gggcaaaaac tttctatgct 360
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<212> DNA
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gaatgactcg tgatgatctt ttcaatatta acgctggcat tgtcaagtca cttgccactg 180
ctatttctaa gtactgcccc catgcccttg ttaacatgat aagcaaccct gtgaactcca 240
ccgttcccat tgctgcagag gttttcaaga aggcagggac atatgacgag aagagattgt 300
ttggggttac aacccttgat gtagtcaggg caaaaacttt ctatgctggg aaagctaaag 360
ttccagttgc cgaggtcaat gtacctgtta taggaggcca tgcaggagtt actattctcc 420
cattattttc tcaggcaaca cctcaagcca atctggatga tgataccatt aaggctctaa 480
cggcaaggac acaagatgga ggaacagaag ttgtgaccgc caaggctgga aagggttctg 540
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caatccaata tcatctntga ccttcctttc tttgcttcca aggnnnggat tgggaagaat 120

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<222> (447)..(447)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (450)..(450)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (460)..(460)
<223> n is a, c, g, or t

<400> 270
gngngttcca gatgttatng agtgctntat gtgcatcnat atntctctga ccttcctttc 60

tttgcttcca ggtgaggatt gggaagaatg gtgtggaaga aattctgggc ttaggttctc 120

tcacagattt cgagcaacaa ggccttgaaa acctcaaggc tgaactcaaa tcatctattg 180

aaaagggaat caaatttgcc tcccagtaat cgaacatgtc atacattact ggatttttcc 240

atttagaacc agatcaaatt ttgcaaattc agaacaattg tttgtaatgt tgccggtagg 300

tataccccta gatttaataa gtaaatctgc gagagcagtt tattgctgca gggactgaaa 360

ttaaaaccag ttttaggttg gcctttccat tcgtaatggc ccttcattgt tgcatgnttt 420

catataatgc aattgaaggg tgntggncan cgatacacan ccccc 465

<210> 271
<211> 598
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<400> 271
gggtaggcgg agatttnaac ccattttcct cttaaatctc tctcaacttc tctttccatt 60

cccattacca ttcattccca gaggtcgaga tggcagcatc agcagcagct acttttacta 120

ttggaactgc ccaaacaggg aggccacttc ctcaatcaaa cccttttggt ttgaaagtca 180

attcccaggt taattttaag accttctctg gtctcaaggc catgtcatct ctaagatgcg 240

agtctgaatc atctttcttt ggcaacgaaa ctagtgctgc tctgcgtgca acttttgcac 300

ccaaagctca aaaggaaaac caaaacatca accgcaattt gcatcctcag gcatcctaca 360

aagtggcggt tcttggtgct gcaggaggaa ttggtcagcc actggcactt ctcattaaga 420

tgtcgccttt ggtttccgac ctgcatcttt atgatatcgc gaatgttaag ggagttgctg 480

ctgatatcag tcattgcaac actccttcaa aggttttgga tttcacaggt gcttctgagt 540

tggcaaattg tttgaaaggt gtggatgtag ttgttatacc tgctggtgtt cccagaaa 598

<210> 272
<211> 169
<212> PRT
<213> Trifolium repens

<400> 272

Met Ala Ala Ser Ala Ala Ala Thr Phe Thr Ile Gly Thr Ala Gln Thr
1 5 10 15

Gly Arg Pro Leu Pro Gln Ser Asn Pro Phe Gly Leu Lys Val Asn Ser
20 25 30

Gln Val Asn Phe Lys Thr Phe Ser Gly Leu Lys Ala Met Ser Ser Leu
35 40 45

Arg Cys Glu Ser Glu Ser Ser Phe Phe Gly Asn Glu Thr Ser Ala Ala
50 55 60

Leu Arg Ala Thr Phe Ala Pro Lys Ala Gln Lys Glu Asn Gln Asn Ile
65 70 75 80

Asn Arg Asn Leu His Pro Gln Ala Ser Tyr Lys Val Ala Val Leu Gly
85 90 95

Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Leu Leu Ile Lys Met Ser
100 105 110

Pro Leu Val Ser Asp Leu His Leu Tyr Asp Ile Ala Asn Val Lys Gly
115 120 125

Val Ala Ala Asp Ile Ser His Cys Asn Thr Pro Ser Lys Val Leu Asp
130 135 140

Phe Thr Gly Ala Ser Glu Leu Ala Asn Cys Leu Lys Gly Val Asp Val
145 150 155 160

Val Val Ile Pro Ala Gly Val Pro Arg
165

<210> 273
<211> 554
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (44)..(44)
<223> n is a, c, g, or t

<400> 273
gngtaggcgg agatttnaac ccattttcct cttaaatctc tctnaacttc tctttccatt 60

cccattacca ttcattccca gaggtcgaga tggcagcatc agcagcagct acttttacta 120

ttggaactgc ccaaacaggg aggccacttc ctcaatcaaa ccctttttggt ttgaaagtca 180

attcccaggt taattttaag accttctctg gtctcaaggc catgtcatct ctaagatgcg 240

agtctgaatc atctttcttt ggcaacgaaa ctagtgctgc tctgcgtgca acttttgcac 300

ccaaagctca aaaggaaaac caaaacatca accgcaattt gcatcctcag gcatcctaca 360

aagtggcggt tcttggtgct gcaggaggaa ttggtcagcc actggcactt ctcattaaga 420

tgtcgccttt ggtttccgac ctgcatcttt atgatatcgc gaatgttaag ggagttgctg 480

ctgatatcag tcattgcaac actccttcaa aggttttgga tttcacaggt gcttctgagt 540

tggcaaattg tttg 554

<210> 274
<211> 593
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (15)..(16)
<223> n is a, c, g, or t

<400> 274
gttaggcgga gattnnaacc cattttcctc ttaaatctct ctcacttctc tttccattcc 60

cattaccatt cattcccaga ggtcgagatg gcagcatcag cagcagctac ttttactatt 120

ggaactgccc aaacagggag gccacttcct caatcaaacc cttttggttt gaaagtcaat 180
tcccaggtta attttaagac cttctctggt ctcaaggcca tgtcatctct aagatgcgag 240
tctgaatcat ctttctttgg caacgaaact agtgctgctc tgcgtgcaac ttttgcaccc 300
aaagctcaaa aggaaaacca aaacatcaac cgcaatttgc atcctcaggc atcctacaaa 360
gtggcggttc ttggtgctgc aggaggaatt ggtcagccac tggcacttct cattaagatg 420
tcgcctttgg tttccgacct gcatctttat gatatcgcga atgttaaggg agttgctgct 480
gatatcagtc attgcaacac tccttcaaag gttttggatt tcacaggtgc ttctgagttg 540
gcaaattgtt tgaaaggtgt ggatgtagtt gttatacctg ctggtgttcc cag 593

<210> 275
<211> 590
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a, c, g, or t

<400> 275
gggagatttn aacccatttt cctcttaaat ctctcccact tctccttcca ttcccattac 60
cattcattcc cagacgttga gatggcagca tcagcagcag ctacttttac tattggaact 120
gcccaaacag ggaggtcact tcctcaatca aacccttttg gtttgaaagt caattcccag 180
gttaatttta agaccttctc tggtctcaag gccatgtcgt ctctaagatg cgagtctgaa 240
tcatctttct ttggcaacga aacttgtgct gctctgcgtg caacttttgc acccaaagct 300
caaaaggaaa accgaaacat caaccgcaat ttgcagcctc aggcatccta caaagtggcg 360
gttctcggtg ctgcaggagg aattggtcag ccacttgcac ttctcattaa gatgtcgcct 420
ttggtttccg acctgcatct ttatgacatt gcgaatgtta agggagttgc tgctgatatc 480
agccattgca acactccttc aaaggttttg gatttcacag gtgcttctga gctagcaaat 540
tgtttgaaag gtgtggatgt tgttgttata cctgctggtg ttcctagaaa 590

<210> 276
<211> 1230
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(5)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (43)..(43)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (48)..(48)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (834)..(834)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (846)..(846)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (898)..(898)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (900)..(900)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1162)..(1162)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1192)..(1192)
<223> n is a, c, g, or t

<400> 276
ttntntttat tttatgtttt ttncctccta catataactc ttnacttngc atacactgtg 60

tctctcaatt attattagtc cttagaaatg gaagcacatg cagctggagc caatcagagg 120

attgcaagaa tctctgctca tcttcaacct ccaaatttcc aggaaggagg tgatgttgca 180

attagcaaag ctaactgcag agcaaaaggt ggggcgccgg gattcaaagt agcaatcttg 240

ggggctgctg gtggaattgg tcaatccctt tctttgctgt tgaagatcaa tccattggtt 300

tcagttcttc atctttatga tgttgtcaac actcctggtg tcactgctga tgttagtcac 360

attgacaccg gtgctgtggt tcgtggcttt ctagggcagg cacaacttga gaatgcactt 420

acaggcatgg acttggtcgt tatacctgct ggtgtgccga ggaaacctgg aatgacaagg 480

gatgacttat ttaagataaa tgctggaatt gtgaggactc ttagcgaagg aattgccaag 540

agctgtccta atgcaattgt caacttgatt agcaatccag tgaattccac tgtgccaatt 600

gctgctgagg ttttcaagaa agccggtaca tatgatccaa agcgactttt aggggttaca 660

accctcgatg ttgtgagggc aaatacctttt gtggcagaag tacttggtgt tgatccaaga 720

gaggttgatg ttccagtggt aggagggcac gcaggagtca caatattacc tcttttgtca 780
caggttaagc ctcccagtag cttcaccgca gaagaaaccg aatacctgac aaancgcatt 840
caaaanggcg gaacacaagt tgttgaggca aaggctgggg ctggttcggc aacactantn 900
atggcctatg cagctgccaa gtttgctaac gcatgcctcc gtggcttgaa aggagaagcc 960
gggatagtgg agtgtgcttt tgttgattct caggttacgg aacttccttt ctttgcagcc 1020
aaggttcgtc ttggtcgcgg tggagcagaa gagatatatc aacttggtcc ccttaatgag 1080
tatgagagga ttggattaga aaaagcgaag aaagagttag caggaagcat ccagaaggga 1140
gtagaattca tcaaaaaaaa anaaagataa ggaaaaatta gttttgtatt gnctctttct 1200
atatctataa agaacttgtg taataattcc 1230

<210> 277
<211> 359
<212> PRT
<213> Trifolium repens

<220>
<221> misc_feature
<222> (249)..(249)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (253)..(253)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (358)..(358)
<223> Xaa can be any naturally occurring amino acid

<400> 277

Met Glu Ala His Ala Ala Gly Ala Asn Gln Arg Ile Ala Arg Ile Ser
1 5 10 15

Ala His Leu Gln Pro Pro Asn Phe Gln Glu Gly Gly Asp Val Ala Ile
20 25 30

Ser Lys Ala Asn Cys Arg Ala Lys Gly Gly Ala Pro Gly Phe Lys Val
35 40 45

Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Ser Leu Ser Leu Leu
50 55 60

Leu Lys Ile Asn Pro Leu Val Ser Val Leu His Leu Tyr Asp Val Val
65 70 75 80

Asn Thr Pro Gly Val Thr Ala Asp Val Ser His Ile Asp Thr Gly Ala
85 90 95

Val Val Arg Gly Phe Leu Gly Gln Ala Gln Leu Glu Asn Ala Leu Thr

100 105 110

Gly Met Asp Leu Val Val Ile Pro Ala Gly Val Pro Arg Lys Pro Gly
115 120 125

Met Thr Arg Asp Asp Leu Phe Lys Ile Asn Ala Gly Ile Val Arg Thr
130 135 140

Leu Ser Glu Gly Ile Ala Lys Ser Cys Pro Asn Ala Ile Val Asn Leu
145 150 155 160

Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val Phe
165 170 175

Lys Lys Ala Gly Thr Tyr Asp Pro Lys Arg Leu Leu Gly Val Thr Thr
180 185 190

Leu Asp Val Val Arg Ala Asn Thr Phe Val Ala Glu Val Leu Gly Val
195 200 205

Asp Pro Arg Glu Val Asp Val Pro Val Val Gly Gly His Ala Gly Val
210 215 220

Thr Ile Leu Pro Leu Leu Ser Gln Val Lys Pro Pro Ser Ser Phe Thr
225 230 235 240

Ala Glu Glu Thr Glu Tyr Leu Thr Xaa Arg Ile Gln Xaa Gly Gly Thr
245 250 255

Gln Val Val Glu Ala Lys Ala Gly Ala Gly Ser Ala Thr Leu Met Ala
260 265 270

Tyr Ala Ala Ala Lys Phe Ala Asn Ala Cys Leu Arg Gly Leu Lys Gly
275 280 285

Glu Ala Gly Ile Val Glu Cys Ala Phe Val Asp Ser Gln Val Thr Glu
290 295 300

Leu Pro Phe Phe Ala Ala Lys Val Arg Leu Gly Arg Gly Gly Ala Glu
305 310 315 320

Glu Ile Tyr Gln Leu Gly Pro Leu Asn Glu Tyr Glu Arg Ile Gly Leu
325 330 335

Glu Lys Ala Lys Lys Glu Leu Ala Gly Ser Ile Gln Lys Gly Val Glu
340 345 350

Phe Ile Lys Lys Lys Xaa Arg
355

<210> 278

<211> 673
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(5)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (43)..(43)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (48)..(48)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (651)..(651)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (670)..(670)
<223> n is a, c, g, or t

<400> 278
ttntntttat tttatgtttt ttncctccta catataactc ttnacttngc atacactctg 60

tctctaatta ttattagtcc ttcgaaatgg aagcacatgc agctggtacc aatcagagga 120

ttgcaagaat ctctgctcat cttcagcctc caaatttcca ggaaggaggt gatgttgcaa 180

ttagcaaagc taactgcaga gcaaaaggtg gggcgccggg attcaaagta gcaatcttgg 240

gggctgctgg tggaattggt caatcccttt ctttgctgtt gaagatcaat ccattggttt 300

cagttcttca tctttatgat gttgtcaaca ctcctggtgt cactgctgat gttagtcaca 360

ttgacaccgg tgctgtggtt cgtggctttc tagggcaggc acaacttgag aatgcactta 420

caggcatgga cttggtcgtt atacctgctg gtgtgccgag gaaacctgga atgacaaggg 480

atgacttatt taagataaat gctggaattg tgaggactct tagcgaagga attgccaaga 540

gctgtcctaa tgcaattgtc aacttgatta gcaatccagt gaattccact gtgccaattg 600

ctgctgaggt tttcaagaaa gccggtacat atgatccaaa gcgactttta ngggtaacaa 660

ccctcgatgn tgt 673

<210> 279
<211> 574

<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<400> 279
gngtctctca attattatta gtccttagaa atggaagcac atgcagctgg tgccaatcag 60
aggattgcaa gaatctctgc tcatcttcaa cctccaaatt tccaggaagg aggtgatgtt 120
gcaattagca aagctaactg cagagcaaaa ggtggggcgc cgggattcaa agtagcaatc 180
ttgggggctg ctggtggaat tggtcaatcc ctttctttgc tgttgaagat caatccattg 240
gtttcagttc ttcatcttta tgatgttgtc aacactcctg gtgtcactgc tgatgttagt 300
cacattgaca ccggtgctgt ggttcgtggc tttctagggc aggcacaact tgagaatgca 360
cttacaggca tggacttggt cgttatacct gctggtgtgc cgaggaaacc tggaatgaca 420
agggatgact tatttaagat aaatgctgga attgtgagga ctcttagcga aggaattgcc 480
aagagctgtc ctaatgcaat tgtcaacttg attagcaatc cagtgaattc cactgtgcca 540
attgctgctg aggttttcaa gaaagccggt acat 574

<210> 280
<211> 543
<212> DNA
<213> Trifolium repens

<400> 280
gtgtctctca attattatta gtccttagaa atggaagccc atgcagctgg agccaatcag 60
aggattgcaa gaatctctgc tcatcttcaa cctccaaatt tccaggaagg aggtgatgtt 120
gcaattagca aagctaactg cagagcgaaa ggtggggcgc cgggattcaa agtagcaatc 180
ttgggggctg ctggtggaat tggtcaatcc ctttctttgc tgttgaagat caatccattg 240
gtttcagttc ttcatcttta tgatgttgtc aacactcctg gtgtcactgc tgatgttagt 300
cacattgata ccggtgctgt ggttcgtggc tttctagggc aggcacaact tgagaatgca 360
cttacaggca tggacttggt cgttatacct gctggtgtgc cgaggaaacc tggaatgaca 420
agggatgact tatttaagat aaatgctgga attgtgagga ctctttctga aggaattgtc 480
aagagctgtc ctaatgcaat tgtcaacttg attagcaatc cagtgaattc cactgtgcca 540
att 543

<210> 281
<211> 593
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (11)..(11)
<223> n is a, c, g, or t

<400> 281
gnagtcctta naaatggaag cacatgcagc tggagccatc gaggattgca agaatctctg 60

ctcatcttcg cctccaaatt tccaggaagg aagtgatgtc gcaattagca aagctaactg 120

cagagcaaaa ggtggggcgc cgggattcaa agtagcaatc ttgggggctg ctggtggaat 180

tggtcaatcc ctttctttgc tgttgaagat caatccattg gtttcggttc ttcatcttta 240

tgatgttgtc aacactcctg gtgtcactgc tgatgttagt cacattgaca ccggtgctgt 300

ggttcgtggc tttctagggc aggcacaact tgagaatgca cttacaggca tggacttggc 360

cgttatacct gctggtgtgc cgaggaaacc tggaatgaca agggatgact tatttaagat 420

aaatgctgga attgtgagga ctctttctga aggaattgtc aagagctgtc ctaatgcaat 480

tgtcaacttg attagcaatc cagtgaattc cactgtgcca attgctgctg aggtcttcaa 540

gaaagccggt acatatgatc caaaacgact tttaggagtt acaaccctcg atg 593

<210> 282
<211> 693
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (545)..(545)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (562)..(562)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (584)..(584)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (592)..(592)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (615)..(615)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (619)..(619)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (625)..(625)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (631)..(631)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (638)..(638)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (644)..(644)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (647)..(647)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (653)..(653)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (670)..(670)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (674)..(674)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (680)..(680)
<223> n is a, c, g, or t

<400> 282
gagaaatgga agcacatgca gctggagcca atcagaggat tgcaagaatc tctgctcatc 60

ttcaacctcc aaatttccag gaaggaggtg atgttgcaat tagcaaagct aactgcagag 120

caaaaggtgg ggcgccggga ttcaaagtag caatcttggg ggctgctggt ggaattggtc 180

aatccctttc tttgctgttg aagatcaatc cattggtttc ggttcttcat ctttatgatg 240

ttgtcaacac tcctggtgtc actgctgatg ttagtcacat tgacaccggt gctgtggttc 300

gtggctttct agggcaggca caacttgaga atgcacttac aggcatggac ttggtcgtta 360

tacctgctgg tgtgccgagg aaacctggaa tgacaaggga tgacttattt aagataaatg 420

ctggaattgt gaggactctt tctgaaggaa ttgtcaagag ctgtcctaat gcaattgtca 480

acttgattag caatccagtg aattccactg tgccaattgc tggtgaggtc ttcaagaaag 540

ccggnacata tgatccaaaa cnacttttaa gggttacaac cctngatgtt gngagggcaa 600

atacttttgt ggcanaagnc ttggngttga ncccaaanag ggtnatnttc cantggtagg 660

agggcccccn ggantacaan attacccttt ttt 693

<210> 283

<211> 555
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (4)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(19)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (21)..(22)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (50)..(50)
<223> n is a, c, g, or t

<400> 283
ccantgcagc tggtgccant nngaggattg cagaatctct gctcatcttn acctccaatt 60

tccaggaagg aggtgatgtt gcaattagca aagctaactg cagagcaaaa ggtggggcgc 120

cgggattcaa agtagcaatc ttgggggctg ctggtggaat tggtcaatcc ctttctttgc 180

tgttgaagat caatccattg gtttcagttc ttcatcttta tgatgttgtc aacactcctg 240

gtgtcactgc tgatgttagt cacattgaca ccggtgctgt ggttcgtggc tttctagggc 300

aggcacaact tgagaatgca cttacaggca tggacttggt cgttatacct gctggtgtgc 360

cgaggaaacc tggaatgaca agggatgact tatttaagat aaatgctgga attgtgagga 420

ctcttagcga aggaattgcc aagagctgtc ctaatgcaat tgtcaacttg attagcaatc 480

cagtgaattc cactgtgcca attgctgctg aggttttcaa gaaagccggt acatatgatc 540

caaagcgact tttag 555

<210> 284
<211> 473
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (42)..(42)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (339)..(339)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (356)..(356)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (394)..(394)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (401)..(401)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
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<222> (414)..(414)
<223> n is a, c, g, or t

<220>
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<222> (432)..(432)
<223> n is a, c, g, or t

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<222> (434)..(434)
<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<400> 284
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gaggaaacct ggaatgacaa gggatgactt atttaagata aatgctggaa ttgtgaggac 120

tcttagcgaa ggaattgcca agagctgtcc taatgcaatt gtcaacttga ttagcaatcc 180

agtgaattcc actgtgccaa ttgctgctga ggttttcaag aaagccggta catatgattc 240

aaagcgactt ttaggggtaa caaccctcga tgttgtgagg gcaaatacct ttgtggcaga 300

agtacttggt gttgatccaa gagaggttga tgttccagng gtaggatggc acgcangagt 360

acaatattac ctcttttgtc acaggttaag cctnccagta ncttaccgna gaanaaaccg 420

aatacctgac anancgnatt caaaanggcg gaacacaagt cgttgaggca aag 473

<210> 285
<211> 598
<212> DNA
<213> Trifolium repens

<220>
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<223> n is a, c, g, or t

<220>
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<222> (560)..(560)
<223> n is a, c, g, or t

<400> 285
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ggcagaagta cttggtgttg atccaagaga ggttgatgtt ccagtggtag gagggcacgc 120
aggagtcaca atattacctc ttttgtcaca ggttaagcct cccagtagct tcactgcaga 180
agaaaccgaa tacctgacaa atcgcattca aaatggtgga acagaagttg ttgaggcaaa 240
ggctggggct ggttcggcaa cactantaat ggcatatgca gctgccaagt ttgctaacgc 300
atgcctccgt ggcttgaaag gagaagccgg gatagtggag tgtgcttttg ttgattctca 360
ggttacggaa cttcctttct ttgcagccaa ggttcgtctt ggtcgcggtg gagcagaaga 420
gatataccaa cttggtcccc ttaatgagta tgagaggatt gggttggaaa aagcgaagaa 480
tgagttagcg ggaagcatcc agaagggagt agaattcatc agaaaataag tcagataagg 540
aaaaattagt tttgtattgn ctctttctat atctataaag aacttgtgta ataattcc 598

<210> 286
<211> 306
<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

<220>
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<222> (42)..(42)
<223> n is a, c, g, or t

<220>
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<222> (298)..(298)
<223> n is a, c, g, or t

<220>
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<222> (304)..(304)
<223> n is a, c, g, or t

<400> 286
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aagtttgcta acgcatgcct ccgtggcttg aaaggagaag ccgggatagt ggagtgtgct 120
tttgttgatt ctcaggttac ggaacttcct ttctttgcag ccaaggttcg tcttggtcgc 180
ggtggagcag aagagatata tcaacttggt ccccttaatg agtatgagag gattggatta 240
gaaaaagcga agaaagagtt agcaggaagc atccagaagg gagtagaatt catcacanaa 300
aaanaa 306

<210> 287
<211> 299
<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<220>
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<222> (38)..(38)
<223> n is a, c, g, or t

<220>
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<222> (299)..(299)
<223> n is a, c, g, or t

<400> 287
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tgctaacgca tgcctccgtg gcttgaaagg agaagccggg atagtggagt gtgcttttgt 120

tgattctcag gttacggaac ttcctttctt tgcagccaag gttcgtcttg gtcgcggtgg 180

agcagaagag atatatcaac ttggtcccct taatgagtat gagaggattg gattagaaaa 240

agcgaagaaa gagttagcag gaagcatcca gaagggagta gaattcatca aaaaaaaan 299

<210> 288
<211> 866
<212> DNA
<213> Trifolium repens

<220>
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<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
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<222> (14)..(14)
<223> n is a, c, g, or t

<220>
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<222> (38)..(38)
<223> n is a, c, g, or t

<220>
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<222> (280)..(280)
<223> n is a, c, g, or t

<400> 288
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ttatggagcc aaattcagat gcaaatcaac gaatcgcaag aatctccggc cacctaaatc 120

ctcccaattt caagatgaat gaacatggtg attcttcttt gacaagtttc cattgccgtg 180

caaaaggtgg agcacctgga ttcaaagttg caattttagg tgctgctggt ggcataggtc 240

aacctctttc aatgttgatg aagatgaatc ctttggtttn agttcttcat ctttatgatg 300

ttgttaatac tcctggtgtt acttctgata ttagtcatat ggatactgct gctgttgttc 360

gagggttttt ggggcaaaat cagcttgagg atgcacttac aggtatggat ttggtaatca 420

ttcctgccgg tgttccccgt aaacctggaa tgacaagaga tgatctcttc aatataaatg 480

ccgggatcgt taaaacactc tgtgaagcaa ttgcaaagcg atgtcctaag gcgattgtca 540

acgtgattag taatccggtt aactccactg tccccattgc ggctgaagtt ttcaaaagag 600

ccggtactta tgatcccaag agacttttgg gagtgacaat gcttgatgtg gttcgggcca 660

atacgtttgt ggctgaagtt cttggtcttg atccaaggga tgtggatgtc ccagttgtcg 720

gaggacatgc cggaatcacc attttacctc tgctttctca ggttaaacca cattcctctt 780

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ttgaggccaa agctggagct ggctct 866

<210> 289
<211> 268
<212> PRT
<213> Trifolium repens

<220>
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<222> (73)..(73)
<223> Xaa can be any naturally occurring amino acid

<400> 289

Met Glu Pro Asn Ser Asp Ala Asn Gln Arg Ile Ala Arg Ile Ser Gly
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His Leu Asn Pro Pro Asn Phe Lys Met Asn Glu His Gly Asp Ser Ser
20 25 30

Leu Thr Ser Phe His Cys Arg Ala Lys Gly Gly Ala Pro Gly Phe Lys
35 40 45

Val Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ser Met
50 55 60

Leu Met Lys Met Asn Pro Leu Val Xaa Val Leu His Leu Tyr Asp Val

65 70 75 80

Val Asn Thr Pro Gly Val Thr Ser Asp Ile Ser His Met Asp Thr Ala
85 90 95

Ala Val Val Arg Gly Phe Leu Gly Gln Asn Gln Leu Glu Asp Ala Leu
100 105 110

Thr Gly Met Asp Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro
115 120 125

Gly Met Thr Arg Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys
130 135 140

Thr Leu Cys Glu Ala Ile Ala Lys Arg Cys Pro Lys Ala Ile Val Asn
145 150 155 160

Val Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val
165 170 175

Phe Lys Arg Ala Gly Thr Tyr Asp Pro Lys Arg Leu Leu Gly Val Thr
180 185 190

Met Leu Asp Val Val Arg Ala Asn Thr Phe Val Ala Glu Val Leu Gly
195 200 205

Leu Asp Pro Arg Asp Val Asp Val Pro Val Val Gly Gly His Ala Gly
210 215 220

Ile Thr Ile Leu Pro Leu Leu Ser Gln Val Lys Pro His Ser Ser Phe
225 230 235 240

Thr Thr Lys Glu Ile Glu Tyr Leu Thr Asp Arg Ile Gln Asn Gly Gly
245 250 255

Thr Glu Val Val Glu Ala Lys Ala Gly Ala Gly Ser
260 265

<210> 290
<211> 572
<212> DNA
<213> Trifolium repens

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<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (38)..(38)
<223> n is a, c, g, or t

<400> 290
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ttatggagcc aaattcagat gcaaatcaac gaatcgcaag aatctccggc cacctaaatc 120

ctcccaattt caagatgaat gaacatggtg attcttcttt gacaagtttc cattgccgtg 180

caaaaggtgg agcacctgga ttcaaagttg caattttagg tgctgctggt ggcataggtc 240

aacctctttc aatgttgatg aagatgaatc ccttggttta gttcttcatc tttatgatgt 300

tgttaatact cctggtgtta cttctgatat tagtcacatg gatactggtg ctgttgttcg 360

aggatttttg gggcaaaatc agcttgagga tgcacttaca ggtatggatt tggtaatcat 420

tcctgctggt gttccccgta aacctggaat gacaagagat gatctcttca atataaatgc 480

cgggatcgtt aaaacactct gtgaagcaat tgcgaagcga tgtcctaagg cgattgtcaa 540

cgtgattagt aatccggtta actccactgt cc 572

<210> 291
<211> 576
<212> DNA
<213> Trifolium repens

<220>
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<222> (4)..(4)
<223> n is a, c, g, or t

<220>
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<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<400> 291
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ctttatgatg ttgttaatac tcctggtgtt acttctgata ttagtcatat ggatactgct 120

gctgttgttc gagggttttt ggggcaaaat cagcttgagg atgcacttac aggtatggat 180

ttggtaatca ttcctgccgg tgttccccgt aaacctggaa tgacaagaga tgatctcttc 240

aatataaatg ccgggatcgt taaaacactc tgtgaagcaa ttgcaaagcg atgtcctaag 300

gcgattgtca acgtgattag taatccggtt aactccactg tccccattgc ggctgaagtt 360

ttcaaaagag ccggtactta tgatcccaag agacttttgg gagtgacaat gcttgatgtg 420

gttcgggcca atacgtttgt ggctgaagtt cttggtcttg atccaaggga tgtggatgtc 480

ccagttgtcg gaggacatgc cggaatcacc attttacctc tgctttctca ggttaaacca 540

cattcctctt tcacgacaaa ggaaattgag tacttg 576

<210> 292
<211> 592
<212> DNA
<213> Trifolium repens

<220>
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<222> (9)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(19)
<223> n is a, c, g, or t

<400> 292
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gtatatggat actgctgctg ttgttcgagg gtttttgggg caaaatcagc ttgaggatgc 120

acttacaggt atggatttgg taatcattcc tgccggtgtt ccccgtaaac ctggaatgac 180

aagagatgat ctcttcaata taaatgccgg gatcgttaaa acactctgtg aagcaattgc 240

aaagcgatgt cctaaggcgg ttgtcaacgt gattagtaat ccggttaact ccactgtccc 300

cattgcggct gaagttttca aaagagccgg tacttatgat cccaagagac ttttgggagt 360

gacaatgctt gatgtggttc gggccaatac gtttgtggct gaagttcttg gtcttgatcc 420

aagggatgtg gatgtcccag ttgtcggagg acatgccgga atcaccattt tacctctgct 480

ttctcaggtt aaaccacatt cctctttcac gacaaaggaa attgagtact tgacagatcg 540

catacaaaac ggtggaactg aagttgttga ggccaaagct ggagctggct ct 592

<210> 293
<211> 599
<212> DNA
<213> Trifolium repens

<220>
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<222> (199)..(199)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (210)..(210)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (271)..(271)
<223> n is a, c, g, or t

<400> 293
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tacggtcctt aaaaaatctg ttcttgtttt attttgtact tttttgtttt ggaagatcgt     120
tagatacatg tgtggtcttc tcaaagttga taaggaacca gtcactgtat tggtcactgg     180
tgctgcagga caaattggnt atgctcttgn tccaatgatt gcaagaggga tgatgctagg     240
cccaaatcaa cctggaattc ttcatatgct ngatattgaa ccaggattag aggcccttaa     300
aggggtgaag atggaactga ttgatggtgc tttcccactt cttagaggtg ttgttgctac     360
tacggatgtt gttgaagcat gcaaggatgt taacattgct gttatgcttg gtggatcccc     420
aaggaaggaa ggaatggaaa gaaaagatgt aatgtctaag aatgtttcaa tttacaaggc     480
tcaagcttca gctttggagg agcatgctgc tgcagattgt aaagtgctag tggtagccaa     540
tccagcaaac acaaatgctc taatattgaa agaatttgct ccatcaatcc ctgagaaaa      599
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<210>  294
<211>  157
<212>  PRT
<213>  Trifolium repens


<220>
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<222>  (24)..(24)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (28)..(28)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (48)..(48)
<223>  Xaa can be any naturally occurring amino acid

<400>  294

Met Cys Gly Leu Leu Lys Val Asp Lys Glu Pro Val Thr Val Leu Val
1               5                   10                  15


Thr Gly Ala Ala Gly Gln Ile Xaa Tyr Ala Leu Xaa Pro Met Ile Ala
            20                  25                  30


Arg Gly Met Met Leu Gly Pro Asn Gln Pro Gly Ile Leu His Met Xaa
        35                  40                  45


Asp Ile Glu Pro Gly Leu Glu Ala Leu Lys Gly Val Lys Met Glu Leu
    50                  55                  60


Ile Asp Gly Ala Phe Pro Leu Leu Arg Gly Val Val Ala Thr Thr Asp
65                  70                  75                  80


Val Val Glu Ala Cys Lys Asp Val Asn Ile Ala Val Met Leu Gly Gly
                85                  90                  95


Ser Pro Arg Lys Glu Gly Met Glu Arg Lys Asp Val Met Ser Lys Asn
            100                 105                 110
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Val Ser Ile Tyr Lys Ala Gln Ala Ser Ala Leu Glu Glu His Ala Ala
115 120 125

Ala Asp Cys Lys Val Leu Val Val Ala Asn Pro Ala Asn Thr Asn Ala
130 135 140

Leu Ile Leu Lys Glu Phe Ala Pro Ser Ile Pro Glu Lys
145 150 155

<210> 295
<211> 276
<212> DNA
<213> Trifolium repens

<220>
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<222> (197)..(197)
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<220>
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<222> (208)..(208)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
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<222> (237)..(237)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (239)..(239)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

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<222> (271)..(271)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

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cggtccttaa aaaatctgtt cttgttttat tttgtacttt tttgttttgg aagatcgtta 120
gatacatgtg tggtcttctc aaagttgata aggaaccagt cactgtattg gtcactggtg 180
ctgcaggaca aattggntat gctcttgntn caatgattgc nanagggatg atgctangnc 240
caaatcnacc tggnattgtt gatatgctng ntnttg 276

<210> 296
<211> 594
<212> DNA
<213> Trifolium repens

<220>
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<222> (2)..(3)
<223> n is a, c, g, or t

<400> 296
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tccttaaaaa atctgttctt gttttatttt gtactttttt gttttggaag atcgttagat 120
acatgtgtgg tcttctcaaa gttgataagg aaccagtcac tgtattggtc actggtgctg 180
caggacaaat tggttatgct cttgttccaa tgattgcaag agggatgatg ctaggcccaa 240
atcaacctgt aattcttcat atgcttgata ttgaaccagg attagaggcc cttaaagggg 300
tgaagatgga actgattgat ggtgctttcc cacttcttag aggtgttgtt gctactacgg 360
atgttgttga agcatgcaag gatgttaaca ttgctgttat gcttggtgga tccccaagga 420
aggaaggaat ggaaagaaaa gatgtaatgt ctaagaatgt ttcaatttac aaggctcaag 480
cttcagcttt ggaggagcat gctgctgcag attgtaaagt gctagtggta gccaatccag 540
caaacacaaa tgctctaata ttgaaagaat ttgctccatc aatccctgag aaaa 594

<210> 297
<211> 866
<212> DNA
<213> Trifolium repens

<220>
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<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (38)..(38)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (280)..(280)
<223> n is a, c, g, or t

<400> 297
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ttatggagcc aaattcagat gcaaatcaac gaatcgcaag aatctccggc cacctaaatc 120

ctcccaattt caagatgaat gaacatggtg attcttcttt gacaagtttc cattgccgtg 180

caaaaggtgg agcacctgga ttcaaagttg caattttagg tgctgctggt ggcataggtc 240

aacctctttc aatgttgatg aagatgaatc ctttggtttn agttcttcat ctttatgatg 300

ttgttaatac tcctggtgtt acttctgata ttagtcatat ggatactgct gctgttgttc 360

gagggttttt ggggcaaaat cagcttgagg atgcacttac aggtatggat ttggtaatca 420

ttcctgccgg tgttccccgt aaacctggaa tgacaagaga tgatctcttc aatataaatg 480

ccgggatcgt taaaacactc tgtgaagcaa ttgcaaagcg atgtcctaag gcgattgtca 540

acgtgattag taatccggtt aactccactg tccccattgc ggctgaagtt ttcaaaagag 600

ccggtactta tgatcccaag agacttttgg gagtgacaat gcttgatgtg gttcgggcca 660

atacgtttgt ggctgaagtt cttggtcttg atccaaggga tgtggatgtc ccagttgtcg 720

gaggacatgc cggaatcacc attttacctc tgctttctca ggttaaacca cattcctctt 780

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ttgaggccaa agctggagct ggctct 866

<210> 298
<211> 268
<212> PRT
<213> Trifolium repens

<220>
<221> misc_feature
<222> (73)..(73)
<223> Xaa can be any naturally occurring amino acid

<400> 298

Met Glu Pro Asn Ser Asp Ala Asn Gln Arg Ile Ala Arg Ile Ser Gly
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His Leu Asn Pro Pro Asn Phe Lys Met Asn Glu His Gly Asp Ser Ser
20 25 30

Leu Thr Ser Phe His Cys Arg Ala Lys Gly Gly Ala Pro Gly Phe Lys
35 40 45

Val Ala Ile Leu Gly Ala Ala Gly Gly Ile Gly Gln Pro Leu Ser Met
50 55 60

Leu Met Lys Met Asn Pro Leu Val Xaa Val Leu His Leu Tyr Asp Val
65 70 75 80

Val Asn Thr Pro Gly Val Thr Ser Asp Ile Ser His Met Asp Thr Ala
85 90 95

Ala Val Val Arg Gly Phe Leu Gly Gln Asn Gln Leu Glu Asp Ala Leu
100 105 110

Thr Gly Met Asp Leu Val Ile Ile Pro Ala Gly Val Pro Arg Lys Pro
115 120 125

Gly Met Thr Arg Asp Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Lys
130 135 140

Thr Leu Cys Glu Ala Ile Ala Lys Arg Cys Pro Lys Ala Ile Val Asn
145 150 155 160

Val Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile Ala Ala Glu Val
165 170 175

Phe Lys Arg Ala Gly Thr Tyr Asp Pro Lys Arg Leu Leu Gly Val Thr
180 185 190

Met Leu Asp Val Val Arg Ala Asn Thr Phe Val Ala Glu Val Leu Gly
195 200 205

Leu Asp Pro Arg Asp Val Asp Val Pro Val Val Gly Gly His Ala Gly
210 215 220

Ile Thr Ile Leu Pro Leu Leu Ser Gln Val Lys Pro His Ser Ser Phe
225 230 235 240

Thr Thr Lys Glu Ile Glu Tyr Leu Thr Asp Arg Ile Gln Asn Gly Gly
245 250 255

Thr Glu Val Val Glu Ala Lys Ala Gly Ala Gly Ser
260 265

<210> 299
<211> 572
<212> DNA

<213> Trifolium repens

<220>
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<223> n is a, c, g, or t

<220>
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<220>
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<222> (38)..(38)
<223> n is a, c, g, or t

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ttatggagcc aaattcagat gcaaatcaac gaatcgcaag aatctccggc cacctaaatc 120
ctcccaattt caagatgaat gaacatggtg attcttcttt gacaagtttc cattgccgtg 180
caaaaggtgg agcacctgga ttcaaagttg caattttagg tgctgctggt ggcataggtc 240
aacctctttc aatgttgatg aagatgaatc ccttggttta gttcttcatc tttatgatgt 300
tgttaatact cctggtgtta cttctgatat tagtcacatg gatactggtg ctgttgttcg 360
aggatttttg gggcaaaatc agcttgagga tgcacttaca ggtatggatt tggtaatcat 420
tcctgctggt gttccccgta aacctggaat gacaagagat gatctcttca atataaatgc 480
cgggatcgtt aaaacactct gtgaagcaat tgcgaagcga tgtcctaagg cgattgtcaa 540
cgtgattagt aatccggtta actccactgt cc 572

<210> 300
<211> 576
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (4)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (22)..(22)
<223> n is a, c, g, or t

<400> 300
gtgncatagg tnaccctctt tnatgttgat gaagatgaat cctatggttt agttcttcat 60

ctttatgatg ttgttaatac tcctggtgtt acttctgata ttagtcatat ggatactgct 120
gctgttgttc gagggttttt ggggcaaaat cagcttgagg atgcacttac aggtatggat 180
ttggtaatca ttcctgccgg tgttccccgt aaacctggaa tgacaagaga tgatctcttc 240
aatataaatg ccgggatcgt taaaacactc tgtgaagcaa ttgcaaagcg atgtcctaag 300
gcgattgtca acgtgattag taatccggtt aactccactg tccccattgc ggctgaagtt 360
ttcaaaagag ccggtactta tgatcccaag agacttttgg gagtgacaat gcttgatgtg 420
gttcgggcca atacgtttgt ggctgaagtt cttggtcttg atccaaggga tgtggatgtc 480
ccagttgtcg gaggacatgc cggaatcacc attttacctc tgctttctca ggttaaacca 540
cattcctctt tcacgacaaa ggaaattgag tacttg 576

<210> 301
<211> 592
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (9)..(10)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (19)..(19)
<223> n is a, c, g, or t

<400> 301
tttggtttnn gttcttatnc tttatgatgt tgtaatactc ctggtgtact tctgatatta 60
gtatatggat actgctgctg ttgttcgagg gtttttgggg caaaatcagc ttgaggatgc 120
acttacaggt atggatttgg taatcattcc tgccggtgtt ccccgtaaac ctggaatgac 180
aagagatgat ctcttcaata taaatgccgg gatcgttaaa acactctgtg aagcaattgc 240
aaagcgatgt cctaaggcgg ttgtcaacgt gattagtaat ccggttaact ccactgtccc 300
cattgcggct gaagttttca aaagagccgg tacttatgat cccaagagac ttttgggagt 360
gacaatgctt gatgtggttc gggccaatac gtttgtggct gaagttcttg gtcttgatcc 420
aagggatgtg gatgtcccag ttgtcggagg acatgccgga atcaccattt tacctctgct 480
ttctcaggtt aaaccacatt cctctttcac gacaaaggaa attgagtact tgacagatcg 540
catacaaaac ggtggaactg aagttgttga ggccaaagct ggagctggct ct 592

<210> 302
<211> 647
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<400> 302
gnaatcctct ttgnctcccc taccctcctt ttttttcctt ccttcttaca ccttctctta 60
tcaactttcc acctctgaac aaaacttcaa tcttttctca ttttcttata ccctttttaca 120
aacttcttca taaagtgtta ggtttttttt tattactctt ttcaagaacc acaaaaacag 180
tgtttcttga attctttgga attttttttt tcctgcaacc atggccttgg cacacttaaa 240
caaccccact tgctcaaaaa ctcaacttca ctcatcacaa ctctcatttc tctctaggac 300
tctccctagg caatatcact gtacttttgc accacttcac agaactcaac atggcagaat 360
tacttgttct gttgcaccaa atcaagtgca ggctccagct gtacaatcac aggatcccaa 420
gaataagcct gattgctatg gtgtcttctg ccttacctat gatttgaagg ctgaagagga 480
gacaaaatcc tggaagaaat taatcaacat tgcagtctca ggtgctgctg gaatgatttc 540
caatcatcta cttttcaagc ttgcatctgg tgaagttttt ggcccaaatc aacctattgc 600
gctgaaatta ttaggatcag aaaggtcctt ccaagctctt gaaggtg 647

<210> 303
<211> 142
<212> PRT
<213> Trifolium repens

<400> 303

Met Ala Leu Ala His Leu Asn Asn Pro Thr Cys Ser Lys Thr Gln Leu
1   5   10   15

His Ser Ser Gln Leu Ser Phe Leu Ser Arg Thr Leu Pro Arg Gln Tyr
            20   25   30

His Cys Thr Phe Ala Pro Leu His Arg Thr Gln His Gly Arg Ile Thr
        35   40   45

Cys Ser Val Ala Pro Asn Gln Val Gln Ala Pro Ala Val Gln Ser Gln
    50   55   60

Asp Pro Lys Asn Lys Pro Asp Cys Tyr Gly Val Phe Cys Leu Thr Tyr
65   70   75   80

Asp Leu Lys Ala Glu Glu Glu Thr Lys Ser Trp Lys Lys Leu Ile Asn
                85   90   95

Ile Ala Val Ser Gly Ala Ala Gly Met Ile Ser Asn His Leu Leu Phe
            100   105   110

Lys Leu Ala Ser Gly Glu Val Phe Gly Pro Asn Gln Pro Ile Ala Leu
        115   120   125

Lys Leu Leu Gly Ser Glu Arg Ser Phe Gln Ala Leu Glu Gly
130 135 140

<210> 304
<211> 602
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<400> 304
gnaatcctct ttgnctcccc taccctcctt ttttttcctt ccttcttaca cttctcttct 60
caactttcca cctctgaaca aaacttctat cttttctcat tttcttatac ccttttagaa 120
acttcttcat aaagtgttat ttttttttat tactcttttc aagaatcaca aaaacagtgt 180
ttcttgaatt ctttgtaatt ttttttttcc tgcaaccatg gccttggcac agttaaacaa 240
tcccacttgc tcaaaaactc aacttcactc atcacaactc tcatttttgt ctaggactct 300
ccctaggcaa tatcactgta cttttgcacc acttcacaga actcaacatg gcagaattac 360
ttgttctgtt gcaccaaatc aagtgcaggc tccagctgta caatcacagg atcccaagaa 420
taagcctgat tgctatggtg tcttctgcct tacctatgat ttgaaggctg aagaggagac 480
aaaatcctgg aagaaattaa tcaacattgc agtctcaggt gctgctggaa tgatttccaa 540
tcatctactt ttcaagcttg catctggtga agtttttggt ccaaatcaac ctattgcgct 600
ga 602

<210> 305
<211> 599
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (27)..(27)
<223> n is a, c, g, or t

<400> 305
ttcttagacc ttctcttata actttcnacc tctgaaccaa attaatcttt tctattttct 60
tatacccttt tacaaacttc ttcataaagt gttgggtttt tttttattac tcttttcaag 120
aaccacaaaa acagtgtttc ttgaattctt ggaatttttt tttcctgcaa ccatggcttt 180
ggcacactta aacaacccca cttgctcaaa aactcaactt cattcatcac agctctcatt 240
tctctctagg actctcccta ggcaatatca ctgtactttt gcaccacttc acagaactca 300
acatggcaga attacttgtt ctgttgcacc aaatcaagtg caggctccag ctgtacaatc 360

acaggatccc aagaataagc ctgattgcta tggtgtcttc tgccttacct atgatttgaa 420

ggctgaagag gagacaaaat cctggaagaa attaatcaac attgcagtct caggtgctgc 480

tggaatgatt tccaatcatc tacttttcaa gcttgcatct ggtgaagttt ttggcccaaa 540

tcaacctatt gcgctgaaat tattaggatc agaaaggtcc ttccaagctc ttgaaggtg 599

<210> 306
<211> 569
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<400> 306
gcaaagcnct cncngacctg gtgtggagcg agcagctttg ctagacataa atgggcagat 60

ttttgcggag cagggaaaag ctctaaatgc agtcgcatct cgcaatgtca aagttatagt 120

tgtgggaaac ccttgcaata caaatgcatt aatatgcttg aagaatgctc caaatattcc 180

tgcaaaaaat tttcatgctt taacccgttt agatgagaac agagcaaaat gtcagctagc 240

cctcaaggca ggtgtcttct acgataaagt gtcgaatatg acgatatggg gaaaccactc 300

aactactcag gtccccgatt tcttaaatgc cagaatcgat ggtttgcctg tcaaagaagt 360

gattaaggat caaaagtggt tagaggaaga gttcaccgaa aaagttcaaa agagaggtgg 420

cgtgcttatt caaaagtggg gaagatcgtc tgctgcatca acttctgtgt cgatagttga 480

tgccatacga tctttgatca ctcctactcc ggagggtgat tggttttcta ctggtgtgta 540

tacagctgga aatccttatg gaatagctg 569

<210> 307
<211> 189
<212> PRT
<213> Trifolium repens

<220>
<221> misc_feature
<222> (3)..(5)
<223> Xaa can be any naturally occurring amino acid

<400> 307

Gln Ser Xaa Xaa Xaa Pro Gly Val Glu Arg Ala Ala Leu Leu Asp Ile
1   5   10   15

Asn Gly Gln Ile Phe Ala Glu Gln Gly Lys Ala Leu Asn Ala Val Ala
20 25 30

Ser Arg Asn Val Lys Val Ile Val Val Gly Asn Pro Cys Asn Thr Asn
35 40 45

Ala Leu Ile Cys Leu Lys Asn Ala Pro Asn Ile Pro Ala Lys Asn Phe
50 55 60

His Ala Leu Thr Arg Leu Asp Glu Asn Arg Ala Lys Cys Gln Leu Ala
65 70 75 80

Leu Lys Ala Gly Val Phe Tyr Asp Lys Val Ser Asn Met Thr Ile Trp
85 90 95

Gly Asn His Ser Thr Thr Gln Val Pro Asp Phe Leu Asn Ala Arg Ile
100 105 110

Asp Gly Leu Pro Val Lys Glu Val Ile Lys Asp Gln Lys Trp Leu Glu
115 120 125

Glu Glu Phe Thr Glu Lys Val Gln Lys Arg Gly Gly Val Leu Ile Gln
130 135 140

Lys Trp Gly Arg Ser Ser Ala Ala Ser Thr Ser Val Ser Ile Val Asp
145 150 155 160

Ala Ile Arg Ser Leu Ile Thr Pro Thr Pro Glu Gly Asp Trp Phe Ser
165 170 175

Thr Gly Val Tyr Thr Ala Gly Asn Pro Tyr Gly Ile Ala
180 185

<210> 308
<211> 558
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<400> 308
gngtagaacc cgtgaagcct tttccctccg gtctccccgc ttgcgccgtc gccgtcaatt 60

gctgcttgtg tcgtcgcctc cagctcctcc tcctccactg tgccaaccga attacaaacc 120

aaaaaaatgg cgacttgttt gcaaacacaa ctcctccaca caagaccttt tcagtttcgg 180

tcttcctcgt cgacaagacc aacttcccta agatgttccg ccgccacccc atccaccaaa 240

aaatcctaca aaatcactct tcttccgggt gatggcatag gtcctgaagt cgtttccgtc 300

gctaaagacg ttcttctcct cactggatcc atccatggga ttaaacttga gtttcaagag 360
aagcttttgg gtggtgctgc tcttgatgct actggagttc ctttacctga tgatactctt 420
tctgttgcta agcaatctga tgctgttctt cttggtgcta ttggagggta taaatgggat 480
aaaaatgaga aacagctgaa gccagaaact ggattgcttc agctacgaga agggcttcaa 540
gtttttgcta atctcaga 558

<210> 309
<211> 144
<212> PRT
<213> Trifolium repens

<400> 309

Met Ala Thr Cys Leu Gln Thr Gln Leu Leu His Thr Arg Pro Phe Gln
1 5 10 15

Phe Arg Ser Ser Ser Ser Thr Arg Pro Thr Ser Leu Arg Cys Ser Ala
20 25 30

Ala Thr Pro Ser Thr Lys Lys Ser Tyr Lys Ile Thr Leu Leu Pro Gly
35 40 45

Asp Gly Ile Gly Pro Glu Val Val Ser Val Ala Lys Asp Val Leu Leu
50 55 60

Leu Thr Gly Ser Ile His Gly Ile Lys Leu Glu Phe Gln Glu Lys Leu
65 70 75 80

Leu Gly Gly Ala Ala Leu Asp Ala Thr Gly Val Pro Leu Pro Asp Asp
85 90 95

Thr Leu Ser Val Ala Lys Gln Ser Asp Ala Val Leu Leu Gly Ala Ile
100 105 110

Gly Gly Tyr Lys Trp Asp Lys Asn Glu Lys Gln Leu Lys Pro Glu Thr
115 120 125

Gly Leu Leu Gln Leu Arg Glu Gly Leu Gln Val Phe Ala Asn Leu Arg
130 135 140

<210> 310
<211> 713
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (663)..(663)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (713)..(713)
<223> n is a, c, g, or t

<400> 310
gnnacattnc cgaatgctgc tgaactaggg agtgattccc ttggagccta tgtcatctct 60

atggcctcaa gtgcaagcga tgtccttgca gtagagcttt tacagaagga tgcacgtctt 120

acagtttgtg gagaattagg aagagcatgt ccgggtggaa cgcttcgggt ggttcctcta 180

tttgaaactg tgcaagacct gagaggagct ggtgcagtta tcagaaaact tttatcaatc 240

gattggtacc gccaacacat cattaagaac cataacggac accaagaggt tatggtcggt 300

tattctgatt ctggtaaaga tgccgggcgc tttactgctg cttgggaact ttacaaagct 360

caagaggatg tagtggctgc ttgcaataag tacgatacta aggttacttt gttccacggc 420

cgcggaggga gtattggacg tggcggaggc ccaacatatc tggctattca gtcccagcca 480

cctggctctg tgatgggaac ccttcggtca actgagcagg gagagatggt gcaggccgag 540

tttgggttgc cacagacagc agttagacaa cttgaaatat acacaacagc tgtgctactt 600

gctacacgtc gtccaccact cccacctcga gaagaaaaat ggcgtaatct aatggaagac 660

atntcaaaaa tcagttgtca gtcctaccgc agtgtagtct atgaaaatcc agn 713

<210> 311
<211> 237
<212> PRT
<213> Trifolium repens

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (221)..(221)
<223> Xaa can be any naturally occurring amino acid

<400> 311

Xaa Thr Xaa Pro Asn Ala Ala Glu Leu Gly Ser Asp Ser Leu Gly Ala
1 5 10 15

Tyr Val Ile Ser Met Ala Ser Ser Ala Ser Asp Val Leu Ala Val Glu
20 25 30

Leu Leu Gln Lys Asp Ala Arg Leu Thr Val Cys Gly Glu Leu Gly Arg
35 40 45

Ala Cys Pro Gly Gly Thr Leu Arg Val Val Pro Leu Phe Glu Thr Val
50 55 60

Gln Asp Leu Arg Gly Ala Gly Ala Val Ile Arg Lys Leu Leu Ser Ile
65 70 75 80

Asp Trp Tyr Arg Gln His Ile Ile Lys Asn His Asn Gly His Gln Glu
85 90 95

Val Met Val Gly Tyr Ser Asp Ser Gly Lys Asp Ala Gly Arg Phe Thr
100 105 110

Ala Ala Trp Glu Leu Tyr Lys Ala Gln Glu Asp Val Val Ala Ala Cys
115 120 125

Asn Lys Tyr Asp Thr Lys Val Thr Leu Phe His Gly Arg Gly Gly Ser
130 135 140

Ile Gly Arg Gly Gly Gly Pro Thr Tyr Leu Ala Ile Gln Ser Gln Pro
145 150 155 160

Pro Gly Ser Val Met Gly Thr Leu Arg Ser Thr Glu Gln Gly Glu Met
165 170 175

Val Gln Ala Glu Phe Gly Leu Pro Gln Thr Ala Val Arg Gln Leu Glu
180 185 190

Ile Tyr Thr Thr Ala Val Leu Leu Ala Thr Arg Arg Pro Pro Leu Pro
195 200 205

Pro Arg Glu Glu Lys Trp Arg Asn Leu Met Glu Asp Xaa Ser Lys Ile
210 215 220

Ser Cys Gln Ser Tyr Arg Ser Val Val Tyr Glu Asn Pro
225 230 235

<210> 312
<211> 576
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (575)..(576)
<223> n is a, c, g, or t

<400> 312
gnnacattnc cgaatgctgc tgaactaggg agtgattccc ttggagccta tgtcatctct 60

atggcctcaa gtgcaagcga tgtccttgca gtagagcttt tcagaaggat gcacgacttg 120

ctgctattgg agagttcgga agagcatgtc ctggtggaac gttgcgggtt gtccctctat 180

ttgaaactgt gaaggaccta agaggagctg gttcagttat ccggaaactt ttatcgatag 240

actggtaccg tgaacacatc attaagaacc acaatggaca tcaagaggtt atggttggat 300

attctgattc gggtaaagat gctggccgct tcactgctgc ttgggaactt tacaaagctc 360

aggaggatgt tgtagctgct tgcaatgatt atggtattaa agttacactg tttcatggcc 420

gtggaggcag tattggtcga ggtggtggcc ctacatatct ggctattcag tcccaaccac 480

ctgggtctgt gatgggaaca cttcggtcta ctgagcaggg agaaatggta gaggccaagt 540

ttgggttacc acagatagct gttagacaac ttgann 576

<210> 313
<211> 570
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (570)..(570)
<223> n is a, c, g, or t

<400> 313
gnacttttac agaaggatgc acgtcttaca gtttgtggag aattaggaag agcatgtccg 60

ggtggaacgc ttcgggtggt tcctctattt gaaactgtgc aagacctgag aggagctggt 120

gcagttatca gaaaactttt atcaatcgat tggtaccgcc aacacatcat taagaaccat 180

aacggacacc aagaggttat ggtcggttat tctgattctg gtaaagatgc cgggcgcttt 240

actgctgctt gggaacttta caaagctcaa gaggatgtag tggctgcttg caataagtac 300

gatactaagg ttactttgtt ccacggccgc ggagggagta ttggacgtgg cggaggccca 360

acatatctgg ctattcagtc ccagccacct ggctctgtga tgggaaccct tcggtcaact 420

gagcagggag agatggtgca ggccgagttt gggttgccac agacagcagt tagacaactt 480

gaaatataca caacagctgt gctacttgct acacgtcgtc caccactccc acctcgagaa 540

gaaaaatggc gtaatctaat ggaagacatn 570

<210> 314
<211> 619

<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (619)..(619)
<223> n is a, c, g, or t

<400> 314
agcttttaca ganggatgca cgtcttacag tttgtggaga attaggaaga gcatgtccgg 60

gtggaacgct tcgggtggtt cctctatttg aaactgtgca agacctgaga ggagctggtg 120

cagttatcag aaaactttta tcaatcgatt ggtaccgcca acacatcatt aagaaccata 180

acggacacca agaggttatg gtcggttatt ctgattctgg taaagatgcc gggcgcttta 240

ctgctgcttg ggaactttac aaagctcaag aggatgtagt ggctgcttgc aataagtacg 300

atactaaggt tactttgttc cacggccgcg gagggagtat tggacgtggc ggaggcccaa 360

catatctggc tattcagtcc cagccacctg gctctgtgat gggaaccctt cggtcaactg 420

agcagggaga gatggtgcag gccgagtttg ggttgccaca gacagcagtt agacaacttg 480

aaatatacac aacagctgtg ctacttgcta cacgtcgtcc accactccca cctcgagaag 540

aaaaatggcg taatctaatg gaagacattt caaaaatcag ttgtcagtcc taccgcagtg 600

tagtctatga aaatccagn 619

<210> 315
<211> 598
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<400> 315
gnaagggaca agctctatcg tactcgtgag cggtctcgct atctcttagc tcatggctat 60

tctgaaattc ctgaagaagc cacattcacc gatgttgatg agttcttgga acctcttgaa 120

ctatgctaca gatcactctg tgcttgtggt gatcgtgcga ttgccgatgg aagccttctt 180

gatttcttga ggcaagtttc cacttttgga ctgtcactgg taagacttga tataaggcaa 240

gagtcagatc gtcacacgga cgtgatggat gccattacca aacatttgga aattggatcc 300

taccaagact ggtctgaaga aaaaagacag gaatggcttt tgtctgagtt ggttggcaaa 360

aggccgcttt ttggacctga cctacctcaa accgatgaaa ttagagaagt tttagagaca 420

tttcatgtca tagcagaact tccatcagac aactttggag cctatatcat ttcgatggca 480

actgccccgt ctgatgtgct agcggttgaa cttcttcaac gtgaatgcaa aatcaagaat 540

ccgttaagag ttgttccgtt gtttgagaaa cttgctgatc tcgagtctgc tcctgctg 598

<210> 316
<211> 199
<212> PRT
<213> Trifolium repens

<220>
<221> misc_feature
<222> (1)..(1)
<223> Xaa can be any naturally occurring amino acid

<400> 316

Xaa Arg Asp Lys Leu Tyr Arg Thr Arg Glu Arg Ser Arg Tyr Leu Leu
1 5 10 15

Ala His Gly Tyr Ser Glu Ile Pro Glu Glu Ala Thr Phe Thr Asp Val
20 25 30

Asp Glu Phe Leu Glu Pro Leu Glu Leu Cys Tyr Arg Ser Leu Cys Ala
35 40 45

Cys Gly Asp Arg Ala Ile Ala Asp Gly Ser Leu Leu Asp Phe Leu Arg
50 55 60

Gln Val Ser Thr Phe Gly Leu Ser Leu Val Arg Leu Asp Ile Arg Gln
65 70 75 80

Glu Ser Asp Arg His Thr Asp Val Met Asp Ala Ile Thr Lys His Leu
85 90 95

Glu Ile Gly Ser Tyr Gln Asp Trp Ser Glu Glu Lys Arg Gln Glu Trp
100 105 110

Leu Leu Ser Glu Leu Val Gly Lys Arg Pro Leu Phe Gly Pro Asp Leu
115 120 125

Pro Gln Thr Asp Glu Ile Arg Glu Val Leu Glu Thr Phe His Val Ile
130 135 140

Ala Glu Leu Pro Ser Asp Asn Phe Gly Ala Tyr Ile Ile Ser Met Ala
145 150 155 160

Thr Ala Pro Ser Asp Val Leu Ala Val Glu Leu Leu Gln Arg Glu Cys
165 170 175

Lys Ile Lys Asn Pro Leu Arg Val Val Pro Leu Phe Glu Lys Leu Ala
180 185 190

Asp Leu Glu Ser Ala Pro Ala
195

<210> 317
<211> 598
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<400> 317
gnaagggaca agctctatcg tactcgtgag cggtctcgct atctcttagc tcatggctat 60
tctgaaattc ctgaagaagc cacattcacc gatgttgatg agttcttgga acctcttgaa 120
ctatgctaca gatcactctg tgcttgtggt gatcgtgcga ttgccgatgg aagccttctt 180
gatttcttga ggcaagtttc cacttttgga ctgtcactgg taagacttga tataaggcaa 240
gagtcagatc gtcacacgga cgtgatggat gccattacca aacatttgga aattggatcc 300
taccaagact ggtctgaaga aaaaagacag gaatggcttt tgtctgagtt ggttggcaaa 360
aggccgcttt ttggacctga cctacctcaa accgatgaaa ttagagaagt tttagagaca 420
tttcatgtca tagcagaact tccatcagac aactttggag cctatatcat ttcgatggca 480
actgccccgt ctgatgtgct agcggttgaa cttcttcaac gtgaatgcaa aatcaagaat 540
ccgttaagag ttgttccgtt gtttgagaaa cttgctgatc tcgagtctgc tcctgctg 598

<210> 318
<211> 584
<212> DNA
<213> Trifolium repens

<220>
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<222> (584)..(584)
<223> n is a, c, g, or t

<400> 318
gtaagggaca agctctatcg tactcgtgag cggtctcgct atctcttagc tcatggctat 60
tctgaaattc ctgaagaagc cacattcacc gatgttgatg agttcttgga acctcttgaa 120
ctatgctaca gatcactctg tgcttgtggt gatcgtgcga ttgccgatgg aagccttctt 180
gatttcttga ggcaagtttc cacttttgga ctgtcactgg taagacttga tataaggcaa 240
gagtcagatc gtcacacgga cgtgatggat gccattacca aacatttgga aattggatcc 300
taccaagact ggtctgaaga aaaaagacag gaatggcttt tgtctgagtt ggttggcaaa 360
aggccgcttt ttggacctga cctacctcaa accgatgaaa ttagagaagt tttagagaca 420
tttcatgtca tagcagaact tccatcagac aactttggag cctatatcat ttcgatggca 480
actgccccgt ctgatgtgct agcggttgaa cttcttcaac gtgaatgcaa aatcaagaat 540
ccgttaagag ttgttccgtt gtttgagaaa cttgctgatc tcgn 584

<210> 319
<211> 575

<212> DNA
<213> Trifolium repens

<220>
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<222> (15)..(15)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (575)..(575)
<223> n is a, c, g, or t

<400> 319
gtcacatgac aaacnatatc tccctttctc taactccgtg atcaaggcgt tagttagtta 60
cacaaattgc tgttaggttt cgttgtactt tcccgtgcaa tccatagtat cttggaggaa 120
caaactagat tttccaccta ggtcgtcacg agattttcct cttcactatt tttctttttc 180
atataataac tcaacacttt ttctagctac ttactagtac tgtgtaacac aaattttatt 240
cattatggct actcctcgca acattgaaaa aatggcttca attgatgctc aattgagact 300
actagcacca aggaaagttt ctgatgatga taaacttgtc gagtatgatg ctttgttatt 360
ggatcgattc cttgacattc ttcaagattt gcatggagaa gatatcagac aaactgttca 420
agattgttat gagttatcgg cagagtatga aggggagctt aagccggaga aattggagga 480
acttgggaat atgcttactg gtcttgatgc tggagattct attgttatag caaaatcatt 540
ttctcatatg cttaatttgg caaacttggc agagn 575

<210> 320
<211> 110
<212> PRT
<213> Trifolium repens

<400> 320

Met Ala Thr Pro Arg Asn Ile Glu Lys Met Ala Ser Ile Asp Ala Gln
1 5 10 15

Leu Arg Leu Leu Ala Pro Arg Lys Val Ser Asp Asp Asp Lys Leu Val
20 25 30

Glu Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp Ile Leu Gln Asp
35 40 45

Leu His Gly Glu Asp Ile Arg Gln Thr Val Gln Asp Cys Tyr Glu Leu
50 55 60

Ser Ala Glu Tyr Glu Gly Glu Leu Lys Pro Glu Lys Leu Glu Glu Leu
65 70 75 80

Gly Asn Met Leu Thr Gly Leu Asp Ala Gly Asp Ser Ile Val Ile Ala
85 90 95

Lys Ser Phe Ser His Met Leu Asn Leu Ala Asn Leu Ala Glu

100 105 110

<210> 321
<211> 575
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (575)..(575)
<223> n is a, c, g, or t

<400> 321
gtcacatgac tnactatatc tccctttctc taactccgtg atcaaggcgt tagttagtta 60
cacaaattgc tgttaggttt cgttgtactt tcccgtgcaa tccatagtat cttggaggaa 120
caaactagat tttccaccta ggtcgtcacg agattttcct cttcactatt tttctttttc 180
atataataac tcaacacttt ttctagctac ttactagtac tgtgtaacac aaattttatt 240
cattatggct actcctcgca acattgaaaa aatggcttca attgatgctc aattgagact 300
actagcacca aggaaagttt ctgatgatga taaacttgtc gagtatgatg ctttgttatt 360
ggatcgattc cttgacattc ttcaagattt gcatggagaa gatatcagac aaactgttca 420
agattgttat gagttatcgg cagagtatga aggggagctt atgccggaga aattggagga 480
acttgggaat atgcttactg gtcttgatgc tggagattct attgttatag caaaatcatt 540
ttctcatatg cttaatttgg caaacttggc agagn 575

<210> 322
<211> 537
<212> DNA
<213> Trifolium repens

<220>
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<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (537)..(537)
<223> n is a, c, g, or t

<400> 322
tgacaaacna tatctccctt tctctaactc cgtgatcaag gcgttagtta gttacacaaa 60
ttgctgttag gtttcgttgt actttcccgt gcaatccata gtatcttgga ggaacaaact 120
agattttcca cctaggttgt cacgagattt tcctcttcac tatttttctt tttcatataa 180
taattcaaca ctttttctag ctacttacta gtactgtgta acacaaattt tattcattat 240
ggctactcct cgcaacattg aaaaaatggc ttcaattgat gctcaattga gactactagc 300

accaaggaaa gtttctgatg atgataaact tgtcgagtat gatgctttgt tattggatcg 360
attccttgac attcttcaag atttgcatgg agaagatatc agacaaactg ttcaagattg 420
ttatgagtta tcggcagagt atgaagggga gcttaagccg gagaaattgg aggaacttgg 480
gaatatgctt actggtcttg atgctggaga ttctattgtt atagcaaaat cattttn 537

<210> 323
<211> 854
<212> DNA
<213> Trifolium repens

<220>
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<222> (583)..(583)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (589)..(589)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (596)..(596)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (602)..(602)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (608)..(608)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (708)..(708)
<223> n is a, c, g, or t

<220>
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<222> (737)..(737)
<223> n is a, c, g, or t

<220>
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<222> (762)..(762)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (775)..(775)
<223> n is a, c, g, or t

<220>
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<222> (786)..(786)
<223> n is a, c, g, or t

<220>
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<222> (789)..(789)

<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (795)..(797)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (816)..(816)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (830)..(830)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (834)..(834)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (853)..(854)
<223> n is a, c, g, or t

<400> 323
agaagatctc atgtttgagt tgtctatgtg gcgctgcaac gacgagctcc gtgttagagc 60
tgaagagctt catagatcct caaagaaaga tgcaaaacat tatattgagt tttggaaaca 120
gattcctcca aacgagccat atcgtgttat tcttggaggt gtgagggaca aactgtataa 180
tacacgtgaa cgtgctcgac agttattagc aaatggaacc tctgacatcc ttgaagagac 240
aaccttcacg aatgttgagc agtttctgga gcctcttgaa ctgtgttata ggtcactttg 300
tgcatgtggt gaccgatcaa tagcagacgg aagccttctt gatttcttgc gacaagtttc 360
tacatttgga ctttcacttg taagactcga catccgtcaa gagtcagaca ggcacacaga 420
cgttatggat gcaattacaa aacacttgga gattggatct taccgagaat ggtcggaaga 480
acgcaggcag gaatggctct tgtctgagct tagtggaaaa cgccctctct tcggccatga 540
tcttcctaag acagaagaaa ttgccgatgt tttagatacc ttncacgtna tttcanaact 600
tncctcanat agctttggtg cctatatcat ctcaatggca acctccccat ctgatgtgct 660
agctgtcgag cttttacaac gtgaatgtca tgtgaagcag ccgttaanag ttgttccact 720
gtttgaaaag ctcgccngtc ttgagtctgc tcctgctgcg gnagcgcgtt ttttnttaga 780
ttgggncana accgnnntaa tggaaagcag aagttntgat aggtactcan actngggaaa 840
agatgctggc cgnn 854

<210> 324
<211> 284
<212> PRT
<213> Trifolium repens

<220>
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<222> (194)..(194)

<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (196)..(196)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (199)..(199)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (201)..(201)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (203)..(203)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (236)..(236)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (246)..(246)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (254)..(254)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (258)..(258)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (262)..(263)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (265)..(266)
<223> Xaa can be any naturally occurring amino acid

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<223> Xaa can be any naturally occurring amino acid

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<222> (277)..(278)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (284)..(284)
<223> Xaa can be any naturally occurring amino acid

<400> 324

Glu Asp Leu Met Phe Glu Leu Ser Met Trp Arg Cys Asn Asp Glu Leu
1 5 10 15

Arg Val Arg Ala Glu Glu Leu His Arg Ser Ser Lys Lys Asp Ala Lys
20 25 30

His Tyr Ile Glu Phe Trp Lys Gln Ile Pro Pro Asn Glu Pro Tyr Arg
35 40 45

Val Ile Leu Gly Gly Val Arg Asp Lys Leu Tyr Asn Thr Arg Glu Arg
50 55 60

Ala Arg Gln Leu Leu Ala Asn Gly Thr Ser Asp Ile Leu Glu Glu Thr
65 70 75 80

Thr Phe Thr Asn Val Glu Gln Phe Leu Glu Pro Leu Glu Leu Cys Tyr
85 90 95

Arg Ser Leu Cys Ala Cys Gly Asp Arg Ser Ile Ala Asp Gly Ser Leu
100 105 110

Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly Leu Ser Leu Val Arg
115 120 125

Leu Asp Ile Arg Gln Glu Ser Asp Arg His Thr Asp Val Met Asp Ala
130 135 140

Ile Thr Lys His Leu Glu Ile Gly Ser Tyr Arg Glu Trp Ser Glu Glu
145 150 155 160

Arg Arg Gln Glu Trp Leu Leu Ser Glu Leu Ser Gly Lys Arg Pro Leu
165 170 175

Phe Gly His Asp Leu Pro Lys Thr Glu Glu Ile Ala Asp Val Leu Asp
180 185 190

Thr Xaa His Xaa Ile Ser Xaa Leu Xaa Ser Xaa Ser Phe Gly Ala Tyr
195 200 205

Ile Ile Ser Met Ala Thr Ser Pro Ser Asp Val Leu Ala Val Glu Leu
210 215 220

Leu Gln Arg Glu Cys His Val Lys Gln Pro Leu Xaa Val Val Pro Leu
225 230 235 240

Phe Glu Lys Leu Ala Xaa Leu Glu Ser Ala Pro Ala Ala Xaa Ala Arg
245 250 255

Phe Xaa Leu Asp Trp Xaa Xaa Thr Xaa Xaa Met Glu Ser Arg Ser Xaa
260 265 270

Asp Arg Tyr Ser Xaa Xaa Gly Lys Asp Ala Gly Xaa
        275   280

<210> 325
<211> 693
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (573)..(573)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (592)..(593)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (639)..(639)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (641)..(641)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (644)..(644)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (654)..(656)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (663)..(663)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (669)..(669)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (675)..(675)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (679)..(679)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (685)..(686)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (691)..(693)
<223> n is a, c, g, or t

<400> 325
gttcactgtc tctctgncca attttcctcc cttgtcttct ttttcttctt cttcctcgta 60

tcttactgcc tcattacacg ggtgagaagg agtgaattgc tccaatggca acaaacaaaa 120

tggaaaaaat ggcatcaatt gatgcacagc ttagacaatt agtaccagca aaagttagtg 180

aagatgataa acttattgag tatgatgctt tgttgttgga tcggtttctt gatatccttc 240

aggatttaca tggagaggat ctgaaagatt ctgttcaaga agtgtatgaa ctttctgcgg 300

agtatgaaag aaagcatgat cctaagaaac ttgaagagct cggaaatttg ataacaagtt 360

tagatgcagg agattcaatt gttgttgcta agtccttttc gcacatgctt aacttggcca 420

acttagctga agaggttcag attgctcatc gtcgaaggaa caagttgaag aaaggagatt 480

ttagggatga gagcaatgca actaccgaat cagacatcga agaaactctt aagagacttg 540

tgtttaatat gaagaaatct cctcaggaag ttnttgatgc gttgaagaac cnnaccgttg 600

atttggttct tactgctcat cccactcagt ccgttcgang nccnctgctt cccnnngcct 660

ggnacgggna ccgcnctgnc tatcnnactg nnn 693

<210> 326
<211> 196
<212> PRT
<213> Trifolium repens

<220>
<221> misc_feature
<222> (157)..(157)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (163)..(163)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (179)..(180)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (184)..(184)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (187)..(187)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (189)..(189)

<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (191)..(192)
<223> Xaa can be any naturally occurring amino acid

<220>
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<222> (194)..(194)
<223> Xaa can be any naturally occurring amino acid

<220>
<221> misc_feature
<222> (196)..(196)
<223> Xaa can be any naturally occurring amino acid

<400> 326

Met Ala Thr Asn Lys Met Glu Lys Met Ala Ser Ile Asp Ala Gln Leu
1 5 10 15

Arg Gln Leu Val Pro Ala Lys Val Ser Glu Asp Asp Lys Leu Ile Glu
20 25 30

Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp Ile Leu Gln Asp Leu
35 40 45

His Gly Glu Asp Leu Lys Asp Ser Val Gln Glu Val Tyr Glu Leu Ser
50 55 60

Ala Glu Tyr Glu Arg Lys His Asp Pro Lys Lys Leu Glu Glu Leu Gly
65 70 75 80

Asn Leu Ile Thr Ser Leu Asp Ala Gly Asp Ser Ile Val Val Ala Lys
85 90 95

Ser Phe Ser His Met Leu Asn Leu Ala Asn Leu Ala Glu Glu Val Gln
100 105 110

Ile Ala His Arg Arg Arg Asn Lys Leu Lys Lys Gly Asp Phe Arg Asp
115 120 125

Glu Ser Asn Ala Thr Thr Glu Ser Asp Ile Glu Glu Thr Leu Lys Arg
130 135 140

Leu Val Phe Asn Met Lys Lys Ser Pro Gln Glu Val Xaa Asp Ala Leu
145 150 155 160

Lys Asn Xaa Thr Val Asp Leu Val Leu Thr Ala His Pro Thr Gln Ser
165 170 175

Val Arg Xaa Xaa Leu Leu Pro Xaa Ala Trp Xaa Gly Xaa Arg Xaa Xaa
180 185 190

Tyr Xaa Thr Xaa

195

<210> 327
<211> 1307
<212> DNA
<213> Trifolium repens

<220>
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<222> (2)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (8)..(8)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (33)..(33)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (988)..(988)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1307)..(1307)
<223> n is a, c, g, or t

<400> 327
gnnncncnac cattacatta atnacacttt ccnctttcgc cttgttcttt ctcttctcaa 60
tataaagacc aattcaattc ccaattcttt tggatccgaa atcattcatt ctacgcgtct 120
tctctcttct ctgcgtttca aaccctagtt gttttgttga ttgatctaaa tggcgttctt 180
tcgaagcgtt tctgcgcttt caaaactacg atctcgtgtg ggtcaacaac ctagtcttgc 240
taattcagtt agatggctcc aaactccaag ctccagtaac actgatcttt attctgagat 300
gaaggagcta gttccagagt atcaggaacg tgttaagaag ttgaagaaag accatggaag 360
tgttgaattg ggaaaaatca cagctgatat ggtacttggt ggaatgagag gaatgactgc 420
tttagtgtgg ctaggctcag ctgttgaccc agatgaggga attcgcttta ggggcatgac 480
aattcctgac tgccagaaaa cacttccagg tgcttttcct ggtggggagc ctttgcccga 540
ggctatactg tggcttctat tgaccggaaa ggtaccaagt aaagagcaag tagattcatt 600
agctcacgaa ttgcgaagtc gtgcaaaaat cccagagtat gcttacaagg caattgatgc 660
actgcctgtt tctgctcatc caatgacaca atttagtact ggtgtaatgg ccctccaggt 720

ggagagtgag tttacaaagg catacgagag tgggatacat aagtcaaggt attgggagcc 780
aacttatgag gatagcttga atttaattgc tcgtttgcct ggaattgctg cctatattta 840
tcgacggata tacaaggatg gaaaaatcat accattggat gattctttgg attatggtgc 900
aaactatgct cacatgttag gatttgatga tccagaaacg ctggagttta tgaggctgta 960
tatttctatc catagtgatc atgaaggngg caacgttagt tctcacacag ctcacctagt 1020
tgctagttca ctatcagatc cttatcttgc attcgcagct gctctgaatg gtttagctgg 1080
cccactgcat ggtttagcca atcaggaagt tctacgatgg atcagaaaca tagttaagga 1140
gtttggaact ccaaacataa gtacagaaca attgagcgac tacattcata aaacattgaa 1200
cagtggccag gttgtgcctg gatatggaca tggagttttg cgcaatacag acccaagata 1260
cacttgccag agggagtttg cattgaagca tttgcctaat gatccan 1307

<210> 328
<211> 378
<212> PRT
<213> Trifolium repens

<400> 328

Met Ala Phe Phe Arg Ser Val Ser Ala Leu Ser Lys Leu Arg Ser Arg
1 5 10 15

Val Gly Gln Gln Pro Ser Leu Ala Asn Ser Val Arg Trp Leu Gln Thr
20 25 30

Pro Ser Ser Ser Asn Thr Asp Leu Tyr Ser Glu Met Lys Glu Leu Val
35 40 45

Pro Glu Tyr Gln Glu Arg Val Lys Lys Leu Lys Lys Asp His Gly Ser
50 55 60

Val Glu Leu Gly Lys Ile Thr Ala Asp Met Val Leu Gly Gly Met Arg
65 70 75 80

Gly Met Thr Ala Leu Val Trp Leu Gly Ser Ala Val Asp Pro Asp Glu
85 90 95

Gly Ile Arg Phe Arg Gly Met Thr Ile Pro Asp Cys Gln Lys Thr Leu
100 105 110

Pro Gly Ala Phe Pro Gly Gly Glu Pro Leu Pro Glu Ala Ile Leu Trp
115 120 125

Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asp Ser Leu
130 135 140

Ala His Glu Leu Arg Ser Arg Ala Lys Ile Pro Glu Tyr Ala Tyr Lys
145 150 155 160

Ala Ile Asp Ala Leu Pro Val Ser Ala His Pro Met Thr Gln Phe Ser
165 170 175

Thr Gly Val Met Ala Leu Gln Val Glu Ser Glu Phe Thr Lys Ala Tyr
180 185 190

Glu Ser Gly Ile His Lys Ser Arg Tyr Trp Glu Pro Thr Tyr Glu Asp
195 200 205

Ser Leu Asn Leu Ile Ala Arg Leu Pro Gly Ile Ala Ala Tyr Ile Tyr
210 215 220

Arg Arg Ile Tyr Lys Asp Gly Lys Ile Ile Pro Leu Asp Asp Ser Leu
225 230 235 240

Asp Tyr Gly Ala Asn Tyr Ala His Met Leu Gly Phe Asp Asp Pro Glu
245 250 255

Thr Leu Glu Phe Met Arg Leu Tyr Ile Ser Ile His Ser Asp His Glu
260 265 270

Gly Asn Val Ser Ser His Thr Ala His Leu Val Ala Ser Ser Leu Ser
275 280 285

Asp Pro Tyr Leu Ala Phe Ala Ala Ala Leu Asn Gly Leu Ala Gly Pro
290 295 300

Leu His Gly Leu Ala Asn Gln Glu Val Leu Arg Trp Ile Arg Asn Ile
305 310 315 320

Val Lys Glu Phe Gly Thr Pro Asn Ile Ser Thr Glu Gln Leu Ser Asp
325 330 335

Tyr Ile His Lys Thr Leu Asn Ser Gly Gln Val Val Pro Gly Tyr Gly
340 345 350

His Gly Val Leu Arg Asn Thr Asp Pro Arg Tyr Thr Cys Gln Arg Glu
355 360 365

Phe Ala Leu Lys His Leu Pro Asn Asp Pro
370 375

<210> 329
<211> 692
<212> DNA
<213> Trifolium repens

<220>
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<222> (2)..(4)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (6)..(6)
<223> n is a, c, g, or t

<220>
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<223> n is a, c, g, or t

<220>
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<222> (33)..(33)
<223> n is a, c, g, or t

<220>
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<222> (692)..(692)
<223> n is a, c, g, or t

<400> 329
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tataaagacc aattcaattc ccaattcttt tggatccgaa atcattcatt ctacgcttct 120

tctctcttct ctgcgtttca aaccctagtt gttttgttga ttgatcttaa tggcgttctt 180

tcgaagcgtt tctgcgcttt caaaactacg atctcgtgtg ggtcaacaac ctagtcttgc 240

taattcagtt agatggctcc aaactccaag ctccagtaac actgatcttt attctgagat 300

gaaggagcta gttccagagt atcaggaacg tgttaagaag ttgaagaaag accatggaag 360

tgttgaattg ggaaaaatca cagctgatat ggtacttggt ggaatgagag gaatgactgc 420

tttagtgtgg ctaggctcag ctgttgaccc agatgaggga attcgcttta ggggcatgac 480

aattcctgac tgccagaaaa cacttccagg tgcttttcct ggtggggagc ctttgcccga 540

ggctatactg tggcttctat tgaccggaaa ggtaccaagt aaagagcaag tagattcatt 600

agctcacgaa ttgcgaagtc gtgcaaaaat cccagagtat gcttacaagg caattgatgc 660

actgcctgtt tctgctcatc caatgacaca an 692

<210> 330
<211> 588
<212> DNA
<213> Trifolium repens

<220>
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<222> (9)..(9)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (588)..(588)
<223> n is a, c, g, or t

<400> 330

acattcgtna tncttttctc tttcgccttg ttctttctct tctaatataa agaccattca 60
attcccaatt cttttggatc cgaaatcatt cattctacgc ttcttctctc ttctctgcgt 120
ttcaaaccct agttgttttg ttgattgatc ttaatggcgt tctttcgaag cgtttctgcg 180
ctttcaaaac tacgatctcg tgtgggtcaa caacctagtc ttgctaattc agttagatgg 240
ctccaaactc caagctccag taacactgat ctttattctg agatgaagga gctagttcca 300
gagtatcagg aacgtgttaa gaagttgaag aaagaccatg gaagtgttga attgggaaaa 360
atcacagctg atatggtact tggtggaatg agaggaatga ctgctttagt gtggctaggc 420
tcagctgttg acccagatga gggaattcgc tttaggggca tgacaattcc tgactgccag 480
aaaacacttc caggtgcttt tcctggtggg gagcctttgc ccgaggctat actgtggctt 540
ctattgaccg gaaaggtacc aagtaaagag caagtagatt cattagcn 588

<210> 331
<211> 681
<212> DNA
<213> Trifolium repens

<220>
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<222> (6)..(6)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (13)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (26)..(26)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (32)..(32)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (35)..(35)
<223> n is a, c, g, or t

<220>
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<222> (38)..(38)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (45)..(45)
<223> n is a, c, g, or t

<220>

<221> misc_feature
<222> (681)..(681)
<223> n is a, c, g, or t

<400> 331
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aaccctagtt gttttgttga ttgatctaaa tggcgttctt tcgaagcgtt tctgcgcttt 120
caaaactacg atctcgtgtg ggtcaacaac ctagtctcgc taattcagtt agatggctcc 180
aaactccaag ctccagtaac actgatcttt attctgagat gaaggagcta gttccagagt 240
atcaggaacg tgttaagaag ttgaagaaag atcatggaag tgttgaattg ggaaaagtca 300
cagctgatat ggtacttggt ggaatgagag gaatgacagc tttagtgtgg ctaggctcag 360
ctgttgaccc agatgaggga attcgcttta ggggcatgac aattcctgac tgccagaaaa 420
cacttccagg tgcttttcct ggtggggagc ctttgcccga ggctatactg tggctgccat 480
tgaccggaaa ggtaccaagt aaagagcaag tagattcatt agctcacgaa ttgcgaagtc 540
gtgcaaaaat cccagagtat gcttacaagg caattgatgc actgcctgtt tctgctcatc 600
caatgacaca atttagtact ggtgtaatgg ccctccaggt ggagagtgag tttacaaagg 660
catatgagag tgggatacat n 681

<210> 332
<211> 456
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (12)..(13)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (29)..(29)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (42)..(42)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (339)..(339)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (405)..(405)
<223> n is a, c, g, or t

<220>
<221> misc_feature

<222> (417)..(417)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (423)..(423)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (426)..(426)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (441)..(441)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (444)..(444)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (455)..(456)
<223> n is a, c, g, or t

<400> 332
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cgttctttcg aagcgtttct gcgctttcaa aactacgatc tcgtgtgggt caacaaccta 120

gtcttgctaa ttcagttaga tggctccaaa ctccaagctc cagtaacact gatctttatt 180

ctgagatgaa ggagctagtt ccagagtatc aggaacgtgt taagaagttg aagaaagacc 240

atggaagtgt tgaattggga aaaatcacag ctgatatggt acttggtgga atgagaggaa 300

tgactgcttt agtgtggcta ggctcagctg ttgacccana tgagggaatt cgctttaggg 360

gcatgacaat tcctgactgc cacaaaacac ttgcaggtgc ttttnctggc ggggagnctt 420

tgnccnaggc tatactgcgg nttntattga ccggnn 456

<210> 333
<211> 601
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (601)..(601)
<223> n is a, c, g, or t

<400> 333
gnggaaaaat acagctgata tggtacttgg tggaatgaga ggaatgactg ctttagtgtg 60

gctaggctca gctgttgacc cagatgaggg aattcgcttt aggggcatga caattcctga 120

ctgccagaaa acacttccag gtgctcttcc tggtggggag cctttgcccg aggctatact 180

gtggcttcta ttgaccggaa aggtaccaag taaagagcaa gtagattcat tagctcacga 240
attgcgaagt cgtgcaaaaa tcccagagta tgcttacaag gcaattgatg cactgcctgt 300
ttctgctcat ccaatgacac aatttagtac tggtgtaatg gccctccagg tggagagtga 360
gtttacaaag gcatacgaga gtgggataca taagtcaagg tattgggagc caacttatga 420
ggatagcttg aatttaattg ctcgtttgcc tggaattgct gcctatattt atcgacggat 480
atacaaggat ggaaaaatca taccattgga tgattctttg gattatggtg caaactatgc 540
tcacatgtta ggatttgatg atccagaaac gctggagttt atgaggctgt atatttctat 600
n 601

<210> 334
<211> 581
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (33)..(33)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (581)..(581)
<223> n is a, c, g, or t

<400> 334
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tttaggggca tgacaattcc tgactgccag aaacacttcc aggtgctttt cctggtgggg 120
agcctttgcc cgaggctata ctgtggcttc tattgaccgg aaaggtacca agtaaagagc 180
aagtagattc attagctcac gaattgcgaa gtcgtgcaaa aatcccagag tatgcttaca 240
aggcaattga tgcactgcct gtttctgctc atccaatgac acaatttagt actggtgtaa 300
tggccctcca ggtggagagt gagtttacaa aggcatacga gagtgggata cataagtcaa 360
ggtattggga gccaacttat gaggatagct tgaatttaat tgctcgtttg cctggaattg 420
ctgcctatat ttatcgacgg atatacaagg atggaaaaat cataccattg gatgattctt 480
tggattatgg tgcaaactat gctcacatgt taggatttga tgatccagaa acgctggagt 540
ttatgaggct gtatatttct atccatagtg atcatgaagg n 581

<210> 335
<211> 559
<212> DNA
<213> Trifolium repens

<220>

<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (14)..(14)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (559)..(559)
<223> n is a, c, g, or t

<400> 335
cntcagagtg ggancntagt aaggattggg agccacttat gaggatgctt gaatttaatt 60

gctcgtttgc ctggaattgc tgcctatatt tatcgacgga tatacaagga tggaaaaatc 120

ataccattgg atgattcttt ggattatggt gcaaactatg ctcacatgtt aggatttgat 180

gatccagaaa cgctggagtt tatgaggctg tatatttcta tccatagtga tcatgaaggt 240

ggcaacgtta gttctcacac agctcaccta gttgctagtt cactatcaga tccttatctt 300

gcattcgcag ctgctctgaa tggtttagct ggcccactgc atggtttagc caatcaggaa 360

gttctacgat ggatcagaaa catagttaag gagtttggaa ctccaaacat aagtacagaa 420

caattgagcg actacattca taaaacattg aacagtggcc aggttgtgcc tggatatgga 480

catggagttt tgcgcaatac agacccaaga tacacttgcc agagggagtt tgcattgaag 540

catttgccta atgatccan 559

<210> 336
<211> 1244
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (124)..(124)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (1243)..(1244)
<223> n is a, c, g, or t

<400> 336

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attactaatt actagtacta attagtaata ccgatccctt tttctcgaac ccattcattc 120
aagnagaaga aggaaaaaca aaatccacac aaacaaacat cttacaacaa tgtcaacgac 180
aactactaca accgacgaat ccaagctgca cgacgctgca cggaaccgtt tggccaccct 240
ctcagctcac ttgcttcctt cctccacaac ctccgccgcg ctcctccatc ctattcacct 300
ttcttcttcc tccgggatct ccccaccgtc taatgtcaaa ggaacactca ccgttgttga 360
tgaacgtacc gggaagaagt ataccattga ggtctctcct gatggcaccg ttaaagccaa 420
tgatttcaag aagatatcaa ctgggaagaa tgataaggga ctcaaacttt atgatcctgg 480
atatttaaac actgctcctg tgcgatcaac aatttcttat attgatggtg atgagggaat 540
ccttagatat agaggatacc ccattgagga gttggccgag aaaagcacct ttccggaagt 600
ggcatatctc atattgtatg gaaatttgcc ttctgcaaat cagttacaag aatgggaatt 660
tgctatatct cagcattcag ccttacctca aggagttttg gatctcatac aatcaatgcc 720
tcaagatgca catcctatgg gcgtcctagt gaatgcaata agcgctctgt ctgtttttca 780
tcctgacgca aatcctgctc tcagaggtct tgacatctac aactcaaagc aagtgagaga 840
caaacaaata gcacggatta ttggaaagat aacaacaatt gctgctgcaa ttaatcttag 900
aatggcagga aggccacctg tgcttccatc caacaaacta tcttacacag agaacttcct 960
atacatgctt gattctctag gcaatcggtc atataaaccc aaccctcagc taactcgtgc 1020
actagacatc atcttcatcc tgcatgcaga acatgaaatg aattgctcta catctgctgt 1080
acgacacctt gcatcaagcg gcgtcgatgt atacactgct attgctggag gtgttggagc 1140
tctgtatgga cctcttcatg gtggagctaa tgaggcggtc cttaaaatgc tgagtgaaat 1200
tggaagtgtc gataacattc cagagttcat tgaaggtgtt aann 1244

<210> 337
<211> 358
<212> PRT
<213> Trifolium repens

<220>
<221> misc_feature
<222> (358)..(358)
<223> Xaa can be any naturally occurring amino acid

<400> 337

Met Ser Thr Thr Thr Thr Thr Thr Asp Glu Ser Lys Leu His Asp Ala
1 5 10 15

Ala Arg Asn Arg Leu Ala Thr Leu Ser Ala His Leu Leu Pro Ser Ser
20 25 30

Thr Thr Ser Ala Ala Leu Leu His Pro Ile His Leu Ser Ser Ser Ser
35 40 45

Gly Ile Ser Pro Pro Ser Asn Val Lys Gly Thr Leu Thr Val Val Asp
50 55 60

Glu Arg Thr Gly Lys Lys Tyr Thr Ile Glu Val Ser Pro Asp Gly Thr
65 70 75 80

Val Lys Ala Asn Asp Phe Lys Lys Ile Ser Thr Gly Lys Asn Asp Lys
85 90 95

Gly Leu Lys Leu Tyr Asp Pro Gly Tyr Leu Asn Thr Ala Pro Val Arg
100 105 110

Ser Thr Ile Ser Tyr Ile Asp Gly Asp Glu Gly Ile Leu Arg Tyr Arg
115 120 125

Gly Tyr Pro Ile Glu Glu Leu Ala Glu Lys Ser Thr Phe Pro Glu Val
130 135 140

Ala Tyr Leu Ile Leu Tyr Gly Asn Leu Pro Ser Ala Asn Gln Leu Gln
145 150 155 160

Glu Trp Glu Phe Ala Ile Ser Gln His Ser Ala Leu Pro Gln Gly Val
165 170 175

Leu Asp Leu Ile Gln Ser Met Pro Gln Asp Ala His Pro Met Gly Val
180 185 190

Leu Val Asn Ala Ile Ser Ala Leu Ser Val Phe His Pro Asp Ala Asn
195 200 205

Pro Ala Leu Arg Gly Leu Asp Ile Tyr Asn Ser Lys Gln Val Arg Asp
210 215 220

Lys Gln Ile Ala Arg Ile Ile Gly Lys Ile Thr Thr Ile Ala Ala Ala
225 230 235 240

Ile Asn Leu Arg Met Ala Gly Arg Pro Pro Val Leu Pro Ser Asn Lys
245 250 255

Leu Ser Tyr Thr Glu Asn Phe Leu Tyr Met Leu Asp Ser Leu Gly Asn
260 265 270

Arg Ser Tyr Lys Pro Asn Pro Gln Leu Thr Arg Ala Leu Asp Ile Ile
275 280 285

Phe Ile Leu His Ala Glu His Glu Met Asn Cys Ser Thr Ser Ala Val
290 295 300

Arg His Leu Ala Ser Ser Gly Val Asp Val Tyr Thr Ala Ile Ala Gly
305 310 315 320

Gly Val Gly Ala Leu Tyr Gly Pro Leu His Gly Gly Ala Asn Glu Ala
325 330 335

Val Leu Lys Met Leu Ser Glu Ile Gly Ser Val Asp Asn Ile Pro Glu
340 345 350

Phe Ile Glu Gly Val Xaa
355

<210> 338
<211> 609
<212> DNA
<213> Trifolium repens

<220>
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<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (7)..(7)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (609)..(609)
<223> n is a, c, g, or t

<400> 338
cntttcnttt ccacagcatc ctaatcctaa tcctaatcct aatcctatta ctaattacta 60

attactaatt actagtacta attagtaata ccgatccctt tttctcgaac ccattcattc 120

aattcaaaga aggaaaaaca aaatcacaca aacaaacatc ttacaacaat gtcaacgaca 180

actactacaa ccgacgaatc caagctgcac gacgctgcac ggaaccgttt ggctaccctc 240

tcagctcact tgcttccttc ctccacaaac tccgctgcgc ttctccatcc tatccacctt 300

tcttcttcct ctgggatctc cccaccgtct aatgtcaaag gaacactcac cgttgttgat 360

gaacgtaccg ggaagaagta taccattgag gtctctcctg atggcaccgt taaagccaat 420

gatttcaaga agatatcaac tgggaagaat gataaggggc tcaaacttta tgatcctgga 480

tatttaaaca ctgctcctgt gcgatcaaca atttcttata ttgatggtga tgagggaatc 540

cttagatata gaggataccc cattgaagag ttggccgaga aaagcacctt tccggaagtg 600

gcatatctn 609

<210> 339
<211> 589
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(5)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (16)..(16)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (589)..(589)
<223> n is a, c, g, or t

<400> 339
gnagnagaag gaaacncaaa tccacaaaca aaactcttac aacaatgtca accacaacta 60

ctacaaccga cgaatccaag ctgcacgacg ctgcacggaa ccgtttggcc accctctcag 120

ctcacttgct tccttcctcc acaacctccg ccgcgctcct ccatcctatt cacctttccg 180

cttcctccgg gatctcccca ccgtctaatg tcaaaggaac actcaccgtt gttgatgaac 240

gtaccgggaa gaagtataac attgaggtct cacctgatgg caccgttaaa gccaatgatt 300

tcaagaagat atcaactggg aagaatgata agggactcaa actttatgat cctggatatt 360

taaacactgc tcctgtgcga tcaacaattt cttatattga tggtgatgag ggaatcctta 420

gatatagagg ataccccatt gaggagttgg ccgagaaaag caccctttccg gaagtggcat 480

atctcatatt gtatggaaat ttgccttctg caaatcagtt acaagaatgg gaatttgcta 540

tatctcagca ttcagcctta cctcaaggag ttttggatct catacaatn 589

<210> 340
<211> 594
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(3)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (5)..(5)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (23)..(23)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (593)..(594)
<223> n is a, c, g, or t

<400> 340
gnngnagaag gaaacacaaa atncacaaac aaaaacatct tacaacaatg tcaaccacaa 60

ctactacaac cgacgaatcc aagctgcacg acgctgcacg gaaccgtttg gccaccctct 120

cagctcactt gcttccttcc tccacaacct ccgccgcgct cctccatcct attcaccttt 180
ccgcttcctc cgggatctcc ccaccgtcta atgtcaaagg aacactcacc gttgttgatg 240
aacgtaccgg gaagaagtat aacattgagg tctcacctga tggcaccgtt aaagccaatg 300
atttcaagaa gatatcaact gggaagaatg ataagggact caaactttat gatcctggat 360
atttaaacac tgctcctgtg cgatcaacaa tttcttatat tgatggtgat gagggaatcc 420
ttagatatag aggatacccc attgaggagt tggccgagaa aagcaccttt ccggaagtgg 480
catatctcat attgtatgga aatttgcctt ctgcaaatca gttacaagaa tgggaatttg 540
ctatatctca gcattcagcc ttacctcaag gagttttgga tctcatacaa tcnn 594

<210> 341
<211> 570
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (20)..(20)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (570)..(570)
<223> n is a, c, g, or t

<400> 341
gnaaagagga aaaacaaatn cacaaacaac atcttacaca atgtcacgac aactactaca 60
accgacgaat ccaagctgca cgacgctgca cggaaccgtt tagccaccct ctcagctcac 120
ttgcttcctt cctccacaac ctccgccgcg ctcctccatc ctattcacct ttcttcttcc 180
tccgggatct ccccaccgtc taatgtcaaa ggaacactca ccgttgttga tgaacgtacc 240
gggaagaagt ataccattga ggtctctcct gatggcaccg ttaaagccaa tgatttcaag 300
aagatatcga ctgggaagaa tgataaggga ctcaaacttt atgatcctgg atatttaaac 360
actgctcctg tgcgatcaac aatttcttat attgatggtg atgagggaat ccttagatat 420
agaggatacc ccattgagga gttggccgag aaaagcacct ttccggaagt ggcatatctc 480
atattgtatg gaaatttgcc ttctgcaaat cagttacaag aatgggaatt tgctatatct 540
cagcattcag ccttacctca aggagttttn 570

<210> 342
<211> 592
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature

<222> (2)..(2)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (17)..(17)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (591)..(592)
<223> n is a, c, g, or t

<400> 342
gnaaggaaaa acaaatncca aacaactctt acacaatgtc acgacaacta ctacaaccga 60

cgaatccaag ctgcacgacg ctgcacggaa ccgtttggct accctctcag ctcacttgct 120

tccttcctcc acaaactccg ctgcgcttct ccatcctatc cacctttctt cttcctctgg 180

gatctcccca ccgtctaatg tcaaaggaac actcaccgtt gttgatgaac gtaccgggaa 240

gaagtatacc attgaggtct ctcctgatgg caccgttaaa gccaatgatt tcaagaagat 300

atcaactggg aagaatgata aggggctcaa actttatgat cctggatatt taaacactgc 360

tcctgtgcga tcaacaattt cttatattga tggtgatgag ggaatcctta gatatagagg 420

ataccccatt gaagagttgg ccgagaaaag cacctttccg gaagtggcat atctcatatt 480

gtatggaaat ttgccttctg caaatcagtt acaagaatgg gaatttgcta tatctcagca 540

ttcagcctta cctcaaggag ttttggatct catacaatca atgcctcaag nn 592

<210> 343
<211> 579
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (12)..(12)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (579)..(579)
<223> n is a, c, g, or t

<400> 343
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aatgtatgga agtttaccta ctgaaagtaa gttagctgaa tggaatttcg ctatatctca 120

gcattcagct gttccagaag gagttttgga tatcatacaa tcaatgcctc atgatgcaca 180

tcctatgggt gtcctagtga atgcaataag cgctctttct gtttttcatc ctgacgccaa 240

tcctgctctt agaggtcttg atatttacga ctcaaaggaa gtgagagaca aacaaatagc 300

acggattatt ggaaagatta taacaattgc tgctgcagtt tatcttagaa tggcaggaag 360

gccacctgtg cttccatcca accaactatc ttacactgag aacttcctat acatgcttga 420

ttctttaggc aatcggtcat ataaacccaa ccctcagcta actcgtgcac tagacattat 480

cttcatcctg catgcagaac atgaaatgaa ttgctctaca tctgctgtcc gacaccttgc 540

atcaagcggc gttgatgtat atactgctat tgctggggn 579

<210> 344
<211> 594
<212> DNA
<213> Trifolium repens

<220>
<221> misc_feature
<222> (593)..(594)
<223> n is a, c, g, or t

<400> 344
agaatgggaa tttgctatat ctagcattag ccttacctca aggagttttg gatctcatac 60

aatcaatgcc tcaagatgca catcctatgg gcgtgcttgt taatgctcta agtgctttgt 120

ctgtttttca tcctgatgca aatcctgctc tcagaggtct tgacatctac aactcaaagc 180

aagtgagaga caaacaaata gtgcggatta ttggaaagat aacaacaatt gctgctgcga 240

ttaatcttag attgggagga aggccacctg ttcttccatc caacaaactt tcttacacag 300

agaacttcct ttacatgctt gattctcttg gcaatcggtc atataaacct aatcctcgtc 360

taactcgtgc actggacatc atcttcatcc ttcatgcaga acatgaaatg aattgctcta 420

catctgctgt acgccacctt gcatcaagtg gtgtcgatgt atacactgct attgctggag 480

gtgttggagc tctgtatgga cctcttcatg gtggagctaa tgaggcggtc cttaaaatgc 540

tgagtgaaat tggaagtgtc gataacattc cagagttcat tgaaggtgtt aann 594

<210> 345
<211> 1738
<212> DNA
<213> Trifolium repens

<400> 345
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accattcatt cccagaggtc gagatggcag catcagcagc agctactttt actattggaa 180

ctgcccaaac agggaggcca cttcctcaat caaacccttt tggtttgaaa gtcaattccc 240

aggttaattt taagaccttc tctggtctca aggccatgtc atctctaaga tgcgagtctg 300

aatcatcttt ctttggcaac gaaactagtg ctgctctgcg tgcaactttt gcacccaaag 360

ctcaaaagga aaaccaaaac atcaaccgca atttgcatcc tcaggcatcc tacaaagtgg 420

cggttcttgg tgctgcagga ggaattggtc agccactggc acttctcatt aagatgtcgc 480

ctttggtttc cgacctgcat ctttatgata tcgcgaatgt taagggagtt gctgctgata 540

tcagtcattg caacactcct tcaaaggttt tggatttcac aggtgcttct gagttggcaa 600

attgtttgaa aggtgtggat gtagttgtta tacctgctgg tgttcccaga aaacctggca 660

tgactcgtga tgaccttttc aacatcaatg ccggtatagt cagggacttg gtcaccgctg 720

ttgcagataa ttgccctggt gcttttattc atgttatcag taacccggtg aactctacag 780
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gtgttactac acttgatgtt gtgagggcaa acacatttgt tgctcagaaa aagaacctga 900
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tagcatcatt tactgcttcc agaacttatg atttaaattt tccatagtat catttctact 1560
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ttttgatcag aaatctcaat agattgttac tatcatgtac tactagaatt ggaaaaatgt 1680
aaacgttgca ttttgaataa tactgccttt ggactagttt gtgtttcgaa aaaaaaa 1738

<210> 346
<211> 408
<212> PRT
<213> Trifolium repens

<400> 346

Met Ala Ala Ser Ala Ala Ala Thr Phe Thr Ile Gly Thr Ala Gln Thr
1 5 10 15

Gly Arg Pro Leu Pro Gln Ser Asn Pro Phe Gly Leu Lys Val Asn Ser
20 25 30

Gln Val Asn Phe Lys Thr Phe Ser Gly Leu Lys Ala Met Ser Ser Leu
35 40 45

Arg Cys Glu Ser Glu Ser Ser Phe Phe Gly Asn Glu Thr Ser Ala Ala
50 55 60

Leu Arg Ala Thr Phe Ala Pro Lys Ala Gln Lys Glu Asn Gln Asn Ile
65 70 75 80

Asn Arg Asn Leu His Pro Gln Ala Ser Tyr Lys Val Ala Val Leu Gly
85 90 95

Ala Ala Gly Gly Ile Gly Gln Pro Leu Ala Leu Leu Ile Lys Met Ser
100 105 110

Pro Leu Val Ser Asp Leu His Leu Tyr Asp Ile Ala Asn Val Lys Gly
115 120 125

Val Ala Ala Asp Ile Ser His Cys Asn Thr Pro Ser Lys Val Leu Asp
130 135 140

Phe Thr Gly Ala Ser Glu Leu Ala Asn Cys Leu Lys Gly Val Asp Val
145 150 155 160

Val Val Ile Pro Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg Asp
165 170 175

Asp Leu Phe Asn Ile Asn Ala Gly Ile Val Arg Asp Leu Val Thr Ala
180 185 190

Val Ala Asp Asn Cys Pro Gly Ala Phe Ile His Val Ile Ser Asn Pro
195 200 205

Val Asn Ser Thr Val Pro Ile Ala Ala Glu Ile Leu Lys Gln Lys Gly
210 215 220

Val Tyr Asp Pro Lys Lys Leu Phe Gly Val Thr Thr Leu Asp Val Val
225 230 235 240

Arg Ala Asn Thr Phe Val Ala Gln Lys Lys Asn Leu Arg Leu Ile Asp
245 250 255

Val Asp Val Pro Val Val Gly Gly His Ala Gly Ile Thr Ile Leu Pro
260 265 270

Leu Leu Ser Lys Thr Arg Pro Ser Ala Asn Phe Thr Asp Glu Glu Ile
275 280 285

Glu Ala Leu Thr Val Arg Ile Gln Asn Ala Gly Thr Glu Val Val Glu
290 295 300

Ala Lys Ala Gly Ala Gly Ser Ala Thr Leu Ser Met Ala Tyr Ala Ala
305 310 315 320

Ala Arg Phe Val Glu Ser Ser Leu Arg Ala Leu Asp Gly Asp Ala Asp
325 330 335

Val Tyr Glu Cys Ser Phe Val Gln Ser Asp Leu Thr Asp Leu Pro Phe
340 345 350

Phe Ala Ser Arg Val Lys Ile Gly Arg Lys Gly Val Glu Ala Leu Ile
355 360 365

Pro Thr Asp Leu Gln Gly Leu Ser Glu Tyr Glu Gln Lys Ala Leu Glu
370 375 380

Ala Leu Lys Pro Glu Leu Lys Ala Ser Ile Glu Lys Gly Ile Ala Phe
385 390 395 400

Ala Gln Lys Gln Thr Val Ser Ala
405

<210> 347
<211> 3372
<212> DNA
<213> Trifolium repens

<400> 347
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acacgggtga gaaggagtga attgctccaa tggcaacaaa caaaatggaa aaaatggcat 180
caattgatgc acagcttaga caattagtac cagcaaaagt tagtgaagat gataaactta 240
ttgagtatga tgctttgttg ttggatcggt ttcttgatat ccttcaggat ttacatggag 300
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atgatcctaa gaaacttgaa gagctcggaa atttgataac aagtttagat gcaggagatt 420
caattgttgt tgctaagtcc ttttcgcaca tgcttaactt ggccaactta gctgaagagg 480
ttcagattgc tcatcgtcga aggaacaagt tgaagaaagg agattttagg gatgagagca 540
atgcaactac cgaatcagac atcgaagaaa ctcttaagag acttgtgttt aatatgaaga 600
aatctcctca ggaagttttt gatgcgttga agaaccagac cgttgatttg gttcttactg 660
ctcatcctac tcagtcggtt cgtaggtcgt tgcttcaaaa gcatggaagg gtaaggaact 720
gtttatctca attgtatgct aaagacatca ctcctgatga taagcaagag ctcgacgaag 780
ctctccagag ggagattcaa gctgcattcc gtaccgatga aatcaagagg acacctccaa 840
caccacaaga tgagatgaga gcagggatga gttacttcca cgaaacaatt tggaagggtg 900
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<210> 348
<211> 967
<212> PRT
<213> Trifolium repens

<400> 348

Met Ala Thr Asn Lys Met Glu Lys Met Ala Ser Ile Asp Ala Gln Leu
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Arg Gln Leu Val Pro Ala Lys Val Ser Glu Asp Asp Lys Leu Ile Glu
            20   25   30

Tyr Asp Ala Leu Leu Leu Asp Arg Phe Leu Asp Ile Leu Gln Asp Leu
        35   40   45

His Gly Glu Asp Leu Lys Asp Ser Val Gln Glu Val Tyr Glu Leu Ser
    50   55   60

Ala Glu Tyr Glu Arg Lys His Asp Pro Lys Lys Leu Glu Glu Leu Gly
65   70   75   80

Asn Leu Ile Thr Ser Leu Asp Ala Gly Asp Ser Ile Val Val Ala Lys
                85   90   95

Ser Phe Ser His Met Leu Asn Leu Ala Asn Leu Ala Glu Glu Val Gln
            100   105   110

Ile Ala His Arg Arg Arg Asn Lys Leu Lys Lys Gly Asp Phe Arg Asp
        115   120   125

Glu Ser Asn Ala Thr Thr Glu Ser Asp Ile Glu Glu Thr Leu Lys Arg
    130   135   140

Leu Val Phe Asn Met Lys Lys Ser Pro Gln Glu Val Phe Asp Ala Leu
145   150   155   160

Lys Asn Gln Thr Val Asp Leu Val Leu Thr Ala His Pro Thr Gln Ser
                165   170   175

Val Arg Arg Ser Leu Leu Gln Lys His Gly Arg Val Arg Asn Cys Leu
            180   185   190

Ser Gln Leu Tyr Ala Lys Asp Ile Thr Pro Asp Asp Lys Gln Glu Leu
        195   200   205

Asp Glu Ala Leu Gln Arg Glu Ile Gln Ala Ala Phe Arg Thr Asp Glu
    210   215   220

Ile Lys Arg Thr Pro Pro Thr Pro Gln Asp Glu Met Arg Ala Gly Met
225   230   235   240

Ser Tyr Phe His Glu Thr Ile Trp Lys Gly Val Pro Lys Phe Leu Arg
                245   250   255

Arg Val Asp Thr Ala Leu Lys Asn Ile Gly Ile Asn Glu Arg Val Pro
            260   265   270

Tyr Asn Ala Pro Leu Ile Gln Phe Ser Ser Trp Met Gly Gly Asp Arg
275 280 285

Asp Gly Asn Pro Arg Val Thr Pro Glu Val Thr Arg Asp Val Cys Leu
290 295 300

Leu Ala Arg Met Met Ala Ala Asn Leu Tyr Tyr Ser Gln Ile Glu Asp
305 310 315 320

Leu Met Phe Glu Leu Ser Met Trp Arg Cys Asn Asp Glu Leu Arg Asp
325 330 335

Arg Ala Glu Glu Leu His Arg Asn Ser Lys Lys Asp Glu Val Ala Lys
340 345 350

His Tyr Ile Glu Phe Trp Lys Lys Ile Pro Leu Asn Glu Pro Tyr Arg
355 360 365

Val Ile Leu Gly Asp Val Arg Asp Lys Leu Tyr Arg Thr Arg Glu Arg
370 375 380

Ser Arg Tyr Leu Leu Ala His Gly Tyr Ser Glu Ile Pro Glu Glu Ala
385 390 395 400

Thr Phe Thr Asn Val Asp Glu Phe Leu Glu Pro Leu Glu Leu Cys Tyr
405 410 415

Arg Ser Leu Cys Ala Cys Gly Asp Arg Ala Val Ala Asp Gly Ser Leu
420 425 430

Leu Asp Phe Leu Arg Gln Val Ser Thr Phe Gly Leu Ser Leu Val Arg
435 440 445

Leu Asp Ile Arg Gln Glu Ser Asp Arg His Thr Asp Val Met Asp Ala
450 455 460

Ile Thr Lys His Leu Glu Ile Gly Ser Tyr Gln Asp Trp Ser Glu Glu
465 470 475 480

Lys Arg Gln Glu Trp Leu Leu Ser Glu Leu Val Gly Lys Arg Pro Leu
485 490 495

Phe Gly Pro Asp Leu Pro Gln Thr Asp Glu Ile Arg Glu Val Leu Glu
500 505 510

Thr Phe His Val Ile Ala Glu Leu Pro Ser Asp Asn Phe Gly Ala Tyr
515 520 525

Ile Ile Ser Met Ala Thr Ala Pro Ser Asp Val Leu Ala Val Glu Leu
530 535 540

Leu Gln Arg Glu Cys Lys Ile Lys Asn Pro Leu Arg Val Val Pro Leu
545 550 555 560

Phe Glu Lys Leu Ala Asp Leu Glu Ser Ala Pro Ala Ala Leu Ala Arg
565 570 575

Leu Phe Ser Ile Asp Trp Tyr Ile Asn Arg Ile Asp Gly Lys Gln Glu
580 585 590

Val Met Ile Gly Tyr Ser Asp Ser Gly Lys Asp Ala Gly Arg Phe Ser
595 600 605

Ala Ala Trp Gln Leu Tyr Lys Ala Gln Glu Asp Leu Ile Asn Val Ala
610 615 620

Gln Lys Tyr Gly Val Lys Leu Thr Met Phe His Gly Arg Gly Gly Thr
625 630 635 640

Val Gly Arg Gly Gly Gly Pro Thr His Leu Ala Ile Leu Ser Gln Pro
645 650 655

Pro Asp Thr Ile His Gly Ser Leu Arg Val Thr Val Gln Gly Glu Val
660 665 670

Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr Leu Gln
675 680 685

Arg Phe Thr Ala Ala Thr Leu Glu His Gly Met Arg Pro Pro Ser Ser
690 695 700

Pro Lys Pro Glu Trp Arg Glu Leu Met Asp Gln Met Ala Val Ile Ala
705 710 715 720

Thr Glu Glu Tyr Arg Ser Ile Val Phe Lys Glu Pro Arg Phe Val Glu
725 730 735

Tyr Phe Arg Leu Ala Thr Pro Glu Met Glu Tyr Gly Arg Met Asn Ile
740 745 750

Gly Ser Arg Pro Ala Lys Arg Arg Pro Cys Gly Gly Ile Glu Thr Leu
755 760 765

Arg Ala Ile Pro Trp Ile Phe Ala Trp Thr Gln Thr Arg Phe His Leu
770 775 780

Pro Val Trp Leu Gly Phe Gly Ala Ala Phe Lys Gln Val Ile Ala Lys
785 790 795 800

Asp Val Lys Asn Leu His Met Leu Gln Glu Met Tyr Asn Gln Trp Pro
805 810 815

Phe Phe Arg Val Thr Ile Asp Leu Val Glu Met Val Phe Ala Lys Gly
820 825 830

Asp Pro Gly Ile Ala Ala Leu Asn Asp Arg Leu Leu Val Ser Gln Asp
835 840 845

Leu Trp Pro Phe Gly Glu Gln Leu Arg Ser Lys Tyr Glu Glu Thr Lys
850 855 860

Lys Leu Leu Leu Gln Val Ala Thr His Lys Glu Val Leu Glu Gly Asp
865 870 875 880

Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Ser Tyr Ile Thr Thr
885 890 895

Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp Pro Asn
900 905 910

Tyr Lys Val Glu Val Arg Pro Arg Val Ser Lys Glu Ser Ala Glu Thr
915 920 925

Ser Lys Ser Ala Asp Glu Leu Val Thr Leu Asn Pro Thr Ser Glu Tyr
930 935 940

Ala Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala
945 950 955 960

Ala Gly Met Gln Asn Thr Gly
965

<210> 349
<211> 2066
<212> DNA
<213> Trifolium repens

<400> 349
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tacattttct ctttcgccat tgttctttct cttctcaata taaagaccaa ttcaattccc 120

aattcttttg gatccgaaat cattcattct acgcttcttc tctcttctct gcgtttcaaa 180

ccctagttgt tttgttgatt gatcttaatg gcgttctttc gaagcgtttc tgcgctttca 240

aaactacgat ctcgtgtggg tcaacaacct agtcttgcta attcagttag atggctccaa 300

actccaagct ccagtaacac tgatctttat tctgagatga aggagctagt tccagagtat 360

caggaacgtg ttaagaagtt gaagaaagac catggaagtg ttgaattggg aaaaatcaca 420

gctgatatgg tacttggtgg aatgagagga atgactgctt tagtgtggct aggctcagct 480

gttgacccag atgagggaat tcgctttagg ggcatgacaa ttcctgactg ccagaaaaca 540

cttccaggtg cttttcctgg tggggagcct ttgcccgagg ctatactgtg gcttctattg 600

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gcaaaaatcc cagagtatgc ttacaaggca attgatgcac tgcctgtttc tgctcatcca 720
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cttgaagatt cgactaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagtact ctgcgttgtt 2040
accactgctt aatcactagt gaattc 2066

<210> 350
<211> 472
<212> PRT
<213> Trifolium repens

<400> 350

Met Ala Phe Phe Arg Ser Val Ser Ala Leu Ser Lys Leu Arg Ser Arg
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Val Gly Gln Gln Pro Ser Leu Ala Asn Ser Val Arg Trp Leu Gln Thr
20 25 30

Pro Ser Ser Ser Asn Thr Asp Leu Tyr Ser Glu Met Lys Glu Leu Val
35 40 45

Pro Glu Tyr Gln Glu Arg Val Lys Lys Leu Lys Lys Asp His Gly Ser
50 55 60

Val Glu Leu Gly Lys Ile Thr Ala Asp Met Val Leu Gly Gly Met Arg
65 70 75 80

Gly Met Thr Ala Leu Val Trp Leu Gly Ser Ala Val Asp Pro Asp Glu
85 90 95

Gly Ile Arg Phe Arg Gly Met Thr Ile Pro Asp Cys Gln Lys Thr Leu
100 105 110

Pro Gly Ala Phe Pro Gly Gly Glu Pro Leu Pro Glu Ala Ile Leu Trp
115 120 125

Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asp Ser Leu
130 135 140

Ala His Glu Leu Arg Ser Arg Ala Lys Ile Pro Glu Tyr Ala Tyr Lys
145 150 155 160

Ala Ile Asp Ala Leu Pro Val Ser Ala His Pro Met Thr Gln Phe Ser
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Thr Gly Val Met Ala Leu Gln Val Glu Ser Glu Phe Thr Lys Ala Tyr
180 185 190

Glu Gly Gly Ile His Lys Ser Arg Tyr Trp Glu Pro Thr Tyr Glu Asp
195 200 205

Ser Leu Asn Leu Ile Ala Arg Leu Pro Gly Ile Ala Ala Tyr Ile Tyr
210 215 220

Arg Arg Ile Tyr Lys Asp Gly Lys Ile Ile Pro Leu Asp Asp Ser Leu
225 230 235 240

Asp Tyr Gly Ala Asn Tyr Ala His Met Leu Gly Phe Asp Asp Pro Glu
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Thr Leu Glu Phe Met Arg Leu Tyr Ile Ser Ile His Ser Asp His Glu
260 265 270

Gly Gly Asn Val Ser Ser His Thr Ala His Leu Val Ala Ser Ser Leu
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Ser Asp Pro Tyr Leu Ala Phe Ala Ala Ala Leu Asn Gly Leu Ala Gly
290 295 300

Pro Leu His Gly Leu Ala Asn Gln Glu Val Leu Arg Trp Ile Arg Asn
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Ile Val Lys Glu Phe Gly Thr Pro Asn Ile Ser Thr Glu Gln Leu Ser
325 330 335

Asp Tyr Ile His Lys Thr Leu Asn Ser Gly Gln Val Val Pro Gly Tyr
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Gly His Gly Val Leu Arg Asn Thr Asp Pro Arg Tyr Thr Cys Gln Arg
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Glu Phe Ala Leu Lys His Leu Pro Asn Asp Pro Leu Phe Gln Leu Val
370 375 380

Ser Lys Ile Lys Glu Val Val Pro Pro Ile Leu Thr Lys Leu Gly Lys
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Val Lys Asn Pro Trp Pro Asn Val Asp Ala His Ser Gly Val Leu Leu
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Asn Tyr Tyr Gly Leu Thr Glu Glu Asn Tyr Tyr Thr Val Leu Phe Gly
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ccctagttgt tttgttgatt gatcttaatg gcgttctttc gaagcgtttc tgcgctttca 240

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gctgatatgg tacttggtgg aatgagagga atgactgctt tagtgtggct aggctcagct 480

gttgacccag atgagggaat tcgctttagg ggcatgacaa ttcctgactg ccagaaaaca 540

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Arg Arg Ile Tyr Lys Asp Gly Lys Ile Ile Pro Leu Asp Asp Ser Leu
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Asp Tyr Gly Ala Asn Tyr Ala His Met Leu Gly Phe Asp Asp Pro Glu
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Thr Leu Glu Phe Met Arg Leu Tyr Ile Ser Ile His Ser Asp His Glu
260 265 270

Gly Gly Asn Val Ser Ser His Thr Ala His Leu Val Ala Ser Ser Leu
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Ser Asp Pro Tyr Leu Ala Phe Ala Ala Ala Leu Asn Gly Leu Ala Gly
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Asp Tyr Ile His Lys Thr Leu Asn Ser Gly Gln Val Val Pro Gly Tyr
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Ser Lys Ile Lys Glu Val Val Pro Pro Ile Leu Thr Lys Leu Gly Lys
385 390 395 400

Val Lys Asn Pro Trp Pro Asn Val Asp Ala His Ser Gly Val Leu Leu
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Asn Tyr Tyr Gly Leu Thr Glu Glu Asn Tyr Tyr Thr Val Leu Phe Gly
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Pro Glu Tyr Gln Glu Arg Val Lys Lys Leu Lys Lys Asp His Gly Ser
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Val Glu Leu Gly Lys Ile Thr Ala Asp Met Val Leu Gly Gly Met Arg
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Gly Met Thr Ala Leu Val Trp Leu Gly Ser Ala Val Asp Pro Asp Glu
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Gly Ile Arg Phe Arg Gly Met Thr Ile Pro Asp Cys Gln Lys Thr Leu
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Pro Gly Ala Phe Pro Gly Gly Glu Pro Leu Pro Glu Ala Ile Leu Trp
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Leu Leu Leu Thr Gly Lys Val Pro Ser Lys Glu Gln Val Asp Ser Leu
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Ala His Glu Leu Arg Ser Arg Ala Lys Ile Pro Glu Tyr Ala Tyr Lys
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Ala Ile Asp Ala Leu Pro Val Ser Ala His Pro Met Thr Gln Phe Ser
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Thr Gly Val Met Ala Leu Gln Val Glu Ser Glu Phe Thr Lys Ala Tyr
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Glu Ser Gly Ile His Lys Ser Arg Tyr Trp Glu Pro Thr Tyr Glu Asp
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Ser Leu Asn Leu Ile Ala Arg Leu Pro Gly Ile Ala Ala Tyr Ile Tyr
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Arg Arg Ile Tyr Lys Asp Gly Lys Ile Ile Pro Leu Asp Asp Ser Leu
225 230 235 240

Asp Tyr Gly Ala Asn Tyr Ala His Met Leu Gly Phe Asp Asp Pro Glu
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Thr Leu Glu Phe Met Arg Leu Tyr Ile Ser Ile His Ser Asp His Glu
260 265 270

Gly Gly Asn Val Ser Ser His Thr Ala His Leu Val Ala Ser Ser Leu
275 280 285

Ser Asp Pro Tyr Leu Ala Phe Ala Ala Ala Leu Asn Gly Leu Ala Gly
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Pro Leu His Gly Leu Ala Asn Gln Glu Val Leu Arg Trp Ile Arg Asn
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Ile Val Thr Glu Phe Gly Thr Pro Asn Ile Ser Thr Glu Gln Leu Ser
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Asp Tyr Ile His Lys Thr Leu Asn Ser Gly Gln Val Val Pro Gly Tyr
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Gly His Gly Val Leu Arg Asn Thr Asp Pro Arg Tyr Thr Cys Gln Arg
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Glu Phe Ala Leu Lys His Leu Pro Asn Asp Pro Leu Phe Gln Leu Val
370 375 380

Ser Lys Ile Lys Glu Val Val Pro Pro Ile Leu Thr Lys Leu Gly Lys
385 390 395 400

Val Lys Asn Pro Trp Pro Asn Val Asp Ala His Ser Gly Val Leu Leu
405 410 415

Asn Tyr Tyr Gly Leu Thr Glu Glu Asn Tyr Tyr Thr Val Leu Phe Gly
420 425 430

Val Ala Arg Ser Ile Gly Val Gly Pro Gln Leu Ile Trp Asp Arg Ala
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000493

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. [7]: A01H 5/00, C12N 15/29

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
WPIDS, CA, MEDLINE, AGRICOLA: phosphoenolpyruvate carboxylase, PEPC, malate dehydrogenase, MDH, plsmt, grass, rye grass, lolium, fescue, festuca, clover, trifolium, medic, medicago, transgenic, transorm, genetic engineer, genetic modify, krebs, TCA, organic acid, soil

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Beaujean A *et al*, "Integration and expression of Sorghum C4 phosphoenolpyruvate carboxylase and chloroplastic NADP+-malate dehydrogenase separately or together in C3 potato plants", *Plant Science*, 2001, 160:1199-1210 whole of document	9, 18
X	Gallardo F *et al*, "Monocotyledonous C4 NADP+-malate dehydrogenase is efficiently synthesized, targeted to chloroplasts and processed to an active form in transgenic plants of the C3 dicotyledon tobacco", *Planta*, 1995, 197:324-332 see page 331, right column, paragraph beginning line 15	9, 18
X	WO 2000/073475 A1 (Pioneer Hi-Bred International) 7 December 2000 page 4 line 16 to 23	9, 18

[X] Further documents are listed in the continuation of Box C   [X] See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
18 June 2004	24 JUN 2004

Name and mailing address of the ISA/AU	Authorized officer
AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustralia.gov.au Facsimile No. (02) 6285 3929	GARETH COOK Telephone No : (02) 6283 2541

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000493

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P, X	Samac DA *et al*, "Plant improvement for tolerance to aluminum in acid soils - a review", *Plant Cell, Tissue and Organ Culture*, December 2003, 75(3):189-207 see pages 202-203	9, 18
E, X	US 2004/116682 A1 (Cheikh *et al*) 17 June 2004 whole of document	9, 18
A	Häusler RE *et al*, "Single and double overexpression of C4-cycle genes had differential effects on the pattern of endogenous enzymes, attenuation of photorespiration and on contents of UV protectants in transgenic potato and tobacco plants", *Journal of Experimental Botany*, 2001, 52(362):1785-1803 whole of document	
A	Häusler RE *et al*, "Overexpression of C4-cycle enzymes in transgenic C3 plants to improve C3-photosynthesis", *Journal of Experimental Botany*, 2002, 53(369):591-607 whole of document	
A	Tesfaye M *et al*, "Overexpression of Malate Dehydrogenase in Transgenic Alfalfa Enhances Organic Acid Synthesis and Confers Tolerance to Aluminum", *Plant Physiology*, 2001, 127:1836-1844 whole of document	
A	EP 1 122 316 A1 (Centro de Investigacion y Estudios Avanzados del Instituto nacional Irapuato) 8 August 2001 whole of document	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000493

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

See supplemental sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 9, 10, 18, 19 as requested by the Applicant.

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000493

Supplemental Box
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No III: Observations where unity of invention is lacking.

The problem addressed by the current application is the modification of organic acid biosynthesis in plants. The solution is provided through the use of polypeptides involved in the organic acid biosynthesis, and their encoding polynucleotides, from clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue *(Festuca)*, specifically polypeptides and their encoding polynucleotides from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*). These polypeptides have been placed into three broad groupings by the Applicant: malate dehydrogenases (MDH), citrate synthases (CS) and phosphenol pyruvate carboxylases (PEPC).

The general concept underlying the application appears to reside in enzymes involved in organic acid biosynthesis. However the enzymes involved in the organic acid biosynthetic pathway through the tricarboxylic acid cycle (TCA) are known in the prior art, as has been admitted by the Applicant page 2 lines 18 to 22 of the specification. Therefore the involvement of the enzymes in organic acid biosynthesis cannot be considered a special technical feature. The enzymes themselves may be from clover, medic, ryegrass or fescue, with the specifically disclosed sequences being from either from white clover or perennial ryegrass. However the species of origin can only constitute a special technical feature if the species of origin makes a contribution over the prior art. There is nothing in the application to indicate that isolation of peptides from white clover makes an inventive contribution over the prior art, therefore the species of origin cannot be considered a special technical feature.

Since there is no obvious special technical feature, it is appropriate to use the Markush approach to analyse the application for unity of invention.

(A) The common property is the involvement of the enzymes in the organic acid biosynthesis in plants.

(B) (1) There is no common structure that is a significant structural element shared by all the polypeptides. A significant structural element is one that forms the contribution of the polypeptides over the prior art, and is disclosed in the application.

(B) (2) There is no single recognised class of compounds embracing all the polypeptides, as the polypeptides belong to different classes of proteins, ie. MDH, CS and PEPC, each carrying out different biological functions.

Unity of invention is therefore lacking in the application.

The Applicant has placed the enzymes into three groups: MDH, CS and PEPC. Each of these groups needs to be analysed to determine if there is unity within the Applicant's groupings. Taking MDH, this group of enzymes is known in the prior art, as has been admitted by the Applicant at page 2 lines 18 to 22 of the specification. As this is a known grouping, Markush practice again needs to be applied to determine if unity exists.

(A) The common property is the involvement of the MDHs in the reversible conversion of malate to oxaloacetate.

(B) (1) There is no common structure that is a significant structural element shared by all the MDH enzymes that has been disclosed in the specification.

(B) (2) There is no single recognised class embracing all MDHs, the recognised class being one where there is an expectation that all members of the class will behave in the same way in the context of the claimed invention. According to the application in the paragraph bridging pages 2 and 3, MADH is important in several metabolic pathways and plants contain multiple forms that differ in coenzyme specificity and subcellular location. The diversity of function of MDHs is also reflected in that there are multiple enzyme classification (EC) numbers into which the enzymes are placed according to function, the numbers being 1.1.1.37, 1.1.1.38, 1.1.1.39, 1.1.1.40, 1.1.1.82 and 1.1.1.83.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/AU2004/000493

Supplemental Box
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No III: Observations where unity of invention is lacking.

Unity in the Applicant's grouping of MDH enzymes is therefore lacking. Each polypeptide sequence within the Applicant's MDH grouping is considered to be a separate invention. Similarly with PEPC each polypeptide sequence is considered a separate invention as no significant structural element has been identified in the application, and there is no single recognised class embracing all PEPCs - the application states at page 3 lines 4 to 10 that PEPCs are widely distributed through most plant tissues filling various physiological roles, and these enzymes have different EC numbers depending on their coenzymes, the EC numbers being 4.1.1.31, 4.1.1.32, 4.1.1.49. The CS group is considered to be a single group for the purposes of unity, there being only one class embracing all CS enzymes.

The application is therefore considered to be to 37 separate inventions. The 37 separate inventions are:

1. citrate synthases (CS)

2 to 37. each separate polypeptide sequence of the Applicant's groupings MDH and PEPC (ie. each polypeptide of SEQ IDs 22, 31, 35, 37, 39, 41, 45, 47, 112, 114, 116, 184, 186, 188, 190, 198, 200, 202, 204, 206, 219, 253, 272, 277, 289, 294, 297, 303, 307, 309, 311, 316, 320, 324, 326 and 348 is a separate invention).

The Applicant requested the search be limited to claims 9, 10, 18 and 19. Claims 9 and 10 are directed to a construct comprising sequences encoding MDH, PEPC and optionally CS. Claims 18 and 19 are directed to a method of modifying organic acid synthesis by transforming a plant with sequences encoding MDH, PEPC and optionally CS. Both a construct comprising sequences encoding MDH and PEPC and a plant transformed with such a construct are disclosed in:

Beaujean A et al, "Integration and expression of Sorghum C4 phosphoenolpyruvate carboxylase and chloroplastic NADP+-malate dehydrogenase separately or together in C3 potato plants", *Plant Science*, 2001, 160:1199-1210

Hence these claims lack unity, *a posteriori.*

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.
PCT/AU2004/000493

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member					
WO	200/073475	AU	51593/00	CA	2 361 912	US	6 653 535
		BR	0010975	EP	1 181 380	US	2004/078839
EP	1 122 316	AU	45533/98	BR	9815878	WO	1999/063100

Due to data integration issues this family listing may not include 10 digit Australian applications filed since May 2001.

END OF ANNEX